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184189

From: Ibrahim, Medina A.
Sent: Tuesday, April 04, 2006 2:10 PM
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CRFE

Please search the following:

1. SEQ ID NO: 1, 3, 5, or 7.
2. DNA encoding SEQ ID NO: 2, 4, 6, or 8.

Thanks

Medina A. Ibrahim
Patent Examiner, GAU-1638
transgenic plants and plant breeding
Remsen-2B07
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:06:24 ; Search time 5558.17 Seconds
(without alignments)
9664.530 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_srs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6	AX427702 Sequence
2	940.2	99.5	1249	15	PAPAPSRIP
3	786.4	83.2	792	6	AX427704 Sequence
4	766.8	81.1	786	15	AB071855
5	761.4	80.6	1092	6	AX427720 Sequence
6	635.8	67.3	1164	15	AY049785
7	634	67.1	1195	6	A42103
8	634	67.1	1195	6	A42103
9	634	67.1	1195	6	I55866
10	632.4	66.9	1379	6	AR009535
11	632.4	66.9	1379	6	AR136704
12	632.4	66.9	1379	6	AX427731
13	632.2	66.9	942	15	AY572976
14	632.2	66.9	1114	15	AF533515
15	631	66.8	1164	15	PAPAP
16	630.8	66.8	1195	6	A36639
17	630.8	66.8	1379	6	AR141172
18	630.4	66.7	1052	15	AY137202

19	629.2	66.6	1378	6	AX427732	AX427732 Sequence
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22	629	66.6	942	15	AY547315	AY547315 Phytolacc
23	624.2	66.1	2472	6	B05033	B05033 DNA encodin
24	624.2	66.1	2472	15	PTCAPP	D10600 P. american
25	588.6	62.3	882	6	A67183	A67183 Sequence 1
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27	586.4	62.1	2369	15	AR141331	AR141331 Phytolacc
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ALIGNMENTS

RESULT 1	AX427702	945 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427702	Sequence 1 from Patent WO0233107.			
DEFINITION	AX427702				
ACCESSION	AX427702				
VERSION	AX427702.1	GI:21537815			
KEYWORDS					
SOURCE					
ORGANISM					
	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE	1				
AUTHORS	Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 1 25-APR-2002;				
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misc_feature	/note="Binding site for primer PSXDR"				
misc_feature	736..777				
variation	/note="Binding site for primer PSXDP"				
	750..759				
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	complement(922..945)				
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Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	ATGAAGGTGATCTGTAGTGTGTGACGTTAATGCGTGCCTCATTCGACCAACT	60		

QY	61	CAACTTGGCCATTAATAACATGACCTTGAATGCGGAAATGCCACCTTAACAAAT	120
Db	61	TCAACTTGGCCATTAATAACATGACCTTGAATGCGGAAATGCCACCTTAACAAAT	120
QY	121	GCACCTTATGGAATCTCTTGGTATCAAGCGAAAGATCCAAACTAAATGCTATGCG	180
Db	121	GCACCTTATGGAATCTCTTGGTATCAAGCGAAAGATCCAAACTAAATGCTATGCG	180
QY	181	ATACCAATGCTACCGTATCTTAATTCGACCCCTTAAGTCTTATGTTAAAGTCCAGGT	240
Db	181	ATACCAATGCTACCGTATCTTAATTCGACCCCTTAAGTCTTATGTTAAAGTCCAGGT	240
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QY	901	TATATATTAATGTCTAATCTTGTGTATCTATTTGAAGATTTCTAA 945	
Db	901	TATATATTAATGTCTAATCTTGTGTATCTATTTGAAGATTTCTAA 945	

RESULT 2			
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LOCUS	1349 bp	mRNA	linear
DEFINITION	P. americana mRNA for pokeweed antiviral protein.		
ACCESSION	X69078		
VERSION	X69078.1	GI:1707648	
KEYWORDS	Pap-S gene; pokeweed antiviral protein (PAP) ; ribosome-inactivating protein.		
SOURCE	Phytolacca americana (American pokeweed)		
ORGANISM	Phytolacca americana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		

REFERENCE	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons, Caryophyllales, Phytolaccaceae, Phytolacca.
AUTHORS	1 Poyet, J.L. and Hoeveler, A.
TITLE	cDNA cloning and expression of pokeweed antiviral protein from seeds in <i>Escherichia coli</i> and its inhibition of protein synthesis in vitro
JOURNAL	FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED	9109394
REFERENCE	2 (bases 1 to 1249)
AUTHORS	Poyet, J.L.
TITLE	Direct Submisjon
JOURNAL	Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Moléculaire, UPR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK	Revised by author 20-SEP-1996
FEATURES	Location/Qualifiers

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Qy	61	TCAACTGTGCATTAATACGATCACCTTTGATGCTGGAATGCCACCTTAACAATAT	120		
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Qy	181	ATACCAATGCTACCTGACTAATTCGACCCCTAAGTACTTATTTGGTTAAGCTCCAAAGT	240		
Db	286	ATACCAATGCTACCTGACTAATTCGACCCCTAAGTACTTATTTGGTTAAGCTCCAAAGT	345		
Qy	241	GCAAACTTAATAACATTACATTAATGCTGAGACGAATAAATTATACGTGATGGGCTAT	300		

Db 346 GCAAACTTAAACCATTAACAATGCTGAGACGAAATACTTAATACGATGGCTAT 405
Qy 301 TCTGATCCCTCAATGCGAATAGTGTGTACCATATATTAATGATTAACAAGCAC 360
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Qy 361 GAACGCACTGATGAGAAATATCTTGTCTCAAGTTTCTAGTTCGTGTCATGTC 420
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Qy 721 AATCCAAAGATGGGGCTTTTACCCAAACCACTGATGATGATGATGATGATGATGAT 780
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Qy 901 TATAATTAATGCTAATCTGATCTATTTGAAGATTTCTAA 945
Db 1006 TATAATTAATGCTAATCTGATCTATTTGAAGATTTCTGA 1050

RESULT 3
AX427704
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704.1 GI:21537816
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bakery: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Nelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 3 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)
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Beet Local Similarity 99.9%; Pred. No. 2.1e-173;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 133 GAATCTCTGTAAATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTA 192
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Db 784 ACAACTTA 791

RESULT 4
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LOCUS Phytolacca americana paps2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855 GI:19570839
VERSION
KEYWORDS Phytolacca americana (American pokeweed)
SOURCE Phytolacca americana
ORGANISM Bukayocra; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
1
REFERENCE
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 786)
Watanabe, K. and Honjo, E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail: watanake@cc.saga-u.ac.jp, Tel:81-952-28-8774, Fax:81-952-28-8774)
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Db 361 AGCTTATATCCGACCTTGGAAAAGAAAGAAAGTAACTCAAGAAATCAAGTCAAATG 420
Qy 493 GGAATTCAAATATCTGACAGTGCATTTGGAAAATCTCTGAGTTGATTCATTCCTGTGA 552
Db 421 GGAATTCAAATATCTGACAGTGCATTTGGAAAATCTCTGAGTTGATTCATTCCTGTGA 480
Qy 553 AAAATCGAGGCTTTTCTTCTACCTGTAGCCATCCAAATGTTTCAAGAGGAGGCGATTC 612
Db 481 AAAATCGAGGCTTTTCTTCTACCTGTAGCCATCCAAATGTTTCAAGAGGAGGCGATTC 540
Qy 613 AAGTACATAGAGAACCAAGTCAAGCACTAATTTTAAATAGAGCAATTCACCTGATCCAA 672
Db 541 AAGTACATAGAGAACCAAGTCAAGCACTAATTTTAAATAGAGCAATTCACCTGATCCAA 600
Qy 673 GTAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 732
Db 601 GTAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 660
Qy 733 GGGGCTTTTACCCCAACCACTTGAAGTATGATGCCAAAGGTAAGCAAGTGAATGTTCTT 792
Db 661 GGGGCTTTTACCCCAACCTTGAAGTATGATGCCAAAGGTAAGCAAGTGAATGTTCTT 720
Qy 793 AGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852
Db 721 AGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 853 ACAACT 858
Db 781 GCCACT 786

RESULT 5
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Neelam, A.; Atkinson, H.J.; Mcpherson, M.J. and Thomas, C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source
1..1092
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"
1..29
misc_feature
/note="Binding site for primer PS1BP"
variation
681..686
/note="Modified XbaI site"
misc_feature
complement(742..786)
/note="Binding site for primer PCS-PAPER"
misc_feature
766..806
/note="Binding site for primer PCS-Delta86F"
misc_feature
766..786
/note="TEV N1A protease cleavage site"
misc_feature
complement(1066..1092)
/note="Binding site for primer SYNPOTDelta86SR"
ORIGIN
Query Match 80.6%; Score 761.4; DB 6; Length 1092;
Best Local Similarity 99.9%; Pred. No. 1.4e-167;

QY 726 CAAAGATGGGGCTTTACCCAAACCACTTGAAGTGGATGCCAAGATCAAGAGTGGAT 785
DB 721 CAAAGATGGAGTTTACCCAAACCTTCGAGTAGTGGATGCCAGTGGTCCAAAGTGGAT 780
QY 786 AGTTCTTAAGTGGAGTAATCAATGCTGATGGGCACTCCTTAAGTACCTTAATGGAAC 845
DB 781 AGTTTGAAGTGGAGTAATCAAGCTGATGGAGCACTCTTAACACCTGAGTGGAG 840
QY 846 CTGTCCAGACAATT---ACCAAAATGCCATGTTCTCTCAAGTATAATTTCTACTATTA 902
DB 841 CTGCCAAACAACTTAATCAACAAATGCCATGTTCTCTCAACTTAATGCTACTATTA 900
QY 903 TAATTATATGCTTAATCTTGTGATCTTAATTTGAAGATCTTA 945
DB 901 TAATTATATGCTTAATCTTGTGATCTTAATTTGAAGATCTTGA 943

RESULT 7
A42103 1195 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 1 from Patent EP0637591.
DEFINITION A42103
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS

SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana

REFERENCE Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 1195)
Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.

A novel expression vector for phytolacca antiviral protein
JINRO LIMITED (KR)
Patent: EP 0637591-A 1 08-FEB-1995;

COMMENT Other publication JP 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
Location/Qualifiers

FEATURES
1. 1195
source
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

ORIGIN

Query Match 67.1%; Score 634; DB 6; Length 1195;

Best Local Similarity 80.1%; Pred. No. 8.9e-138; Indels 3; Gaps 1;

Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 3 GAAGGTGATGCTTGTAGTGTGATGAGCTTAATAGCGTGGCTCATTTGCTGCACCACTTC 62
DB 29 GAAGATGAGTGCATCTGTGTGATCAATATATGATGCTCATTTGCTGCACCACTTC 88
QY 63 AACTGTGTCATTAATACATCATCTTTGATGTGGAAATGCCACATTAACCAATATGC 122
DB 89 AACTGGGTGTGAATAACATCATCTTAATGTGGAAATGCCACATTAACCAATATGC 148
QY 123 CACTTTATGATCTCTTGTATCAAGGAAATGCCAAATTAATTAATGCTATGCAT 182
DB 149 CACTTTTGTGATGATCTTGTATCAAGGAAATGCCAAATTAATTAATGCTATGCAT 208
QY 183 ACCAATGCTACCTGATCTTAATTTGACCCCTTAATGCTTAATTTGATTTAGCTCCAGGTGC 242
DB 209 ACCAATGCTGCCAATACCAATTAATCAATCAAGTACGTTGTGAGCTCCAGGTGC 268
QY 243 AAACCTAAACCAATACATTAATGCTGAGCAAAATTAATTAATGCTGAGGTATTC 302
DB 269 AAATATAAAACCAATACATTAATGCTGAGCAAAATTAATTAATGCTGAGGTATTC 328
QY 303 TGAATCCCTTCAATGCAATAGTGTGATTAATATTAATTAATTAATTAATTAATTAAT 362
DB 329 TGAATCCCTTGAACCAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAAT 388

QY 363 ACCGATGATGAGAAATATCTTTGTCTCAAGTCTAGTCTGTGTTGCAATGTCAT 422
DB 389 AGCCCAAGATGTAGAGTACTCTTTGCCAAATGCAATTTCTGTTAGTAAATCAAT 448
QY 423 TAATCAATAGCTTTATTCACCATGAGAAAGAAAGCAAGATTAATCAAGAAATCA 482
DB 449 AAATCTTGTATGCGATATCCCAATGGAATCAAAAGGGGAGTAAATCAAGAAATCA 508
QY 483 AGTCAATGGGAATCAATATCTGAGAGTGCATTGGAAAAATCTCGAGTGTATTC 542
DB 509 AGTCCAACTGGGAATCAATATCTGAGAGTGCATTGGAAAAATCTCGAGTGTATTC 568
QY 543 ATTCCTGTAAAACTGAGGCTTTTCTACTGATGAGCAATCCAAATGTTTCAAGAGC 602
DB 569 ATTCATGAGAAAAAGGAGGAGGAGTTCCTTAATGAGCAATCAATGATGATCAAGGC 628
QY 603 AGCGCATTCAGTATCATGAGAACCAAGTCAAGATTAATTTAATAGCATTTCAACC 662
DB 629 AGCAAGATTCAGTATCATGAGAACCAAGTCAAGATTAATTTAATAGCATTTCAACC 688
QY 663 TGAATCCCAAGTATTAATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722
DB 689 TAATCCCAAGTATTAATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 748
QY 723 TGCAGAAATGGGCTTTACCCAAACCACTTGAAGTGGATGCCAAGATCAAGT 782
DB 749 TGCAGAAATGGGCTTTACCCAAACCTTGAAGTGGATGCCAAGATCAAGT 808
QY 783 GATGTTCTTAAGTGGAGTAATCAATGCTGATGGGCACTCTTAAGTCTTAATG 842
DB 809 GATGTTCTTAAGTGGAGTAATCAATGCTGATGGGCACTCTTAAGTCTTAATG 868
QY 843 AACCTGTCCAGACAATT---ACCAAAATGCCATGTTCTCTCAAGTATAATTTCTACTTA 899
DB 869 GAGCTGTCCAGACAATT---ACCAAAATGCCATGTTCTCTCAAGTATAATTTCTACTTA 928
QY 900 TTAATTAATATGCTTAATCTTGTGATCTTAATTTGAAGATCTTA 945
DB 929 TTAATTAATATGCTTAATCTTGTGATCTTAATTTGAAGATCTTA 974

RESULT 8

I43835 1195 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1 from patent US 5633155.
DEFINITION I43835
ACCESSION I43835
VERSION I43835.1 GI:2468933
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unknown.
1 (bases 1 to 1195)
Klim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.

Expression vector for phytolacca antiviral protein and process for
preparing transgenic plant transformed therewith
Patent: US 5633155-A 1 27-MAY-1997;
Location/Qualifiers

FEATURES
1. 1195
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 67.1%; Score 634; DB 6; Length 1195;

Best Local Similarity 80.1%; Pred. No. 8.9e-138; Indels 3; Gaps 1;

Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 3 GAAGGTGATGCTTGTAGTGTGATGAGCTTAATAGCGTGGCTCATTTGCTGCACCACTTC 62
DB 29 GAAGATGAGTGCATCTGTGTGATCAATATATGATGCTCATTTGCTGCACCACTTC 88
QY 63 AACTGTGTCATTAATACATCATCTTTGATGTGGAAATGCCACATTAACCAATATGC 122


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RESULT 10
AR009535      1379 bp   DNA      linear   PAT 04-DEC-1998
LOCUS         AR009535
DEFINITION    Sequence 1 from patent US 5756322.
ACCESSION     AR009535
VERSION       AR009535.1   GI:3968340
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 1379)
AUTHORS       Tumer,N.E.
TITLE         Pkeweed antiviral protein mutants
JOURNAL       Patent: US 5756322-A 1 26-MAY-1998;
FEATURES
source        1..1379
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY      3 GAAGTGATGCTTGATGTTGGTGACGTTAATAGCGTGGCTGATTGCTGCACCACTTC 62
DB      221 GAAAGATGAAGTGCATGCTTGTTGGTGCACATATCAATATGCTGATCTTGACCACTTC 280
QY      63 AACTGTGCCATTAATACGATCACCTTGTGATGCTGAAATGCAACCATTAACAATATGC 122
DB      281 AACTGGGCTGTGAATACATCATCTACATATGTTGGAAGTACACCATTTGCAATATGCG 340
QY      123 CACCTTTATGGAATCTCTTCTGATATCAAGGGAAGATCCAAACTAAATGCTATGCGAT 182
DB      341 CACTTTTCGAATGATCTTGTATATGAAGCAAGATCCAAAGTTTAAATGCTATGGAAT 400
QY      183 ACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATTTGTTAAGCTCCAGAGTGC 242
DB      401 ACCAATGCTGCCAATACAAATACAAATCCAAAGTACGTGTTGGAGTCCAGGTTTC 460
QY      243 AAACCTAAAAACCATTAACATAATGCTGAGACGAATTAATTATACGTGATGCGTATTC 302
DB      461 AAATAAAAAAACCATCACTAATGCTGAGACGAATTAATTGATGATGATGATTC 520
QY      303 TGATCCCTTCATATGGAATTAAGTGTGTTACCATATATTTAATGATATTAACAAGACCGA 362
DB      521 TGATCCCTTTGAAACCAATTAATGTGTTACATATCTTTAATGATATCTCAGGTACTGA 580
QY      363 ACGCATGATGAGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCAT 422
DB      581 ACGCCAAAGATGTAAGACTACTCTTTGCCCAATGCAATTCCTCGTGTGTAATAAACAAT 640
QY      461 AAATAAAAAAACCATCACTAATGCTGAGACGAATTAATTGATGATGATGATTC 520
DB      303 TGATCCCTTCATATGGAATTAAGTGTGTTACCATATATTTAATGATATTAACAAGACCGA 362
QY      521 TGATCCCTTTGAAACCAATTAATGTGTTACATATCTTTAATGATATCTCAGGTACTGA 580
QY      363 ACGCATGATGAGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCAT 422
DB      581 ACGCCAAAGATGTAAGACTACTCTTTGCCCAATGCAATTCCTCGTGTGTAATAAACAAT 640
QY      483 AGTCCAAATTTGGGAATCAATTAATCAAGCTGACATTTGGAAAAATCTCTGGAAGTTATTC 542
DB      701 GGTCCAACTGGGAATCAATTAATCAAGTAAATATTTGGAAGATTTCTGGAAGTATGTC 760
QY      543 ATTCCCTGTAAAAACGAGGCTTTTCTTCACTGTAGCCATCCAAATGTTTCAGAGGC 602
DB      761 ATTCACTGAGAAAACGAGGCGCAATTCCTATTTGTTGACCATCAATGTTATCAAGGC 820
QY      603 ACGGCAATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCC 662
DB      821 ACCAAGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAAGAGCAATTCACACC 880
QY      663 TGATCCCAAGATTAATTTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAA 722
DB      881 TAATCCCAAGTACTTAATTTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCATGA 940
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QY      723 TGCCAAGATGAGGCTTTTACCAAAACCTTAGCTAGTGTGATGCAAAAGTACCAAGT 782
DB      941 TGCCAAGATGAGGCTTTTACCAAAACCTTAGCTAGTGTGATGCAAAAGTACCAAGT 1000
QY      783 GATAGTCTTGAAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGAT 842
DB      1001 GATAGTGTGAGTGTGATGAATCAAGGCTGATGATGATGATGATGATGATGATGAT 1060
QY      843 AACCTGTGAGCAACT--ACCAAAATGCAATGTTCTGCAAGTATATTTCTACTTA 899
DB      1061 GAGCTGTGAGCAACTTATTAACCAAAATGCAATGTTCTGCAAGTATATTTCTACTTA 1120
QY      900 TTATATATATATGCTAATCTTGTGATGATGATGATGATGATGATGATGATGAT 945
DB      1121 TTATATATATATGCTAATCTTGTGATGATGATGATGATGATGATGATGATGAT 1166

RESULT 11
AR136704      1379 bp   DNA      linear   PAT 16-JUN-2001
LOCUS         AR136704
DEFINITION    Sequence 1 from patent US 6137030.
ACCESSION     AR136704
VERSION       AR136704.1   GI:14477376
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 1379)
AUTHORS       Tumer,N.E.
TITLE         Pap mutants that exhibit anti-viral and/or anti-fungal activity in
JOURNAL       Patent: US 6137030-A 1 24-OCT-2000;
FEATURES
source        1..1379
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ORIGIN
Query Match      66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY      3 GAAGTGATGCTTGATGTTGGTGACGTTAATAGCGTGGCTGATTGCTGCACCACTTC 62
DB      221 GAAAGATGAAGTGCATGCTTGTTGGTGCACATATCAATATGCTGATCTTGACCACTTC 280
QY      63 AACTGTGCCATTAATACGATCACCTTGTGATGCTGAAATGCAACCATTAACAATATGC 122
DB      281 AACTGGGCTGTGAATACATCATCTACATATGTTGGAAGTACACCATTTGCAATATGCG 340
QY      123 CACCTTTATGGAATCTCTTCTGATATCAAGGGAAGATCCAAACTAAATGCTATGCGAT 182
DB      341 CACTTTTCGAATGATCTTGTATATGAAGCAAGATCCAAAGTTTAAATGCTATGGAAT 400
QY      183 ACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATTTGTTAAGCTCCAGAGTGC 242
DB      401 ACCAATGCTGCCAATACAAATACAAATCCAAAGTACGTGTTGGAGTCCAGGTTTC 460
QY      243 AAACCTAAAAACCATTAACATAATGCTGAGACGAATTAATTATACGTGATGCGTATTC 302
DB      461 AAATAAAAAAACCATCACTAATGCTGAGACGAATTAATTGATGATGATGATTC 520
QY      461 AAATAAAAAAACCATCACTAATGCTGAGACGAATTAATTGATGATGATGATTC 520
DB      303 TGATCCCTTCATATGGAATTAAGTGTGTTACCATATATTTAATGATATTAACAAGACCGA 362
QY      521 TGATCCCTTTGAAACCAATTAATGTGTTACATATCTTTAATGATATCTCAGGTACTGA 580
QY      363 ACGCATGATGAGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCAT 422
DB      581 ACGCCAAAGATGTAAGACTACTCTTTGCCCAATGCAATTCCTCGTGTGTAATAAACAAT 640
QY      423 TAACTAATATGCTTATATCCGACCAATGAAAAAGAAAGCAAGATTAATCTCAAGAAATCA 482
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Db 641 AAATTGATAGTCATATCCAACTGGAAATCAAAAGCGAGTAAATCAAGATCA 700
Qy 483 AGTCAATTTGGGAATTCAAATCTGACGAGTGACATTTGAAAATCTCTGAGTTGATTC 542
Db 701 GGTCACTTGGGAATTCAAATCTGACGAGTAAATTTGAAAATTTCTGAGTATGTC 760
Qy 543 ATTCCCTTAAAACTGAGGCTTTTCTACTGTGACCAATCCAAATGTTTCAGAGGC 602
Db 761 ATTCACTGAGAAAACGAAAGCGAATTCCTATTGTGACCAATGATGATCAGAGGC 820
Qy 603 AGCGGATTCGAATCATAGAGAACCAAGTCAAGCTAATTTAATAGACATTCACC 662
Db 821 AGCAAGATTCAGATCATAGAGAACCAAGTCAATTTAATAGACATTCACC 880
Qy 663 TGATCCCAAGTAATTAATTTGAGAGAGAGTGGGGCAAAATCTCTGAGGCAATTCACA 722
Db 881 TAAATCCCAAGTAATTAATTTGAGAGAGAGTGGGGTAAAGATTTACAGCAATTCAGA 940
Qy 723 TGCCAGAAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGGTACCAAGTG 782
Db 941 TGCCAGAAATGGAGTTTACCCAAACCTCTGAGTATGATGACCAAGGTACCAAGTG 1000
Qy 783 GATAGTTTGAAGTGAATGAATCATGATGATGACCTCTTAAGTACGTTAATG 842
Db 1001 GATAGTTTGAAGTGAATGAATCATGATGATGACCTCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGTTCTGCAAGTAAATTTCTACTTA 899
Db 1061 GAGCTGTGAGCAACTTAAATCAAAATGCGATGTTCTCTCAACTTAATTAATGTTACTTA 1120
Qy 900 TTATTAATTAATGTTCTAATCTTGATGATCTAATTTGAAGATTTCTAA 945
Db 1121 TTATTAATTAATGTTCTAATCTTGATGATCTAATTTGAAGATTTCTGA 1166

RESULT 12
AX427731 1379 bp DNA linear PAT 20-JUN-2002

LOCUS AX427731
DEFINITION Sequence 30 from Patent WO0233107.
ACCESSION AX427731
VERSION AX427731.1 GI:21537838

KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

Phytolacca americana
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Neelam,A., Atkinson,H.J., McPherson,M.J. and Thomas,C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 30 25-Apr-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES
Source
1..1379
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

ORIGIN

Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 3 GAAGTATGCTTGTAGTGTGAGCTTAATAGCGTGGCTCATGTGTGACCAACTTC 62
Db 221 GAATATGAAGTCAGTGTGTGGGACAAATTCATATGCTCATTTCTTGACCAACTTC 280
Qy 63 AACTGTGACCAATTAATGATCAGTACCTTGTGATGCTGGAATGCAACATTAACAATATGC 122
Db 281 AACTTGGGCTGTGATTAATCAATCTACAAATGTTGGAAATGCAACATTAACAATATGC 340
Qy 123 CACCTTAATGAATCTCTTGTAAATCAAGCAAAAGATTCMAAATTAATGCTATGGCAT 182

Db 341 CACTTTCTGATGATCTTCTGTAATGAAGCAAAAGATTCAGATTTAAATGCTATGAT 400
Qy 183 ACCAATGCTACTGATTAATTAATTTGACCCCTTAAGTACTTAATTTGTAAGTCTCAAGTGC 242
Db 401 ACCAATGCTGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 460
Qy 243 AAACCTAAAAACATTAATCAATGATGAGAGCAAAATTAATTAATTAATTAATTAATTAAT 302
Db 461 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 520
Qy 303 TGATTCCTTCAATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 362
Db 521 TGATTCCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 580
Qy 363 ACGCAATGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 422
Db 581 ACGCAATGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 640
Qy 423 TAACTCAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 482
Db 641 AAATCTTGAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 700
Qy 483 AGTCAATTTGGGAATTCAAATCTGACGAGTGACATTTGAAAATCTCTGAGTTGATTC 542
Db 701 GGTCACTTGGGAATTCAAATCTGACGAGTAAATTTGAAAATTTCTGAGTATGTC 760
Qy 543 ATTCCCTTAAAACTGAGGCTTTTCTACTGTGACCAATGTTTCAGAGGC 602
Db 761 ATTCACTGAGAAAACGAAAGCGAATTCCTATTGTGACCAATTAATTAATTAATTAAT 820
Qy 603 AGCGGATTCGAATCATAGAGAACCAAGTCAAGCTAATTTAATAGACATTCACC 662
Db 821 AGCAAGATTCAGATCATAGAGAACCAAGTCAATTTAATAGACATTCACC 880
Qy 663 TGATCCCAAGTAATTAATTTGAGAGAGAGTGGGGCAAAATCTCTGAGGCAATTCACA 722
Db 881 TAAATCCCAAGTAATTAATTTGAGAGAGAGTGGGGTAAAGATTTCAAGCAATTCAGA 940
Qy 723 TGCCAGAAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGGTACCAAGTG 782
Db 941 TGCCAGAAATGGAGTTTACCCAAACCTCTGAGTATGATGACCAAGGTACCAAGTG 1000
Qy 783 GATAGTTTGAAGTGAATGAATCATGATGATGACCTCTTAAGTACGTTAATG 842
Db 1001 GATAGTTTGAAGTGAATGAATCATGATGATGACCTCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGTTCTGCAAGTAAATTTCTACTTA 899
Db 1061 GAGCTGTGAGCAACTTAAATCAAAATGCGATGTTCTCTCAACTTAATTAATGTTACTTA 1120
Qy 900 TTATTAATTAATGTTCTAATCTTGATGATCTAATTTGAAGATTTCTAA 945
Db 1121 TTATTAATTAATGTTCTAATCTTGATGATCTAATTTGAAGATTTCTGA 1166

RESULT 13

AY572976 942 bp mRNA linear PLN 05-Apr-2004
LOCUS AY572976
DEFINITION Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
ACCESSION AY572976
VERSION AY572976.1 GI:45826466

KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

Phytolacca americana
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Xiao,Z.A. and Jiang,Y.
TITLE A gene encoding the pokeweed antiviral protein in the leaf of
Phytolacca americana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 942)

REFERENCE	AUTHORS	TITLE
152	CGAAGATATCCAAATCTAAATAATGCTATGCGATACCAATGCTACTGATATCTATATGACCC	211
124	CGAAAGATCCAAATTTAAATGCTATGAGATACCAATGCTGCCAATACAAATCCAGATC	183
212	CTAAGTACTTAATGGTTAAGCTCCAAAGTGCCAAACCTAATAAAACAATTACATAATGCTGA	271
184	CAAAATACGATGGTTGAGCTCCAAAGGTTCAAAATATAAAAAACATACACATAATGCTGA	243
272	GACGAAATPACTTAATACGATATGGGCTATTCTGATCCCTTCAATGGCAATTAATGTCGT	331
244	GACGAAACAAATTTGATATGATGAGGCTATTCTGATCCCTTGGATACCAATTAATGTCGT	303
332	ACCATATATTTAATGATATTAACAACCCGAACGCAATGATGAGGAATACTCTTGGT	391
304	ACCATATCTTTAATATATATCTAGGACTGAACCCGAATATGAGACTACTCTTTGGC	363
392	CAAGTTAGATCTCGATGTTGCATATGCTCATTAACATATAGCTTAATATCCGACATG	451
364	CBAATCCCAATCTCGATGTTAATTAABAAACATTAATATATGATGATTCACAAATGG	423
452	AAAAGAAAGCAGAGTAACTCAGAAATCAAGTCOAATGGGAAATCCAAATACTCAGCA	511
424	AATCAAAAGCCGAGATTAATCAAAAGTCAAGTCAATCGGGAATTCAAATACTTGACA	483
512	GTGACATTTGAAAAATCTCTGAGTGAATTCATCCCTGTAATAAATGAGGCTTTTTC	571
484	GTGACATTTGAAAAATTTCTGAGTGAATTCATCCCTGTAATAAATGAGGCTTTTTC	543
572	TACTGGTACCATCCAAATATGTTTCAAGAGGAGCGCGATTCAGATACATAGAGCAAG	631
544	TACTGGTACCATCCAAATATGTTTCAAGAGGAGCGCGATTCAGATACATAGAGCAAG	603
632	TCAGACTTAATTTAATAGAGCATTCACCTGATCCCAAGTAAATTAATTTGAGAGA	691
604	TGAAATCTAATTTTAAACAGAGCATTCACCTGATCCCAAGTAAATTAATTTGAGAGA	663
692	AGTGGGGGAAATCTCTGAGGCAATTCACAATGCCAAATATGGGCTTTACCCAAACAC	751
664	CATGGGGTAAATTTCTACAGCAATTCATGATGCCAAATATGGGCTTTTACCCAAACCTC	723
752	TTGAGCTATGAGTATCCAAAGGTACCAAGTGAATGATCTTATGATGATGAATCAATC	811
724	TGCAATCTATGATATCCCAAGGTATGATGATGATGATGATGATGATGATGATGATGATG	783
812	GTGATGAGCACTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG	868
784	CTGATGAGCACTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG	843
869	CCATGTTCTTCAAGTATTAATTTTCTATTAATTAATTAATTAATTAATTAATTAATTAAT	928
844	CCATGTTCTTCAAGTATTAATTTTCTATTAATTAATTAATTAATTAATTAATTAATTAAT	903
929	TATTTGAAGATTCCTAA 945	
904	TATTTGAAGATTCCTAA 920	
RESULT 15		
PAPAP	1164 bp	mRNA linear
LOCUS	P.americanana PAP gene for anti-viral protein.	PLN 18-NOV-1991
DEFINITION	X55383.1 GI:20421	
VERSION	X55383.1	
KEYWORDS	antiviral protein; cell wall protein; PAP gene; ribosome inactivating protein.	
SOURCE	Phytolacca americana (American pokeweed)	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.	
REFERENCE	Lin, O.; Chen, Z.C.; Antoniw, J.F. and White, R.F.	
AUTHORS	Isolation and characterization of a cDNA clone encoding the	

JOURNAL	JOURNAL	anti-viral protein from <i>Phytolacca americana</i>
PUBMED	Plant Mol. Biol. 17 (4), 609-614 (1991)	
AUTHORS	2 (bases 1 to 1164)	
TITLE	Antoniw, J.F.	
JOURNAL	Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops Research, dept. of Plant Pathology, Rothamsted Experimental Station, Harpenden, Herts, AL5 2JQ, UK	
FEATURES	source	
gene	1. 1164	
CDS	/organism="Phytolacca americana"	
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	/tissue_type="leaf"	
	/dev_stage="vegetative"	
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	2. .943	
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	/db_xref="GOA:P10297"	
	/db_xref="UniProt/Swiss-Prot:P10297"	
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ORIGIN		
Query Match	66.8%; Score 631; DB 15; Length 1164;	
Best Local Similarity	80.1%; Pred. No.4.5e-137;	
Matches 755; Conservative	0; Mismatches 185; Indels 3; Gaps 1;	
QY	6 GGTGATGCTTGTAGTGTGGTGAAGTAAATAGCTGAGCTCATTTGCTGACCAACTTCAAC	65
DB	1 GATGAATGCAATGCTTGTGGTGAAGTAAATAGCTCATTTGCTGACCAACTTCAAC	60
QY	66 TTGTGCATTAATTCGATCACCCTTTGATGCTGGAATGCAACCTTAACAATATGCGAC	125
DB	61 TTGGGCTGTGAATTCATCATCTTCAATGTTGGAGATGACCACTTAGCAATATGCGAC	120
QY	126 CTTTATGGAATCTCTTGTGTAATGAGGAAGAAAGTCCAAAATTAATGCTATGCAATAC	185
DB	121 TTTTCTGAATGATCTTGTATGATGAAGGAAGTCCAAATTTAAATGCTATGGAATAC	180
QY	186 AATGCTACTGATCTAATTCGACCCCTAAGTACTTATGGTTAAAGCTCCAAAGTGCATA	245
DB	181 AATGCTGCCAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA	240
QY	246 CTTAAAAACATTAACATTAATGCTGAGACGAAATTAATTAATGCTGAGCTATTTCTGA	305
DB	241 TAAAAAACATTAACATTAATGCTGAGACGAAATTAATTAATGCTGAGCTATTTCTGA	300
QY	306 TCCCTTCAATGGAATTAATGCTGATTCATTAATTAATTAATTAATTAATTAATTAATTA	365
DB	301 TCCCTTGAATTAATTAATGCTGATTCATTAATTAATTAATTAATTAATTAATTAATTA	360
QY	366 CACTGATGAGAGAAATCTCTTGGTCAAGTTCAGTTCTCGATGCAATGTCATTAAT	425
DB	361 CCAAGATGAGAGAAATCTCTTGGTCAAGTTCAGTTCTCGATGCAATGTCATTAAT	420
QY	426 CTTCAATAGCTTATTCGACCAATGAGAAAGAAAGCAAGATTAATCTCAAGATTAAGT	485
DB	421 CTTTGAATGCTATTCGACCAATGAGAAAGAAAGCAAGATTAATCTCAAGATTAAGT	480
QY	486 CCAATTTGGGAATTCGAATTAATTCGAGAGATGCAATTTGAGAAAAATCTCTGAGTTGATTCAT	545
DB	481 CCAACTGGGAATTCGAATTAATTCGAGAGATGCAATTTGAGAAAAATCTCTGAGTTGATTCAT	540

QY 546 CCTGTAAAACTGAGGCTTTTCTACTGTAGCCATCCAAATGGTTTCAGAGGCAGC 605
Db 541 CACTGAGAAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGGTATCAGAGGCAGC 600
QY 606 GCGATTCAGTACTATGAGAACCAAGTCAAGACTAATTTAATAGAGCATTTCACTGA 665
Db 601 AAGATTCAGTACATAGAGATCAGGAAACTAATTTAACAAGACATTCACACCTTA 660
QY 666 TCCCAAGTAAATTAATTTGAGAGGAAGTGGGCAAAATCTGAGGCAATTCACAAATGC 725
Db 661 TCCCAAGTAACTTAATTTGAGAGGACATGGGTAAGATTTCAACAGCAATTCATGATGC 720
QY 726 CAAGAAATGGGCTTTAACCCAAACCACTTGAGCTAGTGAATGCCAAAGTACCAAGTGAAT 785
Db 721 CAAGAAATGGGCTTTAACCCAAACCTTCGAGCTAGTGAATGCCAGTGGTCCAAAGTGAAT 780
QY 786 AGTCTTAAGTGAATGAATCAATGCTGATGTGGCACTCCTTAAGTACGTTAATGGAAC 845
Db 781 AGTGTGAGAGTGAATGAATCAAGCTGATGTGACACTCTTAAGTACGTTGAGGAG 840
QY 846 CTGTGAGACAACTT---ACCAAAATGCAATGTTCTCTCAAGTTATAATTTCTACTTATTA 902
Db 841 CTGTGAGACAACTTATAACCAAAATGCAATGTTCTCTCAACTTAATGTCTACTTATTA 900
QY 903 TAATTATATGTCTAATCTTGTGATCTAATTGAAGATTTCTAA 945
Db 901 TAATTACATGTTAATCTTGTGATCTAATTGAAGATTTCTGA 943

Search completed: April 9, 2006, 04:15:08
Job time : 5560.17 secs

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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 23:57:17 ; Search time 569.609 Seconds
(without alignments)
11056.934 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945
Sequence: 1 atgaagctgctgtctgtac.....atctattgaagattctaa 945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
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8: geneseqn2003as: *
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12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6	AAD42715
2	786.4	83.2	792	6	AAD42716
3	761.4	80.6	1092	6	AAD42729
4	634.4	67.1	1154	11	ADM74765
5	632.4	66.9	1378	12	ADG76061
6	632.4	66.9	1379	3	AAZ45197
7	632.4	66.9	1379	3	AAZ59220
8	632.4	66.9	1379	6	AAD42738
9	632.4	66.9	1379	10	ADT05787
10	630.8	66.8	1195	2	AAQ56672
11	630.8	66.8	1195	2	AAQ56672
12	629.2	66.6	1378	4	AAC87929
13	629.2	66.6	1378	6	AAD42739
14	629.2	66.6	1379	3	AAZ59221
15	624.2	66.1	2472	2	AAQ43967
16	597.4	62.3	1154	11	ADM74751
17	588.6	62.1	882	2	AAT99556
18	586.4	62.1	2369	2	AAT99557
19	586.4	62.1	2369	2	ABA96543

20	543.8	57.5	918	2	AAQ64893
21	543.8	57.5	918	2	AAT04782
22	459	48.6	465	6	AAD42717
23	329	34.8	333	6	AAD42718
24	110.8	11.7	934	3	AAZ45198
25	110.8	11.7	934	6	AAD42740
26	97.8	10.3	600	2	ABA96716
27	97.8	10.3	600	2	ABA96547
28	96	10.2	864	1	AAQ91504
29	88.4	9.4	804	2	AAQ53895
30	88.4	9.4	804	2	AAQ53896
31	88.4	9.4	804	2	AAQ53885
32	88.4	9.4	804	2	AAQ53884
33	88.4	9.4	804	2	AAQ99041
34	88.4	9.4	804	2	AAQ99042
35	88.4	9.4	804	2	AAT17962
36	88.4	9.4	804	2	AAT17963
37	88.4	9.4	804	2	AAT17964
38	88.4	9.4	804	3	AAAI2861
39	88.4	9.4	804	3	AAAI2862
40	88.4	9.4	804	9	ACD67204
41	88.4	9.4	804	9	ACD67205
42	88.4	9.4	804	10	ADC34588
43	88.4	9.4	804	10	ADC34589
44	88.4	9.4	804	10	ADH92013
45	88.4	9.4	804	10	ADH92012

ALIGNMENTS

RESULT 1	
AAAD42715	
ID	AAAD42715 standard, DNA, 945 BP.
AC	AAAD42715;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed pro-PAP-S protein encoding DNA.
KW	Neurotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM	gene; ds.
XX	
OS	Phytolacca americana.
PH	
Key	Location/Qualifiers
FT	1..945
FT	/*tag= a
FT	/product= "Pro-PAP-S protein"
FT	1..24
FT	/*tag= b
FT	/bound_moiety= "Primer PPS1BP"
FT	complement (735..776)
FT	/*tag= c
FT	/bound_moiety= "Primer PSXDR"
FT	736..777
FT	/*tag= d
FT	/bound_moiety= "Primer PSXDF"
FT	750..759
FT	/*tag= e
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PN	MO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 PA Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
 PI WPI; 2002-489891/52.
 DR P-PSDB; AAE25918.
 XX
 XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 PS Claim 24; Page 73-74; 87pp; English.
 CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
 CC protein encoding DNA
 XX
 SQ Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
 Query Match 100.0%; Score 945; DB 6; Length 945;
 Best Local Similarity 100.0%; Pred. No. 3.4e-254;
 Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGTGATGCTTGTAGTGTGAGCGTAAATAGCCGTGCTCATTTGCTGACCAACT 60
 DB 1 ATGAAGGTGATGCTTGTAGTGTGAGCGTAAATAGCCGTGCTCATTTGCTGACCAACT 60
 QY 61 TCAACTTGTGCCCTAAATACGATCACCTTGTAGTGTGAAATGCCACCTTAACAATAT 120
 DB 61 TCAACTTGTGCCCTAAATACGATCACCTTGTAGTGTGAAATGCCACCTTAACAATAT 120
 QY 121 GCCACCTTATGGAATCTCTTGTGTAATCAAGCGAAGATCAAAATCTAAATGCTATGCG 180
 DB 121 GCCACCTTATGGAATCTCTTGTGTAATCAAGCGAAGATCAAAATCTAAATGCTATGCG 180
 QY 181 ATACCAATGCTACCTGATACCTAATTCGACCCCTAGTACTTATGTTAGCTCAAGGT 240
 DB 181 ATACCAATGCTACCTGATACCTAATTCGACCCCTAGTACTTATGTTAGCTCAAGGT 240
 QY 241 GCAAACTTAAAAACCTTACATGCTGACGCAAGAAATTAATACGATGGGCTAT 300
 DB 241 GCAAACTTAAAAACCTTACATGCTGACGCAAGAAATTAATACGATGGGCTAT 300
 QY 301 TCTGATCCCTCAATGGAATAGTGTGCTTACCATATATTTAATGATTAACAAGCACC 360
 DB 301 TCTGATCCCTCAATGGAATAGTGTGCTTACCATATATTTAATGATTAACAAGCACC 360
 QY 361 GAAACGACGTATGGAATATCTCTTGTCTCAAGTTCTAGTCTCGTGTGCAATGTCC 420
 DB 361 GAAACGACGTATGGAATATCTCTTGTCTCAAGTTCTAGTCTCGTGTGCAATGTCC 420
 QY 421 ATTAATCAATATGCTTATATTCGACCAATGGAAGAAAGCAAGATTAATCAAGAAAT 480
 DB 421 ATTAATCAATATGCTTATATTCGACCAATGGAAGAAAGCAAGATTAATCAAGAAAT 480
 QY 481 CAAGTCCATTTGGGAATTCGAATACCTCAGACGTACATTTGGAATAATCTCTGAGTTGAT 540
 DB 481 CAAGTCCATTTGGGAATTCGAATACCTCAGACGTACATTTGGAATAATCTCTGAGTTGAT 540
 QY 541 TCATTCCTCTGTAATAAATCTGAGGCTTTTCTAATCTGTAAGCCATCAAAATGTTTCAGAG 600
 DB 541 TCATTCCTCTGTAATAAATCTGAGGCTTTTCTAATCTGTAAGCCATCAAAATGTTTCAGAG 600
 QY 601 GCAGCGCGGATTCAGATACATAGGAACCAAGTCAAGATTAATTTAATAGCATTTCTAC 660
 DB 601 GCAGCGCGGATTCAGATACATAGGAACCAAGTCAAGATTAATTTAATAGCATTTCTAC 660

QY 661 CCTGATCCCAAGTAATTAATTTGAGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
 DB 661 CCTGATCCCAAGTAATTAATTTGAGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
 QY 721 AATGCCAAGATATGGGGCTTTACCCAAACCACTTGAAGTATGATGCCAAGATTCACAG 780
 DB 721 AATGCCAAGATATGGGGCTTTACCCAAACCACTTGAAGTATGATGCCAAGATTCACAG 780
 QY 781 TGGATGTTCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 TGGATGTTCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 GGAACCTGTACAGCAACTTACCAAAATGCGATGTTCTCAAGTATTAATTTCTACTAT 900
 DB 841 GGAACCTGTACAGCAACTTACCAAAATGCGATGTTCTCAAGTATTAATTTCTACTAT 900
 QY 901 TATTAATTAATGTTCTAATCTTGGTATGATGATGATGATGATGATGATGATGAT 945
 DB 901 TATTAATTAATGTTCTAATCTTGGTATGATGATGATGATGATGATGATGATGAT 945

RESULT 2
 AAD42716
 ID AAD42716 standard; DNA; 792 BP.
 XX
 AC AAD42716;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Pokeweed mature PAP-S protein encoding DNA.
 XX
 KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
 KM gene; de.
 OS Phytotheca americana.
 XX
 FH Key Location/Qualifiers
 FT 1..792
 FT CDS /tag= a
 FT primer_bind 1..29 /product= "Mature PAP-S protein"
 FT /tag= b
 FT primer_bind complement(436..462)
 FT /tag= c
 FT primer_bind 463..492 /bound_molecy= "Primer PS1SR"
 FT /tag= d
 FT primer_bind 681..686 /bound_molecy= "Primer PS2BF"
 FT misc_feature 681..686 /tag= e
 FT primer_bind /note= "Sequence replacing removed XbaI site"
 FT /tag= f
 FT primer_bind complement(765..792)
 FT /tag= g
 FT primer_bind /bound_molecy= "Primer PS2SR"
 PN WO200233107-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-GB004593.
 XX
 PR 14-OCT-2000; 2000GB-00025217.
 XX
 PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 PI Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
 XX WPI; 2002-489891/52.
 DR P-PSDB; AAE25918.
 XX
 PT Inducing necrotic effect in specific cells of plant by transforming plant

PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 PS Claim 2; Page 76; 87pp; English.

CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is pokeweed mature PAP
 CC -S protein encoding DNA

XX
 XX Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;

Query Match 83.2%; Score 786.4; DB 6; Length 792;
 Best Local Similarity 99.9%; Pred. No. 8.9e-210;

Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 ATAAATCGATCAGCTTGAATGCTGGAATGCCCATTTAACAATATGCCACTTTATG 132
 DB 4 ATAAATCGATCAGCTTGAATGCTGGAATGCCCATTTAACAATATGCCACTTTATG 63
 QY 133 GAAATCTCTGATATCAAGCGAAAGATCCAAAATTAATGCTATGCAATCAATGCTA 192
 DB 64 GAAATCTCTGATATCAAGCGAAAGATCCAAAATTAATGCTATGCAATCAATGCTA 123
 QY 193 CCGATATCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCAAGGTGCAAACTTAAA 252
 DB 124 CCGATATCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCAAGGTGCAAACTTAAA 183
 QY 253 ACCATTAACCTAATGCTGGAATGCCCATTTAACAATATGCCACTTTATG 312
 DB 184 ACCATTAACCTAATGCTGGAATGCCCATTTAACAATATGCCACTTTATG 243
 QY 313 AATGCGAATAGTGTGCTTACATATATTTAATGATTTAACAAGCAGCAAGCACTGAT 372
 DB 244 AATGCGAATAGTGTGCTTACATATATTTAATGATTTAACAAGCAGCAAGCACTGAT 303
 QY 373 GTGAGAAATACCTTTGCTCAAGTTCTGCTGTGCTGATGTCATTAATCAAT 432
 DB 304 GTGAGAAATACCTTTGCTCAAGTTCTGCTGTGCTGATGTCATTAATCAAT 363
 QY 433 AGCTTATATCCGACATGGAAGAAAGCAAGATTAATCAAGATTCAGATTCAT 492
 DB 364 AGCTTATATCCGACATGGAAGAAAGCAAGATTAATCAAGATTCAGATTCAT 423
 QY 493 GGAATTCAAATATCTCAGCAGTGCATGGAATAATCTCTGAGTTGATTCATCCCTGTA 552
 DB 424 GGAATTCAAATATCTCAGCAGTGCATGGAATAATCTCTGAGTTGATTCATCCCTGTA 483
 QY 553 AAAAAGTGAAGCTTTTCTTACTGTGTAGCATCAAAATGTTTCAAGAGCAGCGATTC 612
 DB 484 AAAAAGTGAAGCTTTTCTTACTGTGTAGCATCAAAATGTTTCAAGAGCAGCGATTC 543
 QY 613 AAGTACATAGAGAACCAAGTCAAGATTAATTTAATGAGCATTTACCTGATCCAAA 672
 DB 544 AAGTACATAGAGAACCAAGTCAAGATTAATTTAATGAGCATTTACCTGATCCAAA 603
 QY 673 GTAATTAATTTGAGGAGGAGGAGGCAAAATCTCTGAGCAATTCACANTGCCAATAAT 732
 DB 604 GTAATTAATTTGAGGAGGAGGAGGCAAAATCTCTGAGCAATTCACANTGCCAATAAT 663
 QY 733 GGGGCTTTTACCAACCACTTGAAGTATGATGATGCCAAGATTCAGATGATGCTT 792
 DB 664 GGGGCTTTTACCAACCACTTGAAGTATGATGATGCCAAGATTCAGATGATGCTT 723
 QY 793 AAGGTGATGAATTCATGCTGATGTGCACTCTTAAAGTACGTTAATGAGACCTGTGAG 852
 DB 724 AAGGTGATGAATTCATGCTGATGTGCACTCTTAAAGTACGTTAATGAGACCTGTGAG 783

QY 853 ACAACTTA 860
 DB 784 ACAACTTA 791

RESULT 3
 ID AAD42729 standard; DNA; 1092 BP.

AC AAD42729;

DT 29-AUG-2003 (revised)

DT 15-NOV-2002 (first entry)

DE Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.

KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;

OS Phytophthora americana.

OS Oryza sativa.

OS Tobacco; Etch virus.

OS Chimeric.

FT Key

FT primer_bind

FT misc_feature

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

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FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is a fusion DNA. This
 CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA

CC and Tobacco Etch virus (TEV) N1a protease cleavage site (PCS). (Updated
 CC on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Query Match 80.6%; Score 761.4; DB 6; Length 1092;
 Best Local Similarity 99.9%; Pred. No. 1e-202;
 Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 ATAAATACGATCACTTGGATGCTGAAATGCCACATTAACAAATATGACCTTATG 132
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 DB 4 ATAAATACGATCACTTGGATGCTGAAATGCCACATTAACAAATATGACCTTATG 63
 |||||
 QY 133 GAATCTCTTGGATATCAAGGAAAGATCAAAAATAAATGCTATGACATACCAATGCTA 192
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 DB 64 GAATCTCTTGGATATCAAGGAAAGATCAAAAATAAATGCTATGACATACCAATGCTA 123
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 QY 193 CCTGATATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCMAACTTAAA 252
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 DB 124 CCTGATATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCMAACTTAAA 183
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 QY 253 ACCATTACCTAATGCTGAGACGAAATTAATTAAGTATGAGTGGGCTATTGCTGATCCCTTC 312
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 DB 184 ACCATTACCTAATGCTGAGACGAAATTAATTAAGTATGAGTGGGCTATTGCTGATCCCTTC 243
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 QY 313 AATGGCAATAGTGTGCTTACCAATATTTAATGATATTAACAAGCACCGACATGAT 372
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 DB 244 AATGGCAATAGTGTGCTTACCAATATTTAATGATATTAACAAGCACCGACATGAT 303
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 QY 373 GTGGAATATCTCTTGGCTCAAGTTCAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
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 DB 304 GTGGAATATCTCTTGGCTCAAGTTCAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
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 QY 433 AGCTTATATCCGACCATGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTTC 492
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 DB 364 AGCTTATATCCGACCATGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTTC 423
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 QY 493 GGAATTCAAATTAATCTCAGCAGTGAATTGAAAAATCTCTGAGTGAATTCATTCCTCTGTA 552
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 DB 424 GGAATTCAAATTAATCTCAGCAGTGAATTGAAAAATCTCTGAGTGAATTCATTCCTCTGTA 483
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 QY 553 AAAACGAGGCTTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
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 DB 484 AAAACGAGGCTTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
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 QY 613 AAGTACATAGAGAACCAAGTCAAGACTTAATTTTATAGACATTTTACCTGATCCCAA 672
 |||||
 DB 544 AAGTACATAGAGAACCAAGTCAAGACTTAATTTTATAGACATTTTACCTGATCCCAA 603
 |||||
 QY 673 GTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAAAATGCCAAGAT 732
 |||||
 DB 604 GTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAAAATGCCAAGAT 663
 |||||
 QY 733 GGGGCTTTACCCCAACCACTTGAGCTAGTGGATGCCAAAGTACCAAGTGAATGTTCTT 792
 |||||
 DB 664 GGGGCTTTACCCCAACCACTTGAGCTAGTGGATGCCAAAGTGAATGTTCTT 723
 |||||
 QY 793 AGAGTGAATGAATCAATGCTGATGTGGCACTCTTAAGTACG 835
 |||||
 DB 724 AGAGTGAATGAATCAATGCTGATGTGGCACTCTTAAGTACG 766
 |||||

RESULT 4
 ADM74765
 ID ADM74765 standard; cDNA; 1164 BP.
 XX
 AC ADM74765;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE HIV-1 inhibition activity related Tat cDNA.
 XX
 KW human immunodeficiency virus; HIV-1; tumour; plant;

KW Chinese phytolacca leaf; trans-acting activation factor; Tat; mutant;
 KW gene; ss.
 XX
 XX Human immunodeficiency virus 1.

OS Key Location/Qualifiers
 FH CDS 2..943
 FT /*tag= a
 FT /product= "Tat HIV-1 protein"

PN CN1400220-A.

PD 05-MAR-2003.

PF 02-AUG-2001; 2001CN-00123911.

PR 02-AUG-2001; 2001CN-00123911.

XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.

XX Peng X, Bai L, Yin B;

XX WPI; 2003-469263/45.

XX P-PSDB; ADM74766.

XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
 its expression, separation and purification method in prokaryon.

PS Example 9; Page 11-12; 17bp; Chinese.

CC The present invention relates to two kinds of cDNA which can inhibit
 CC human immunodeficiency virus (HIV-1) activity, including separation clone
 CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
 CC and application of the cDNA in preparation of preparation for curing the
 CC virus and tumours. One of the described cDNAs is obtained by separation
 CC and cloned from a plant Chinese phytolacca leaf, and one from the trans-
 CC acting activation factor (Tat) mutant coded by human immunodeficiency
 CC virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
 CC used in the HIV-1 inhibition activity of the invention.

XX Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;

Query Match 67.1%; Score 634.2; DB 11; Length 1164;
 Best Local Similarity 80.3%; Pred. No. 4.6e-167;
 Matches 757; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 6 GGTGATGCTTGTAGTGTGCTGATGCTTAATAGGTGGCTCATGCTGCACCAACTTCAAC 65
 |||||
 DB 1 GATGAAGTCGATGCTTGTGCTGATGCTTAATAGGTGGCTCATGCTGCACCAACTTCAAC 60
 |||||
 QY 66 TTGTGCATTAATATGATGATCACTTTGATGCTGGAATGCAACCATTAACAAATATGCAAC 125
 |||||
 DB 61 TTGTGCATTAATATGATGATCACTTTGATGCTGGAATGCAACCATTAACAAATATGCAAC 120
 |||||
 QY 126 CTTTATGAAATCTCTTGTATCAAGCGAAAGATCCAAAATTAATATGCTATGGCATTAC 185
 |||||
 DB 121 TTTTCTGATTAATCTTGTATCAAGCGAAAGATCCAAAATTAATATGCTATGGCATTAC 180
 |||||
 QY 186 AATGCTACGTAATCAATTTCCACCCCTTAAGTCTTATTTGTTAACTCCAAAGTGCMAA 245
 |||||
 DB 181 AATGCTACGTAATCAATTTCCACCCCTTAAGTCTTATTTGTTAACTCCAAAGTGCMAA 240
 |||||
 QY 246 CCTAAACACATTAACATATGCTGAGAGCAAAATTAATATAGTATGATGGGCTATTTCTGA 305
 |||||
 DB 241 TAAABAAACATCAACATATGCTGAGAGCAAAATTAATATAGTATGATGGGCTATTTCTGA 300
 |||||
 QY 306 TCCCTTCAATGSCATTAAGTGTCTTACCAATATTTAATGATATTAACAACCAAGCAGC 365
 |||||
 DB 301 TCCCTTGAATACCAATTAAGTGTCTTACCAATATTTAATGATATTAACAACCAAGCAGC 360
 |||||
 QY 366 CACTGATGTGAGAAATCACTTGTGCTCAAGTCTTACTTCTCGTGTGCAATGTCCATTAA 425
 |||||
 DB 361 CCAAGATGTAGAGACTACTTGTGCTCAAGTCTTACTTCTCGTGTGCAATGTCCATTAA 420
 |||||


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DB      940 TGCAGAAATGAGATTACCCAACTCTGAGCTAGTGGATCCAGTGTCAGAGTG 999
QY      783 GATAGTTCTTAGTGATGAATCANTCGATGATGGCACTCCTTAGTACCTTAATGG 842
DB      1000 GATAGTGTGATGATGATGAATCAAGCCGATGATGCACTTTAACTACGTTGCTGG 1059
QY      843 AACCTGTGACAACTT---ACCAAAATGCGATGTTCTCAAGTTAATTTCTACTTA 899
DB      1060 GAGCTGTGACAACTTATTAACCAAAATGCGATGTTCTCAACTTAAATGTCTACTTA 1119
QY      900 TTTAATTAATGATCTTAATCTTGTGATCTTAATTTGAAGATTCTTA 945
DB      1120 TTTAATTAATGATCTTAATCTTGTGATCTTAATTTGAAGATTCTTA 1165

RESULT 6
AA245197
ID      AA245197 standard; DNA; 1379 BP.
AC      AA245197;
XX
DT      29-FEB-2000 (first entry)
DE      Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
KM      Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
KM      ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
KM      potato virus X; cucumber mosaic virus; CMV; SE;
KM      tomato yellow leaf curl virus.
XX
OS      Phytolacca americana.
XX
FH      Key Location/Qualifiers
FT      CDS 225..1166
FT      /*tag= a
FT      /product= "PAP"
FT      /note= "Pokeweed antiviral protein"

MO960843-AI.
XX
PD      02-DEC-1999.
XX
PF      21-MAY-1999; 99MO-US01301.
XX
PR      22-MAY-1998; 98US-0086374P.
XX
PA      (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI      Turner NE, Wang P;
XX
DR      WPI; 2000-062555/05.
XX
DR      P-PSDB; AAYS8025.
XX
PT      New antiviral DNA useful for generating transgenic plants resistant to
PT      viruses and/or fungi.
XX
PS      Example; Page 4-5; 43pp; English.
XX
XX      This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
CC      a type I ribosome-inhibiting protein (RIP) found in the cell walls of
CC      Phytolacca americana (pokeweed). It is a single polypeptide chain that
CC      catalytically removes a specific adenine residue from a highly conserved
CC      stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
CC      antiviral protein II (PAP II) protein confers antiviral and or antifungal
CC      activities to plants. A DNA molecule encoding a PAP II protein with an
CC      intact catalytic active site amino acid residue (E172) is useful for
CC      generating transgenic plants. PAP II DNA is useful for generating a
CC      transgenic plants (especially cereal crops) through transforming a
CC      prooplast or introducing the DNA directly into a plant part prior to
CC      regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC      activity thus have increased resistance to viruses and/or fungi. Viruses
CC      include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato

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CC      yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC      Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
CC      other plants pests including insects, bacteria and nematodes. PAP II DNA
CC      is also useful for identifying a PAP II protein having reduced
CC      cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC      unlike PAP transgenic plants which are stunted and sterile, PAP II
CC      transgenic plants have a normal and fertile phenotype
XX
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match      66.9%; Score 632.4; DB 3; Length 1379;
Best Local Similarity 80.0%; Pred. No. 1,6e-166;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY      3 GAAAGTGAATGCTTGTAGTGTGGTGAAGTTAATAGGCGGCTCAATGTCGACCAACTTC 62
DB      221 GAAAGTGAATGCTTGTAGTGTGGTGAAGTTAATAGGCGGCTCAATGTCGACCAACTTC 280
QY      63 AACTGTGCGCATTAATACGATCACTTGTGATGCTGGAATGCGACATTAACTAATATGCG 122
DB      281 AACTGTGCGCATTAATACGATCACTTGTGATGCTGGAATGCGACATTAACTAATATGCG 340
QY      123 GACCTTTAATGGAATCTCTTGTATATCAAGCGAAAGTCCAAAATCTAATGCTATGCGAT 182
DB      341 GACCTTTAATGGAATCTCTTGTATATCAAGCGAAAGTCCAAAATCTAATGCTATGCGAT 400
QY      183 ACCAATGCTACCTGATTAATTAATGCAAGCCCTAAGTACTTATGTTAAGTCCAGAGTGC 242
DB      401 ACCAATGCTACCTGATTAATTAATGCAAGCCCTAAGTACTTATGTTAAGTCCAGAGTGC 460
QY      243 AAACCTTAAACCATTAACATTAATGCTGAGACGAAATTAATTAATGCTGAGTATTC 302
DB      461 AAACCTTAAACCATTAACATTAATGCTGAGACGAAATTAATTAATGCTGAGTATTC 520
QY      303 TGATCCCTTCAATGCGAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTA 362
DB      521 TGATCCCTTCAATGCGAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTA 580
QY      363 AGCAGCTGATGATGAGATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 422
DB      581 AGCAGCTGATGATGAGATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 640
QY      423 TAACTCAATTAATGCTTATATCCGACATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 482
DB      641 TAACTCAATTAATGCTTATATCCGACATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 700
QY      483 AGTCCAAATGCGAATTAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTA 542
DB      701 AGTCCAAATGCGAATTAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTA 760
QY      543 ATTCCTGTAAACCATGAGGCTTTTCTACTGATGATGATGATGATGATGATGATGATGATG 602
DB      761 ATTCCTGTAAACCATGAGGCTTTTCTACTGATGATGATGATGATGATGATGATGATGATG 820
QY      603 AGGCGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 662
DB      821 AGGCGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 880
QY      663 TGATCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 722
DB      881 TGATCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 940
QY      723 TGCAGAAATGAGGCTTTTACCCAAACCATGATGATGATGATGATGATGATGATGATGATG 782
DB      941 TGCAGAAATGAGGCTTTTACCCAAACCATGATGATGATGATGATGATGATGATGATGATG 1000
QY      783 GATAGTCTTAGATGATGAATCAATCGATGATGATGATGATGATGATGATGATGATGATG 842
DB      1001 GATAGTCTTAGATGATGAATCAATCGATGATGATGATGATGATGATGATGATGATGATG 1060
QY      843 AACCTGTGACAACTT---ACCAAAATGCGATGTTCTCAAGTTAATTTCTACTTA 899
DB      1061 GAGCTGTGACAACTTATTAACCAAAATGCGATGTTCTCAACTTAAATGTCTACTTA 1120

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XX Thomas CJR, Mcpherson MJ, Atkinson HU, ' Neelam A;
PI WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAVI and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 1.6e-166;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAGGTGATGCTTGTAGTGTGTGAGCGTTAATAGCGTGCCTCATTTGTCACCACTTC 62
DB 221 GAAGATGAGTGTGATGCTGTGTGAGCAATATCAATATGCTCTATTCGACCACTTC 280
QY 63 AACTTGTCCATTAATATGATCACTTTGATGCTGGAATGCAACCATTAATATATG 122
DB 281 AACTTGGGCTGTGAAATCAATCATCTACATGTTGGAAGTACCATTTGCAAAATACGC 340
QY 123 CACCTTATGAGATCTCTGTATATCAAGGAAAGATCCAAACTAAATGATGCAAT 182
DB 341 CACTTTTGTGATGATCTGTATATGAGGAAAGATCCAACTTAAATGCTATGCAAT 400
QY 183 ACCAATGCTACCTGATATCTAATTCGACCCCTAATGCTTATTTAGCTCCAGGTGC 242
DB 401 ACCAATGCTGCCAATATCAATATCAATGCAATGCAATGCTGTGAGTCCAGGTTC 460
QY 243 AAACTTAAATACCTATTAATGCTGAGACGAAATTAATTAACGTGATGCTATTC 302
DB 461 AAATATATATATACCTATTAATGCTGAGACGAAATTAATTAATGCTGATGCTATTC 520
QY 303 TGATCCCTTCAATGAGATTAAGTGTGTTACCATATTAATTAAGATTTAACAAGCCGA 362
DB 521 TGATCCCTTGAACCAATTAATGCTGTACATATCTTTAATGATATCTCAGGTATCGA 580
QY 363 ACGCACTGATGAGATATCTTTGCTCAAGTTCTAGTTCGCTGTTGCAATGTCAT 422
DB 581 ACGCCAAAGATGAGATATCTTTGCTCAAGTTCTAGTTCGCTGTTGCAATGTCAT 640
QY 423 TAACTACATTAATGCTTATTCGACATGAGAAAGAAAGCAAGTAATCAAGAAATCA 482
DB 641 AAACCTTGTAGTGTGATATCAATGATGATGAAAGGCGGAGTAAATCAAGAAATCA 700
QY 483 AACTCAATTTGGGAATCAATATCTGACGATGCAATTTGAAAAATCTCGAGTTGATTC 542
DB 701 GGTTCACACTGGGAATTCATTAATCTGACAGATATTAATTTGAAAGATTTCTGAGTGTG 760
QY 543 ATTCCCTGTAAATCTGAGGCTTTTCTTACTGTAGGCAATCAATGTTTCAAGGC 602
DB 761 ATTCACTGAGAAACCGAAGCGCAATTCATTTGTAGGCAATCAATGTTTCAAGGC 820
QY 603 ACGCGATTCAGATATGAGAACCAAGTCAAGTCAATTTTAAATAGAGATTTCAACC 662
DB 821 ACCAAGATTCAGATATGAGAACCAAGTCAAGTCAATTTTAAAGAGATTTCAACC 880
QY 663 TGATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTCGAGGCAATTCACA 722
DB 881 TAAATCCCAAGTATTAATTTGAGAGAGAGATGGGCTTAAGATTTCAACGCAATTCATGA 940

QY 723 TGCCAAGATGGGGCTTTTACCCAAACCACTTGAAGTATGATGATGCAAGTACCAAGT 782
DB 941 TGCCAAGATGGAGTTTATCCAAACCTCTCAGATGATGATGATGATGATGATGATG 1000
QY 783 GATAGTCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 842
DB 1001 GATAGTCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
QY 843 AACCTGTCAGACACTT---ACCAATGCAATGTTCTGCAAGTATTAATTTCTA 899
DB 1061 GACTGTGACAGCACTTAATTAACCAATGCAATGTTCTGCAAGTATTAATTTCTA 1120
QY 900 TTATATTAATGCTTAATCTTGTGATCTAATTTGAAGATTTCTAA 945
DB 1121 TTATATTAATGCTTAATCTTGTGATCTAATTTGAAGATTTCTGA 1166

RESULT 9
AD105787
ID AD105787 standard; DNA; 1379 BP.
XX
AC AD105787;
XX
DT 15-APR-2004 (first entry)
XX
DE DNA encoding the wild-type pokeweed antiviral protein.
XX
KW ribosome depurination; antifungal; antiviral; virolytic; anti-HIV;
KW cytosolic; immunosuppressive; agricultural biotechnology; pharmaceuticals;
KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
KW de.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT 225..1166
FT CDS /tag= a
FT /product= "wild-type pokeweed antiviral protein"
XX
PN MO200262952-A2.
XX
PD 15-AUG-2002.
XX
PP 01-FEB-2002; 2002MO-US002792.
XX
PR 02-FEB-2001; 2001US-0266396P.
XX
PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE, Hudak KA, Parikh B;
XX
DR WPI; 2003-156656/15.
XX
DR P-PSDB; AD105788.
XX
PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT type PAP, useful in agricultural biotechnology or in the fields of
PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
PT or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 1; 51pp; English.
XX
XX The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
XX that is less toxic than wild-type PAP and exhibits ribosome depurination
XX activity, where the mutant is a central domain mutant or N-terminal
XX domain mutant. The PAP mutants have the following activities: antifungal,
XX antiviral, virolytic, anti-HIV, cytosolic and immunosuppressive. The PAP
XX mutants are useful in agricultural biotechnology as well as in the fields
XX of pharmaceuticals and medicine. The PAP mutants and methods are useful in
XX treating mammals with cancer, AIDS, viral infection or autoimmune
XX diseases associated with proliferations of unwanted T-cells or B-cells.
XX The transgenic plants are useful in exhibiting resistance to a broad

Best Local Similarity 82.2%; Pred. No. 3,9e-164;
Matches 780; Conservative 0; Mismatches 158; Indels 11; Gaps 5;

OY	1	ATGAAGTGAATGCTTGATGTTGGTGAAGTTAATAGGTGGCTCAATGCTGCACCACT	60
Db	1014	ATGAAGATGAATGCTGGTGGTGGTGGTGGATGATGATTTATCATGGCTCATTTCTTAACACCT	1073
OY	61	TCAACTTGTGCCATTAATACGATCACTTTGATGCTGGAATAGCCACATTAAACAATAT	120
Db	1074	TCAACTTGGGCCATTAATATCAATCACTTCGATGTTGGAAATGCAACCACTTAACAAGAT	1133
OY	121	GCCACTTTATGGAATCTCTTGTATATCAAGCGAAAGATCCAAACTTAAATGCTATGGC	180
Db	1134	GCCACTTTATGAAGATCAATCATATATCAAGGAAAGATCCCACTGAAGCTATATGGC	1193
OY	181	ATACCAATGCTACCTGATATCTAATTTGCAACCCCTAATGCTTAATGTTTAAGCTCCAAAGT	240
Db	1194	ATACCAATGTTGCCAATATCTAATTTAGCTCCCAAGTACTTGTGGTATACCTCCAAAT	1253
OY	241	GCAAACTTAAACCACTTACATATATGCTGAGACGAATTAATCTTATACGTATGGGCTAT	300
Db	1254	TCAAGTTTAAACCACTCACTATATGCTGAAGCGAAACAATCTGTATGTATGGGCTAT	1313
OY	301	TCTGATCCCTTCAATGCGAATATAGTGTGTTACATATATTTAATGATATTTACA---AGC	357
Db	1314	GCTGACACTTATATATGGC---AAGGTGTTATCATATATTTAAGATATCTCAAAATCT	1370
OY	358	ACCGAAGCATGATGTTGAGAAATCTCTTTGCTCAAGTTCAATGTTCTGGTGGCAATG	417
Db	1371	ACTGACGAAATGATGTATGATGCTACTTTGGCCAAATCCGAAGTTCTGGTGGTGA	1430
OY	418	TCCAATTACTACATATAGCTTATATCCGACATGAGAAAGAAAGCAGAAATTAATCTCAGA	477
Db	1431	AACATTACTATGATATAGCATTTATCAACATTGGAAGAAAGAAAGTATGAGACG---CMAA	1487
OY	478	AATCAATCTCAATTTGGGAATTCAAATACTCAGCACTGACATTGGAAAAATCTCTGAGTT	537
Db	1488	AGTCAAGTCCAACTCGGAATTCAAATACCTCAACAGTGCATTGGAAAGATCTATGAGTGTG	1547
OY	538	GATTCATTCCTCGTAAACCTGAGGCTTTTTCCTACGTGATAGCATCCAAATGGTTTCA	597
Db	1548	GATTCATTCCTGAGAAACCTGAGGCGGAATTCCTGTTATGATGCGATCCAAATGGTTTCA	1607
OY	598	GAGCAGCGCATTCACATATAGAGAACCAAGTCAAGACTAATTTTAAATAGACATTC	657
Db	1608	GAGCAGCGCGGTTCAATGATCATGAGAAATCAGGTGAAGACTAATTTTAAATAGACATTC	1667
OY	658	TACCTGATCCCAAGTATTAATTTTGGAGAGAAATGGGGCAAAATCTCTGAGGCAAT	717
Db	1668	TACCTGATCCCAAGTACTTAACTTGAAGAGAGATGGGGTAAAGATCTTACGCGAAT	1727
OY	718	CACAAATGCCAAGATTTGGGCTTTTACCCCAACCACTTGAAGTATGATGACCAAGATACC	777
Db	1728	CACAAATGCCAAGATTTGGGCTTTTAAACCAAGTCTCTGAAGCTTAAATAATGCGATAGC	1787
OY	778	AAGTGAATGATCTTAGAGTGAATGAAATCAATCGATGTTGGCAGCTCTTAAGTACGTT	837
Db	1788	AAGTGAATGATCTGAAGTGAATGATATCAACTGATATGGGAGCTCTTAAGTATGTT	1847
OY	838	AATGGAACCTGTCAACAACCTTACCAAAATGCCATGTTCTCTCAAGTTAATATTTCACT	897
Db	1848	AATGGAACCTGTCAAGGCAACTTACCAAAAGTCCATGTTCCCTC-ACCTATATGCTACT	1906
OY	898	TATATATATTTATGTCTAATCTTGGTGA-TCATTTGAAGAGATTTCTTA	945
Db	1907	TATATATATTCATGTCTAATCTTGGTGACTCTATTTGGAAGAGATTTCTTA	1955

Search completed: April 9, 2006, 00:50:33
Job time : 571.609 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 4476.73 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atcaagtcgtctgtctgtac.....atctattgaagattctaa 945

Scoring table: IDENTITY_NUC

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	87	9.2	993	2	BE035039
C 2	80.6	8.5	816	2	BE035038
3	65.6	6.9	1033	2	BE035037
4	62.2	6.6	498	5	BE035036
5	61.6	6.5	829	7	BE035035
6	59	6.2	649	6	BE035034
7	59	6.2	649	6	BE035033
8	59	6.2	649	6	BE035032
9	59	6.2	649	6	BE035031
10	59	6.2	649	6	BE035030
11	59	6.2	649	6	BE035029
12	57.4	6.1	639	6	BE035028
13	55.4	5.9	1038	2	BE035027
14	52.4	5.5	405	8	BE035026
15	50.8	5.4	639	8	BE035025
16	47.2	5.0	837	1	BE035024
17	46.6	4.9	489	2	BE035023
18	45.4	4.8	267	1	BE035022
19	44.6	4.7	1021	2	BE035021
20	44.4	4.7	701	9	BE035020
21	43.6	4.6	919	10	BE035019
22	42.6	4.5	414	10	BE035018

C 23	42.4	4.5	561	9	AQ156306
C 24	42.4	4.5	1101	10	CNS0039G
C 25	41.8	4.4	717	9	BH974953
C 26	41.8	4.4	658	10	CZ857242
C 27	41.6	4.4	571	7	CG298356
C 28	41.1	4.3	788	10	CG690741
C 29	40.8	4.3	1001	10	CNS0078B
C 30	40.4	4.3	228	10	CG503780
C 31	40.4	4.3	307	4	AK190946
C 32	40.4	4.3	431	10	CG517501
C 33	40.4	4.3	525	6	CA548609
C 34	40.4	4.3	526	10	CL256443
C 35	40.4	4.3	557	1	AM230870
C 36	40.4	4.3	553	9	AO670952
C 37	40.4	4.3	575	5	BU743805
C 38	40.4	4.3	579	3	BU365833
C 39	40.4	4.3	616	5	BY729128
C 40	40.4	4.3	630	7	CO102355
C 41	40.4	4.3	635	1	AM323815
C 42	40.4	4.3	685	2	BG920190
C 43	40.4	4.3	812	6	CA751457
C 44	40.4	4.3	812	7	CV557169
C 45	40.4	4.3	813	5	BU961361

ALIGNMENTS

RESULT 1
BE035039/c
LOCUS
DEFINITION
antiviral protein, mRNA sequence.
ACCESSION
BE035039
VERSION
BE035039.1
KEYWORDS
EST.
ORGANISM
Mesembryanthemum crystallinum (common iceplant)

BE035039
NM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.

REFERENCE
AUTHORS
Bohrer, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers
1..993

FEATURES
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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
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/cell_type="epidermal bladder cells"
/dev stage="12 weeks old"
/clone lib="NM"
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

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Best local similarity 60.1%; Pred. No. 5.6e-12;
Matches 163; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

DB 455 AGAAGCAGAGTAACTCAAGAAATCAAGTCAATGGATTCAGAACTCAGCAGT 514
681 AGAAGCTGCGGTCAAGCAGAAACAGTATGAGTTGGGGCTTCAACTAGAGTTTG 622

QY	ACATTTGGAAAAAATCTCTGGAGTTGATTCATTCCTCCGTAAATAACGAGCTTTTTCAC	574
DB	621 CCATGAGTGCATTTATATGTATAAAAAACGATGATGGAACTCGAGGCGAAATTCCTTAC	562
QY	575 TGTGAGCCATCCAAATGGTTTCAGAGGAGCGCGATTCAAGTACATAGAACCAAGT--	632
DB	561 TGATTGCCATCCAGATGGTTTCAGAAAGCAGCAGGTTCCATTATATCGAGACTAAGTGA	502
QY	693 -CAAGACTAATTTTAAATATAGAGATTCTACCTCGATTCGCCAAAGTAAATTAATTTGGAGAGA	691
DB	501 CCGAAGTGGGTCACATGGTTTCGTTCAACCGCATCGAAAGTGAATTAATTCGAGAAC	442
QY	692 AGTGGGCGAAATCTCTGAGGCAATTCACAA	722
DB	441 ACTGGGAAAGATTTCCGATGATGATTCATTA	411
RESULT 2		
LOCUS	BE035038/c	
DEFINITION	BE035038 816 bp mRNA linear EST 07-JUN-2000	
ACCESSION	BE035038	
VERSION	BE035038.1	
KEYWORDS	EST.	
SOURCE	Meesembryanthemum crystallinum (common iceplant)	
ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alizaceae; Meesembryanthemum.	
REFERENCE	1 (bases 1 to 816)	
AUTHORS	Bonner, H. J., Borcherdt, C., Brazille, S., Brooks, J., Baton, M., Ferreira, H., Kwanaki, S., McColough, A., Michalowski, C. B., Palacio, C., Scara, G., Wheeler, M., and Zepeda, G. R.	
TITLE	Functional Genomics of Plant Stresses Tolerance	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Michalowski, C. B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: cbm@u.arizona.edu.	
FEATURES	location/Qualifiers	
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	/mol_type="mRNA"	
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	/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2: XhoI; plants stressed 6 weeks in 500mM NaCl"	
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Query Match	8.5%; Score 80.6; DB 2; Length 816;	
Best Local Similarity	58.7%; Pred. No. 2.8e-10;	
Matches 159; Conservative	0; Mismatches 109; Indels 3; Gaps 1;	
QY	455 AGAAAGCAAGTAACTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAGTG	514
DB	680 AGAAACCTCGCGGTACACCGAAACAGTATGACGTGGGGCTTGCTAAATAGAGTTGG	621
QY	515 ACATTGGAANAATCTCTGAGTGTGATTATCCCGTAAANAAGAGGCTTTTTCAC	574
DB	620 CCATTCGATCAATTTATGTATAAAAAACGATGATGGAACTCGAGGCGAAATTCCTTAC	561
QY	575 TGTGAGCCATCCAAATGGTTTCAGAGGAGCGCGATTCAAGTACATAGAACCAAGT--	632
DB	560 TGATTGCCATCCAGATGGTTTCAGAAAGCAGCAGGTTCCATTATATCGAGACTAAGTGA	501
QY	693 -CAAGACTAATTTTAAATATAGAGATTCTACCTCGATTCGCCAAAGTAAATTAATTTGGAGAGA	691

LOCUS	DEFINITION	LOCUS	DEFINITION
Db	500 CCGAAGGGGTACATGTTTCGTTCAACCCGATCCGAAGGTATTAACTTGGAGAAC 444	Qy	692 AGTGGGGCAAAATCTGTGAGCAATTACCA 722
Db	440 ACTGGGGAAGATTTCGATGATGATTCATAA 410	Db	690 GAAAGTGGGGCAAAATCTTCTGAGGCATTACA 721
RESULT 3		Db	433 CAATTGGGGGAAGATTTCGCAAGATTCATA 464
BE036541	1033 bp mRNA linear EST 07-JUN-2000		
LOCUS	MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to		
DEFINITION	antiviral protein, mRNA sequence.		
ACCESSION	BE036541		
VERSION	BE036541.1 GI:8331550		
KEYWORDS	EST.		
SOURCE	Mesembryanthemum crystallinum (common iceplant)		
ORGANISM	Mesembryanthemum crystallinum		
REFERENCE	Eukaryote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.		
AUTHORS	1 (bases 1 to 1033) Bohner, H.J., Borchert, C., Brazille, S., Brooke, J., Baton, M., Palmer, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacios, C., Scara, G., Wheeler, M. and Zepeda, G.R.		
TITLE	Functional Genomics of Plant Stress Tolerance		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Michalowski, C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: cdm@u.arizona.edu An open reading frame exists. Location/Qualifiers 1..1033 /organism="Mesembryanthemum crystallinum" /mol_type="mRNA" /db_xref="taxon:3544" /feature_type="apical meristem and leaf primordia" /dev_stage="6 weeks" /clone_id="MP" /note="3 d 500mM NaCl"		
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source			
ORIGIN			
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Best Local Similarity	55.1%; Pred. No. 3e-06;		
Matches 150; Conservative	0; Mismatches 119; Indels 3; Gaps 1;		
Qy	453 AAGAAGACAGAACTCAAGAAATCAAGTCCATTGGGAATTCAAATACACAG 512	Qy	573 ACTGGTGCATTCGAATGGTTTCTGAGAGGACGCCGATTCAGATCAATAGAACCAAGT 632
Db	193 AGAGAAAGCTGCAAGCAGCCGAATTCAGATTAAGTTAGGGTGAATTAACTAGAGTT 252	Db	373 GACCCAAAGTGGGTACATGGCTGTTCAATCCGACCCGAAGTGTGATTTGGAGAA 432
Qy	513 TGACATTGGAAAAATCTCTGGAATTGATTGATTCCTGTAAAAATGAGGCTTTTTCT 572		
Db	253 TGCATTCGAGTCGGTTTGTGTAAAGACCCGATTAATGAGCAGGTGAGGCCAAATCTT 312		
Qy	573 ACTGGTGCATTCGAATGGTTTCTGAGAGGACGCCGATTCAGATCAATAGAACCAAGT 632		
Db	313 GCTAATTGCTATACACATGGTTTCTGAGACGACCGGTTTAAGTAAATTGAAGTAAGT 372		
Qy	633 ---CAAGACTAATTTTATAGACATCTTACCCGTGATCCCAAGTAATTAATTATTTGAGAA 689		
Db	373 GACCCAAAGTGGGTACATGGCTGTTCAATCCGACCCGAAGTGTGATTTGGAGAA 432		
Qy	690 GAAAGTGGGGCAAAATCTTCTGAGGCATTACA 721		
Db	433 CAATTGGGGGAAGATTTCGCAAGATTCATA 464		
RESULT 4			
BE0588134	498 bp mRNA linear EST 06-DEC-2002		
LOCUS	BD12317-024-009-G14-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone		
DEFINITION			

024-009-G14 5-PRIME, mRNA sequence.
BQ588134
VERSION BQ588134.1 GI:26117717
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 498)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drunowski,M., Stal,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 498 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
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/mol_type="mRNA"
/culivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184726"
/db_xref="taxon:161934"
/clone="024-009-G14"
/tissue_type="leaf"
/lab_host="EMD10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet library provided by KWS Kleinwanzlebener Saatgut AG Rihbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polYA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN
Query Match 6.6%; Score 62.2; DB 5; Length 498;
Best local Similarity 56.7%; Pred. No. 2.1e-05;
Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;
QY 83 TCACCTTTGATGCTGGAATGCGACATTAAACAATATGCGACCTTATGGAATCTCTTC 142
DB 169 TAACTTTTACCTTGAAGAGCTTCAAGACAAAATATGSCACTTTCTTAAGAACTTAC 228
QY 143 GTATATACGGAAGATCCAAAATCTAAATGCTATGCGCATCAATGCTACTGATATCA 202
DB 229 GGAACATATGGAAGGATTCAAAGCTATGATACGAAGAAATCCAAATGCTCCCGCACCAT 288
QY 203 ATTGACCCCTAGTACTTATGTTAGTCAAGTCCAAAGTGCGAA-----CTTAAAA 253
DB 289 CAAACACGAAATATCTTTTATGCGAGCTTAAAGCTTAAAAAGCCGGTACTGACATTA 348
QY 254 CCATTAAGTAAATGCTGAGACGAATAATCTTATACGTATGAGGCTATTCATCCCTTCA 313
DB 349 CCATCACTGCTGTTAGCAAAAATGACTTATATATGATGAGGCTTTTACGATCAAGTNG 408
QY 314 ATGGCA 320
DB 409 CAGGTAA 415

RESULT 5
LOCUS CN782289
DEFINITION EST00385 cgeed Chenopodium quinoa cDNA clone 802J22 5' similar to antiviral ribosome-inactivating protein CAP308 (Chenopodium album), mRNA sequence.
ACCESSION CN782289
VERSION CN782289.1 GI:47561753
KEYWORDS EST.
SOURCE Chenopodium quinoa (quinoa)
ORGANISM Chenopodium quinoa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
AUTHORS Cole,N.D., Coleman,C.E., Christensen,S.A., Jellen,E.N., Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and Maughan,P.J.
TITLE Development and use of an expressed sequenced tag library in quinoa (Chenopodium quinoa Willd.) for the discovery of single nucleotide polymorphisms
JOURNAL Plant Sci. 168 (2), 439-447 (2005)
COMMENT Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig_coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.
Location/Qualifiers
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/organism="Chenopodium quinoa"
/mol_type="mRNA"
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/clone="802J22"
/tissue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_lib="cgeed"
/note="Vector: pTRIPLEX2; Site 1: SfiI; Site 2: SfiI; Developing Seed cDNA library from Chenopodium quinoa"

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Best local Similarity 51.2%; Pred. No. 3.4e-05;
Matches 291; Conservative 0; Mismatches 244; Indels 33; Gaps 5;
QY 99 AAATGCCACCATTAACAATATGCGACCTTTATGGAATCTTCTGTAATCAAGCGAAGA 158
DB 115 AAAACCTACAGAAATATTATTAACCTTTCTGGAAGATATACGACCAACTAAGA 174
QY 159 TCCAAACCTAAATGCTATGCGATACCAATGCTACTGATTAATTCAGCCCTTAAGA 218
DB 175 TCCAAAGCTATGATGGAAGGATCCCAATGATCCGACCAACCAACCCAGATACATA 234
QY 219 CTATATGTTAGTTCGAAGTCAAGCAACTTAAGC-----CATTAAGTATGCT 269
DB 235 TCTTTTGGTGAACCTTGAATCTTAAAGATTAAGATTAATTCATTAACCTTGCTT 294
QY 270 GAGAGAAATTAATTATACGTATGAGGCTATTTCTGATCCCTTCAATGGCAATAGTGTG 329
DB 295 AAGTGAAGACGACTGATGATGAGGCTTCTGCTATTAATTTGAGGCAAGTTGCGGG 354
QY 330 TTACCATATTTTATATGATATTAACAAGCAGCAAGCACTGATGAGGAATACTCTTG 389
DB 355 CCAATTTCTTTTCAATCTTAACATTGACACCACTTGATTAAGGCAAGAA---AGTTTTC 410
QY 390 CTCAAGTTCTAGTCTCGTGTGCAATGTCATTAATCAATAGCTTATATCCAGCAT 449

Db 411 CAGAACTCAGGTTTTC-----ATAATATTAAGTATGGGAAAGTTACAGTCAAAAT 462
450 GGAAGAAAGAGAGAGTAAGTCAAGAAATCAAGTCAATGGGAATTCAAATCTCAG 509
Qy 463 CGAAGCAATGCTGTGTAACACCGATTAAAGT--TTCCGTTGGGGTTGATTAACCTTAA 519
Qy 510 CAGTGCATTTGAGAAATCTCTGAGTTGATTCATTCCTCTGA-----AAATCTGA 560
Db 520 AACTTACATGAGAAAGCTTATGGGATGATCTAAGGCCAAAGATTATAGCAAACTGA 579
Qy 561 GGCTTTTCTTACTGCTGAGCCATCCAAATGTTTCAGAGGACGCCGATTCAGTACAT 620
Db 580 AGCTCGTTCCTACATCATGCGATTCAAATGTTGACAGAGCGCGCTTTCAGATCAAT 639
Qy 621 AGAGAACCAAGTCAAGACTAATTTAAT 648
Db 640 CCAAGGAGAGCTATGCTTACTACAAAT 667

RESULT 6
CA838757 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5,
mRNA sequence.
ACCESSION CA838757
VERSION CA838757.1 GI:26566522
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)
JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
FEATURES
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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
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/clone="MCT020B02"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Query Match 6.2%; Score 59; DB 6; Length 649;
Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

Qy 453 AAAGAAAGCAGAGTAAGTAACTCAAGAAATCAAGTCCAAATGGGAATTCATATCAGCAG 512
Db 87 AAGAAATGCTGAAACCAACAGACGAGGAGGATTAAGTTAGGGTGAATTAAGTAACTAGAGTT 146
Qy 513 TGCATTTGAGAAATCTCTGAGTTGATTCATTCCTCTGTAATAAAGTACGCTTTTCTCT 572
Db 147 TCGATTCGAGTGGCTTATGTAAGATCGCAAGTCAAGAGAAATGAGGGCCAAATTCCT 206
Qy 573 ACTGGATGCAATCCAAATGTTTCAGAGGACGCGGATTCAGTCAATAGAACCAACAT 632
Db 207 GCTGATGCAATACAGATGTTTCTGAGCAGCAAGTTCAAGTATATGAGATTAAGT 266
Qy 633 CAGACTAATTT-----TAATAGACATTTACCTGATCCCAAGTAATTAATTTGA 686
Db 267 GAACCAAGTGGGCTTAATTAATTAATTCGTTCTTACCCGACCCGAAATGCTCTTTTGA 326
Qy 687 GGAAGATGGGGCAAAATCTCTGAGGCAATTCA 719
Db 327 GACCAATGGGGGAGAGATTTCCGACGAGATTC 359

RESULT 7
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5,
mRNA sequence.
ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)
JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.
FEATURES
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location/Qualifiers
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT026C11"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Query Match 6.2%; Score 59; DB 6; Length 649;

Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAAGTAATACTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAG 512
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Db 87 AGAAGATGCTGCACCAACCAAGAGAGCCATAGATTAGGGGTGATTAATCTAGAGTT 146
| | | | |
QY 513 TGACATTTGAAAAATCTCTGAGAGTTGATTCAATCCCTGTAAATACTGAGCTTTTCTTCT 572
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Db 147 TGGCATGAGTGGGTTTATGTGTAGACATGACAGATGAGGAATGAGCCCAATCTT 206
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QY 573 ACTGTAGCCATCCAAATGTTTCAAGAGCGCCGATTCAGTACATAGAAACCAAGT 632
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Db 207 GCTGATGCCATACAGATGTTTCTGAAGCAGAGGTTCAAGTATATGAGAGTAAGT 266
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QY 633 CAAGACTAATTT-----TAATAGACATTTACCTGATCCCAAGTAATTAATTGGA 686
| | | | |
Db 267 GAACCAAAAGTCCGTAGATTATGAAATGTTCTTACCCGACCCGAAAAATGCTGCTTTTGA 326
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QY 687 GGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCA 719
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Db 327 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 359
| | | | |

RESULT 8
LOCUS CA835532 661 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS038A11.160572 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM); Mesembryanthemum crystallinum cDNA clone MCS038A11.5, mRNA
sequence.

ACCESSION CA835532
VERSION CA835532
KEYWORDS CA835532.1 GI:26563297
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alismaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 661)
Cushman, J.C.

AAn expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC

JOURNAL Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

COMMENT PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
Location/Qualifiers
1. .661

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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS038A11"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.2%; Score 59; DB 6; Length 661;

Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAAGTAATACTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAG 512
| | | | |
Db 98 AGAAGATGCTGCACCAACCAAGAGAGCCATAGATTAGGGGTGATTAATCTAGAGTT 157
| | | | |
QY 513 TGACATTTGAAAAATCTCTGAGAGTTGATTCAATCCCTGTAAATACTGAGCTTTTCTTCT 572
| | | | |
Db 158 TGGCATGAGTGGGTTTATGTGTAGACATGACAGATGACAGAAATGAGCCCAATCTT 217
| | | | |
QY 573 ACTGTAGCCATCCAAATGTTTCAAGAGCGCCGATTCAGTACATAGAAACCAAGT 632
| | | | |
Db 218 GCTGATGCCATACAGATGTTTCTGAAGCAGAGGTTCAAGTATATGAGAGTAAGT 277
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QY 633 CAAGACTAATTT-----TAATAGACATTTACCTGATCCCAAGTAATTAATTGGA 686
| | | | |
Db 278 GAACCAAAAGTCCGTAGATTATGAAATGTTCTTACCCGACCCGAAAAATGCTGCTTTTGA 337
| | | | |
QY 687 GGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCA 719
| | | | |
Db 338 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 370
| | | | |

RESULT 9
LOCUS CA839511 671 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT028D04.172117 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM); Mesembryanthemum crystallinum cDNA clone MCT028D04.5,
mRNA sequence.

ACCESSION CA839511
VERSION CA839511
KEYWORDS CA839511.1 GI:26567276
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alismaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 671)
Cushman, J.C.

An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC

JOURNAL Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

COMMENT PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.
Location/Qualifiers
1. .671

FEATURES
source
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the

according to Stratagene's recommended protocol for the

metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.2%; Score 59; DB 6; Length 689;
 Best Local Similarity 53.8%; Pred. No. 0.0016;
 Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAGAACTGAAGAAATCAAGTCCAAATTCGAAATTAATCTCAGAG 512
 DB 98 AGAATAAGCTGCAACCAACGACGAGACCATAGAGTGGGGTGAATTAATCAGAGTT 157
 QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCTCCCTGTAATAAATGAGGCTTTTCT 572
 DB 158 TGGCATGAGTCGGGTTATGTTAGACATGACATGACATGAGAAATGAGCCAAATTCCT 217
 QY 573 ACTGTAGCCATCCAAATGTTTCAAGGACGCGCATTCAGATACATAGAAACCAAGT 632
 DB 218 GCTGATTGCCATACAGATGTTTCTGAAGCAGCAAGTTCAAGTATATGAGAGTAAAGT 277
 QY 633 CAAGACTAATTT-----TAATAGCATTTCTACCTGATCCCAAGTAATTAATTGGA 686
 DB 278 GAACCAAGTCGTTAGATTGATGATCGTTCTTACCCGACCCGAAATGCTGCTTTTGA 337
 QY 687 GGAGAGTGGGGCAAAATCTCTGAGGCAATTC 719
 DB 338 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 370

RESULT 12

CA835855 639 bp mRNA linear EST 12-DEC-2002
 MCS004G12_161218 Ice plant Lambda Uni-Zap XR expression library, 5
 days 0.5 M NaCl treatment; Crassulacean acid metabolism, phase I (2
 AM). Mesembryanthemum crystallinum cDNA clone MCS004G12 5, mRNA
 sequence.

ACCESSION CA835855
 VERSION CA835855.1
 KEYWORDS GI:26563620
 SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
 Mesembryanthemum crystallinum

REFERENCE Baktayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Alzooaceae; Mesembryanthemum.
 1 (bases 1 to 639)
 Cushman, J.C.

AAn expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 Unpublished (1997)

JOURNAL COMMENT
 Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 004 row: G column: 12
 Seq primer: T3 20mer
 High quality sequence stop: 639.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS004G12"
 /tissue_type="leaf"
 /dev_stage="five-week-old"

ORIGIN

Query Match 6.1%; Score 57.4; DB 6; Length 639;
 Best Local Similarity 53.5%; Pred. No. 0.0043;
 Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAGAACTGAAGAAATCAAGTCCAAATTCGAAATTAATCTCAGAG 512
 DB 98 AGAATAAGCTGCAACCAACGACGAGACCATAGAGTGGGGTGAATTAATCAGAGTT 157
 QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCTCCCTGTAATAAATGAGGCTTTTCT 572
 DB 158 TGGCATGAGTCGGGTTATGTTAGACATGACATGACATGAGAAATGAGCCAAATTCCT 217
 QY 573 ACTGTAGCCATCCAAATGTTTCAAGGACGCGCATTCAGATACATAGAAACCAAGT 632
 DB 218 GCTGATTGCCATACAGATGTTTCTGAAGCAGCAAGTTCAAGTATATGAGAGTAAAGT 277
 QY 633 CAAGACTAATTT-----TAATAGCATTTCTACCTGATCCCAAGTAATTAATTGGA 686
 DB 278 GAACCAAGTCGTTAGATTGATGATCGTTCTTACCCGACCCGAAATGCTGCTTTTGA 337
 QY 687 GGAGAGTGGGGCAAAATCTCTGAGGCAATTC 719
 DB 338 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 370

RESULT 13

BE033546 1038 bp mRNA linear EST 07-JUN-2000
 BE033546
 LOCUS MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
 ribosome-inactivating protein, mRNA sequence.

ACCESSION BE033546
 VERSION BE033546.1
 KEYWORDS GI:8328555
 SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
 Mesembryanthemum crystallinum

REFERENCE Baktayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Alzooaceae; Mesembryanthemum.
 1 (bases 1 to 1038)
 Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
 Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
 Palacio, C., Scarpa, G., Wheeler, M., and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu

An open reading frame exists.
 Location/Qualifiers
 1. 1038
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /tissue_type="Root"
 /dev_stage="5-6 weeks old"
 /clone_lib="MF"
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
 XhoI"

FEATURES

1. 1038
 Location/Qualifiers
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /tissue_type="Root"
 /dev_stage="5-6 weeks old"
 /clone_lib="MF"
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
 XhoI"

ORIGIN

Query Match 5.9%; Score 55.4; DB 2; Length 1038;

Best Local Similarity 52.7%; Pred. No. 0.0016;
Matches 14; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 453 AAGAAAGCAGAAAGTAATCAAGAAATCAAGTCCATTTGGGAAATTCAAATACACAG 512
| | | | |
DB 286 AGAAGAGCTGCAGAAAGAGCCGAAATGCATAGATTAGGGGTGAATTAACAGATT 345
| | | | |
QY 513 TGACATTGAAAATCTCTGAGATTGATTCATTCCTGTAAATACTAGAGCTTTTCT 572
| | | | |
DB 346 CGGATGAGATCGGTTTGGTAAAGACCGATTAATGGGAGGTTGAGGCCAAATCTT 405
| | | | |
QY 573 ACTGTAGCATCCAAATGTTTCAAGAGAGCCGATTCAGATCAATAGAACCAAGT 632
| | | | |
DB 406 GCTGATTGCTATCAGATGGTCTCTGAGAGCAGCGGTTTAAGTTTGAAGTAAAGT 465
| | | | |
QY 633 CA---AGACTAATTTTATAGACATTCACCTGATCCCAAGTAATTAATTGGAGGA 689
| | | | |
DB 466 GACCCAAAGTGGTGTATATGCTTTTCAACCCGACCCGAAAGTCTGAGTTGGTGA 525
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QY 690 GAAGTGGGCAAAATCTCTGAGGCAATTCACAA 722
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DB 526 CAATTGGGTGACATTTTCCATGAGACTCATAA 558
| | | | |

RESULT 14
T24255 405 bp mRNA linear EST 28-JUL-1995
LOCUS t24255 lambdaZAPST Ricinus communis cDNA clone pcrs1345, mRNA
DEFINITION
ACCESSION T24255
VERSION T24255.1 GI:689074
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoidae;
Acalyphaeae; Ricinus.
REFERENCE 1 (bases 1 to 405)
vandeloo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
JOURNAL
COMMENT Contact: Somerville CR
Carnegie Institution
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3
Location/Qualifiers
1. 405
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone_lib="pcrs1345"
/clone="lambdaZAPST"
/note="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI;
Poly(A) + RNA was purified from developing stage III to
Stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN
Query Match 5.5%; Score 52.4; DB 8; Length 405;
Best Local Similarity 59.2%; Pred. No. 0.0084;
Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

QY 555 AACTGAGGCTTTTCTTACTGTGACCATCAATGATTTTCAGAGCAGCGGATTCAA 614

DB 82 AACCTGGCTCGTTCCTTATGTTGATCCAAATGATTCAGAGCAGCAAGATTCCA 141
| | | | |
QY 615 GTACATAGGAACCAAGTCAAGCTAATTT-----AATAGCATTTCAACCTGATCC 668
| | | | |
DB 142 GTACATTGAGGAGAAATGCGCAGAAATTAGGTACACCGAAGATCTGCACACGATCC 201
| | | | |
QY 669 CAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTGTAGAGCAATTCACA-ATGCCA 727
| | | | |
DB 202 TAGGTATATTAACCTTNAAGAAATGTTGGGAGACCTTCCACATTCATAAAGACTA 261
| | | | |
QY 728 AGATGGGCTTTTACCAACCACTTGAGCT 758
| | | | |
DB 262 ACCAAGAGCGCTTGTGATGCCANTTCAACT 292
| | | | |

RESULT 15
BE037217 639 bp mRNA linear EST 07-JUN-2000
LOCUS BE037217
DEFINITION MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein/antiviral protein, mRNA sequence.
ACCESSION BE037217
VERSION BE037217.1 GI:8332233
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Rosaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 639)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Feirer, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
JOURNAL
COMMENT Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
Location/Qualifiers
1. 639
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/ribseq_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN
Query Match 5.4%; Score 50.8; DB 2; Length 639;
Best Local Similarity 61.2%; Pred. No. 0.025;
Matches 104; Conservative 0; Mismatches 57; Indels 9; Gaps 1;

QY 463 GAAGTAATCTCAAGAAATCAAGTCAATGGGAATTCATCAATCTCGAGTCATTTGA 522
| | | | |
DB 308 GAGAGCTAAGGAGAAAGAGATGCATTTGATTTAGTAAGTAATAGTTTCAATAAA 367
| | | | |
QY 523 AAATCTGAGGATTCATTCCTGTAAATAGAGGCTTTTCTTACTGTAGGCC 582
| | | | |
DB 368 AACAGC-----GATTAATGATGAAAAGATGAGGCTTACATTTCTTGTAGTTGG 418
| | | | |
QY 583 ATCCAAATGTTTCAAGAGCAGCGGATTCAGATCATATGAGAACCAAGT 632
| | | | |
DB 419 ATTCAATGTTTGTGAGGCTGACGCTCTCTTACATACAGAGAAAGGT 468
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Job time : 4477.73 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 328.047 Seconds
(without alignments)
5120.590 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	634	67.1	1195	2 US-08-373-858-1	Sequence 1, Appl1
2	634	67.1	1195	2 US-08-342-7868-1	Sequence 1, Appl1
3	632.4	66.9	1379	2 US-08-500-611-1	Sequence 1, Appl1
4	632.4	66.9	1379	2 US-08-500-694-1	Sequence 1, Appl1
5	632.4	66.9	1379	3 US-07-865-169-1	Sequence 1, Appl1
6	632.4	66.9	1379	3 US-09-005-273-1	Sequence 1, Appl1
7	632.4	66.9	1379	6 PCT-US96-11546-1	Sequence 1, Appl1
8	630.8	66.8	1379	3 US-08-501-253A-1	Sequence 1, Appl1
9	629.2	66.6	1379	3 US-07-865-169-2	Sequence 2, Appl1
10	629.2	66.6	1379	3 US-09-005-273-3	Sequence 3, Appl1
11	543.8	57.5	918	2 US-08-138-636-1	Sequence 1, Appl1
12	543.8	57.5	918	2 US-08-319-622A-1	Sequence 1, Appl1
13	543.8	57.5	918	2 US-08-471-564-1	Sequence 1, Appl1
14	88.4	9.4	804	2 US-08-356-161-6	Sequence 6, Appl1
15	88.4	9.4	804	2 US-08-356-161-7	Sequence 6, Appl1
16	88.4	9.4	804	3 US-08-718-904-22	Sequence 22, Appl1
17	88.4	9.4	804	3 US-08-718-904-23	Sequence 22, Appl1
18	88.4	9.4	804	3 US-09-449-249-22	Sequence 22, Appl1
19	88.4	9.4	804	3 US-09-449-249-23	Sequence 23, Appl1
20	88.4	9.4	804	6 PCT-US93-05702-6	Sequence 6, Appl1
21	88.4	9.4	804	6 PCT-US93-05702-7	Sequence 7, Appl1
22	88.4	9.4	804	6 PCT-US95-10973A-6	Sequence 6, Appl1
23	88.4	9.4	804	6 PCT-US95-10973A-7	Sequence 7, Appl1
24	88.2	9.3	774	6 PCT-US91-05766-1	Sequence 1, Appl1

25	82	8.7	804	2 US-08-356-161-4	Sequence 4, Appl1
26	82	8.7	804	3 US-08-718-904-20	Sequence 20, Appl1
27	82	8.7	804	3 US-09-449-249-20	Sequence 20, Appl1
28	82	8.7	804	6 PCT-US93-05702-4	Sequence 4, Appl1
29	82	8.7	804	6 PCT-US95-10973A-4	Sequence 4, Appl1
30	80.4	8.5	804	2 US-08-356-161-3	Sequence 3, Appl1
31	80.4	8.5	804	2 US-08-356-161-5	Sequence 3, Appl1
32	80.4	8.5	804	3 US-08-718-904-19	Sequence 19, Appl1
33	80.4	8.5	804	3 US-08-718-904-21	Sequence 21, Appl1
34	80.4	8.5	804	3 US-09-449-249-19	Sequence 19, Appl1
35	80.4	8.5	804	3 US-09-449-249-21	Sequence 21, Appl1
36	80.4	8.5	804	6 PCT-US93-05702-3	Sequence 3, Appl1
37	80.4	8.5	804	6 PCT-US93-05702-5	Sequence 5, Appl1
38	80.4	8.5	804	6 PCT-US95-10973A-3	Sequence 3, Appl1
39	80.4	8.5	804	6 PCT-US95-10973A-5	Sequence 5, Appl1
40	79.6	8.4	1233	3 US-08-718-904-80	Sequence 80, Appl1
41	79.6	8.4	1233	3 US-09-449-249-80	Sequence 80, Appl1
42	73	7.7	813	2 US-07-901-707-11	Sequence 59, Appl1
43	73	7.7	813	2 US-07-901-707-11	Sequence 11, Appl1
44	73	7.7	813	2 US-07-901-707-57	Sequence 57, Appl1
45	73	7.7	813	2 US-07-908-430-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytoacta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; NUMBER OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA


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Oy 183 ACCAATGCTACCGTAAGTAATTGGAACCCCTAAGTACTTAATGGTTAAGGTCGAAGGTCG 2432
Db 209 ACCAATGCTGCCCAATCAACAAATCAAAATCCAAAGTACGTGTGGTGAAGCTCCAAAGTTC 2688
Oy 243 AAACCTAAAACCATTTACACTAAATGCTGAGACCAAAATTACTTAATACGTGAATGGGCTATTTC 3020
Db 269 AAATTAATAAAACCATCACTAATGCTGAGACCAAAATTTGTATGTGATGGTTATTTC 3288
Oy 303 TGAATCCCTTCGAATGGCAATTAAGTGTGTTACCATATATTAATTAAGATATTACAAAGCACCGA 3622
Db 329 TGAATCCCTTTGAAACCAATAAATGTGTGTTACCATATCTTAAAGATATCTCAGGTACTGA 3888
Oy 363 ACGCACTGAATGAGAAATACTCTTTGGCTCAAGTTGCTAGTTCTGTTGCGTTGCAATGTCAT 4222
Db 389 ACGCCAAAGTATAGAGACTAATCTTTGGCCAAATGCAAAATTCCTGTGTTAGTAAAAAT 4488
Oy 423 TAACTACAAATAGCTTAATATCCGACCATGAAAAAGAAAGACAAAGTAATCTCAAGAAATCA 4822
Db 449 AAACCTTGTATGTCATATCCAACTATGGAAATCAAAAAGCGGAGTAAATTCAGAAAGTCA 5088
Oy 483 AGTCCAAATGGGAATTCAAATATCTCAGCAATGCAATTTGGAAAAATCTCTGGAATTTGATTTC 5422
Db 509 AGTCCAACTGGGAATTCAAATATCTCAGCAAGTATATTTGAAATATTTCTGGAATGATGTC 5688
Oy 543 ATTCCCTGTAAAAACCTGAGGCTTTTCTTTCTACCTGATAGCCATGCAAAATGTTTTCAAGAGC 6022
Db 569 ATTCACTGAGAAAACCGAAGCCGAATTTCTATTGTGATGCCATCAAAATGATATCAAGAGC 6288
Oy 603 AGCGGGAATTCAGATCATAGAGAACCAAGTCAAGACTAATTTTATAGACATTTCAACC 6622
Db 629 AGCAAGATTCAGATCATAGAGATCAGGTGAATAATTTATTAACAGACATTTCAACC 6888
Oy 663 TGATCCCAAGTATTAATTTTGAAGAGAAAGTGGGGCAAAATCTCTGAGCAATTCAGAA 7222
Db 689 TAATCCCAAGTACTTAATTTTGGCAAGACATGCGGTGAAGATTTCAACAGCAATTCATGA 7488
Oy 723 TGCCAAAGATGGGGCTTTATCCCAAAACCACTGTAGTATGAGATGGCCAAAGGTACCAAGTG 7822
Db 749 TGCCAAAGATGAGATTTTATCCCAAAACCTCTCGAGCTAGTGAAGCCAGTGTGCAAGTG 8088
Oy 783 GATAGTCTTAGAGTGAATCAATCAATCGTATGTGCACTCTCTTAAGTACGTTAATGG 8422
Db 809 GATAGTCTTAGAGTGAATCAATCAAGCTGATGTAGCACTTTAAACTAGCTTGGTGG 8688
Oy 843 AACCTGTCAAGACATTT---ACCAAAATGCCATGTTCTCTGAAGTATAATTTCTACTTA 8999
Db 869 GAGCTGTCAAGACATTTATACCAAAATGCCATGTTCTCTCAACTAATTAATGTCTACTTA 9288
Oy 900 TTATATATATATGTCATATCTTGGTATGATCTAATTTGAAGATTTCTAA 945
Db 929 TTATATATTAATGATGTTAATCTTGGTATCTAATTTGAAGATTTCTGA 974

RESULT 3
US-08-500-611-1
; Sequence 1, Application US/08500611
; Patent No. 5756322
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lerner, David, Mittenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

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? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/500,611
? FILING DATE: 11-JUL-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Foley, Shawn P.
? REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 908-654-5000
? TELEFAX: 908-654-7866
? TELEX: 139-125
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1379 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 225..1163
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(233, "a")
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(349, "g")
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(435, "c")
? US-08-500-611-1

```

Query Match	66.9%	Score 632.4	DB 2	Length 1379	
Best Local Similarity	80.0%	Pred. No.3-9e-168			
Matches 757	Conservative 0	Mismatches 186	Indels 3	Gaps 1	
Qy	3	GAAGGTAGTCTTGTAGTTGTGTGACGTTAATAGCGTGTCTCATTTGCGACCAACTTC	62		
Db	221	GAAGATGAAGTCAGATGCTTGTGTGTGACAAATATCAATATGTGTTCTTTGTGACCAACTTC	280		
Qy	63	AACCTTGGCCATAAATACGATCACCTTTGATGCTGAAATGCCACATTAAACAATATGC	122		
Db	281	AACCTGGCGCTGTAAATCAATCACTTCAATATGTTGGAAGTACACCACTTACCAATACGC	340		
Qy	123	CACCTTATGGAATCTCTTGTATTCAGAGGAAAGATCCAAATCAAAATGCTATNGCAT	182		
Db	341	CACCTTTCGTATGATCTTGTATATGAGGCAAAAGATCCAAATTTAAATCTATNGAAT	400		
Qy	183	ACCAATGCTACTGATATCTATTTCGACCCCTTAAGTACTTATGTGTTAAGTCCAAAGTGC	242		
Db	401	ACCAATGCTGCGCAATTAACAATACAAATCCAAATGATGTTGTGTGAGTCCAAAGTTTC	460		
Qy	243	AAACCTTAAAAACCTTACACTAATGCTGAGACCAATATCTTATACGTGATGGGCTATTTC	302		
Db	461	AAATAAAAAAACCACTCACCTAAAGCTGAGACGAAACAATTTGTATGTGAAGGGTATTTC	520		
Qy	303	TGATCCCTCAATGCGACATAGTGTGCTTACATATATTTAATATATTAACAACAACGA	362		
Db	521	TGATCCCTTTGAAACCAATTAATATGTGTTACCATATCTTTATATATATCTCAGTACTGA	580		
Qy	363	ACGCACTGATGTGAGAAATACCTTTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCCAT	422		
Db	581	ACGCGAAGATGTAGAGCTACTCTTTTCCCAAAATGCCAAATTCGTGTGTAGTAAAAACAT	640		
Qy	423	TAACTACAAATGCTTATATCCGACCATGAAAAAGAAAGCAAGTAAATCTCAAGAAATCA	482		
Db	641	AAATTTGTAATGTGATATCCAACTTTGGAATCAAAAGCGGAGTAAATCTCAAGAGTCA	700		
Qy	483	AGTCCAAATTTGGAAATTCAAATATCTCAGCAGTGCATGAAAAAATCTCTGAGTTGATTC	542		
Db	701	GGTCCAACTGGGAATTCAAATATCTCAGCAGTAAATTTGTGAAAGATTTCTGAGATGATGC	760		
Qy	543	ATTCCCTGTAAAAAATGAGGCTTTTTCATCTGTAGTACCAATCCAAATGTGTTGAGAGC	602		

DB 761 ATTCACTGAGAAACCGAACCGAATTCCTATTGTAGCATCAATGATGATCAGAGGC 820
QY 603 AGCGGATTCGAATGATGAGAAACGAAGCAAGCACTAATTTTAATGAGACATTCACCC 662
DB 821 AGCAAGATTCAGTACATGAGATCGAGTGAAGAACTAATTTTAACGAGACATTCACCC 880
QY 663 TGATCCCAAGTAATTAATTTGAGAGAGAAAGTGGGGCAAAATCTGAGGCAATTCACA 722
DB 881 TAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAATTTCAACGCAATTCATGA 940
QY 723 TGGCAAGATGGGGCTTTTACCCAAACCACTTGAGCTAGTGAATGCCAAGTAACAAAGT 782
DB 941 TGCAGAAATGAGGTTTACCCAAACCTTCAGAGTGAAGTGAAGCCAGTGTCCAAAGTG 1000
QY 783 GATAGTCTTAGAGTGAATGAATCAATGATGAGGACCTCTCAAGTAAAGTAAATG 842
DB 1001 GATAGTCTTAGAGTGAATGAATCAAGCTGATGAGACCTTTAACTAGCTTGGTGG 1060
QY 843 AACCTGTCAAGCACTT--ACCAAAATGCCATGTTCTCTCAAGTAAATTTCTACTTA 899
DB 1061 GAGCTGTCAAGCACTTAACTAATCAAAATGCCATGTTCTCTCAAGTAAATTTCTACTTA 1120
QY 900 TTAATAATTAATGCTAATCTTGTGATCTAATTTGAAGATTCTAA 945
DB 1121 TTAATAATTAATGCTAATCTTGTGATCTAATTTGAAGATTCTGA 1166

RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun B.
TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEES: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:

NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 66.9%; Score 632.4; DB 2; Length 1379;
Best Local Similarity 80.0%; Pred. No. 3.9e-168;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAAGTGAATGCTTGTAGTGTGTGAGCGTTAATAGCGGTCTCATTTGCTGCACCACTTC 62
DB 221 GAAGATGAAGTGCATCTGTGGTGAACAATCAATATATGAGCTCATTTGCACCACTTC 280
QY 63 AACTGTGCAATTAATACATACACCTTTGATGCTGGAATATGCAACATTAACAAATATGC 122
DB 281 AACTGTGGCTGTGAATACATATCTACATGTTGGAAGTACACCATTAAGCAAAATATGC 340
QY 123 CACCTTTATGAAATCTCTGTAATCAAGCAAGATCCAAAATCTAAATGCTATGGCAT 182
DB 341 CACTTTTCTGAATGATCTTGTATGAGCAAGAAAGATCCAAATTTAAATGCTATGGAAAT 400
QY 183 ACCAATGCTAAGTATCTAATTCGACCCCTTAAGTACTTAATGTTAAGCTCCAAAGTGC 242
DB 401 ACCAATGCTGCCCAATACAAATACAAATCAAAAGTACGTTGTTGAGCTCCAAAGTTC 460
QY 243 AAAACCTAAACCAATACATTAATGCTGAGAGAAATTAATTAATGATATGAGTGGCTATTC 302
DB 461 AATTAATAAAACCATCACTAATGCTGAGAGAAACAAATTTGATGATGAGTGGTTATTC 520
QY 303 TGATCCCTTCAATGGCAATAGTGTGTTACCATATATTAAATGATTAACAAGCAGCA 362
DB 521 TGATCCCTTGAACCAATTAATGTGTTACCATATCTTAATGATATCTCAGATACCTGA 580
QY 363 AGCGACTAGTGTGAGAAATACTTTTGTCTCAAGTTCTAAGTTCTGTGTTCATATGTCAT 422
DB 581 AGCGCAAGATGTGAGAGACTACTCTTGGCCCAATGCAATTCGCGTTAGTAAACAT 640
QY 423 TAACTACATACCTTATATCCGACCATGAGAAAGAGAGAAAGTAACTCAAGAAATCA 482
DB 641 AAACCTTGAATGATGATATCCAACTGGAAATCAAAAGCGAGTAAATCAAGAGTCA 700
QY 483 AGTCAATTTGGAAATTCGAATACAGCAGTGAATGGAATAATCTCTGAGTGTGATTC 542
DB 701 GGTCCAACTGGGAATTCGAATATCTGACAGTAAATTTGGAAGATTTCTCGAGTATGTC 760
QY 543 ATTCCCTGTAATAAAGTGAAGCTTTTCTTCTAGCTGAGGATCAAAATGTTTCAGAGGC 602
DB 761 ATTCACTGAGAAACCGAAGCCGAATTCCTAATTTGATGAGCATTAATGATGAGAGGC 820
QY 603 AGCGGATTCGAATGATGAGAAACGAAGTCAAGTAAATTTTAATGAGCATTCACCC 662
DB 821 AGCAAGATTCAGTACATGAGAAATCGGTGAAGAACTAATTTTAACAGAGCATTCACCC 880
QY 663 TGATCCCAAGTAATTAATTTGAGAGAGAAAGTGGGGCAAAATCTGAGGCAATTCACA 722
DB 881 TAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTCACAGCAATTCATGA 940
QY 723 TGGCAAGATGGGGCTTTTACCCAAACCACTTGAGCTAGTGAATGCCAAGTAAAGTGA 782
DB 941 TGCAGAAATGAGGTTTACCCAAACCTTCAGAGTGAAGTGAAGCCAGTGTGCCAAAGTG 1000
QY 783 GATAGTCTTAGAGTGAATGAATCAATGATGAGGACCTCTCAAGTAAAGTAAATG 842
DB 1001 GATAGTCTTAGAGTGAATGAATCAAGCTGATGAGACCTTTAACTAGCTTGGTGG 1060
QY 843 AACCTGTCAAGCACTT--ACCAAAATGCCATGTTCTCTCAAGTAAATTTCTACTTA 899
DB 1061 GAGCTGTCAAGCACTTAACTAATCAAAATGCCATGTTCTCTCAAGTAAATTTCTACTTA 1120
QY 900 TTAATAATTAATGCTAATCTTGTGATCTAATTTGAAGATTCTAA 945

PCT-US96-11546-1

Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 3.9e-168;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

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QY 3 GAAGGTGATGCTTGTAGTGTGACCTTAATAGCGGTGCTCAATGCTGACCAACTTC 62
DB 221 GAAGATGAAGTGCATGCTGTGTGACCAATATCAATATGCTCATCTTGACCAACTTC 280
QY 63 AACTTGTGCCATAATATACATCACTTTGATGCTGGAATGCCCACTTAACAATATGC 122
DB 281 AACTTGTGGCTGTGAATCAATCACTCAATCAATGTTGGAAGTCCACATTAACAATATGC 340
QY 123 CACCTTATGGAATCTTGTGTATCAAGGAAAGATCCAAACCTAAATGCTATGCAAT 182
DB 341 CACTTTTCTGAATGATCTTGTGAATGAAGCAAGATCCAAAGTTAAATGCTATGCAAT 400
QY 183 ACCAATGCTAAGTATCTTAATTCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGC 242
DB 401 ACCAATGCTGCCCATAATCAATATCAATCCAAAGTACGTGTGTTGAGTCCAAAGTTC 460
QY 243 AAACCTTAAAAACCTTACATAATGCTGAGACGAATATACCTTAATGCTGATGGCTATTC 302
DB 461 AAATTAATAAAACCATCACTCACTAAATGCTGAGACGAATATGATGATGAGGTTATTC 520
QY 303 TGATCCCTTCAATGGAATATAGTGTGCTTACATATATTAATTAATTAACAACCA 362
DB 521 TGATCCCTTGAACCAATTAATATGCTTACATATCTTAATTAATTAATTAACAACCA 580
QY 363 ACCGATGATGAGATATCTTCTTGTGCTCAAGTCTGATGCTGATGCAATGCTCAT 422
DB 581 ACCGATGATGAGATATCTTCTTGTGCTCAAGTCTGATGCTGATGCAATGCTCAT 640
QY 423 TAATTAATATGCTTATATCCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCA 482
DB 641 AAATCTTGAATATGATATCAATCACTGGAATCAAAAGCGGAGATTAATCAAGAAATCA 700
QY 483 AGTCAATGAGGAAATCAATATCACTGAGATGACATGGAATATCTGAGATGATTC 542
DB 701 GGTCAATGAGGAAATCAATATCACTGAGATGACATGGAATATCTGAGATGATTC 760
QY 543 ATTCCCTGTAAAACTGAGGCTTTTCTTCTGATGCTGATGCTCAATATGCTTCAAGGC 602
DB 761 ATTCACTGAGAAACCGAAGCGCAATCTTATGTTGACCAATATGATATGAGAGGC 820
QY 603 AGCGCATTAAGTATCAATGAGAAACCAAGTCAAGATTAATTAATAGCAATCTTACC 662
DB 821 AGCAAGATTAAGTATCAATGAGAAACCAAGTCAAGATTAATTAATAGCAATCTTACC 880
QY 663 TGATCCCAAGTATTAATTTGAGGAAAGTGGGGCAAAATCTCTGAGCAATTCACAA 722
DB 881 TAATCCCAAGTATTAATTTGAGGAAAGTGGGGCAAAATCTCTGAGCAATTCACAA 940
QY 723 TGCCAAAGATGAGGCTTTAACCAACCACTTGAAGTATGAGTCCAAAGTATCAAGTGC 782
DB 941 TGCCAAAGATGAGGCTTTAACCAACCACTTGAAGTATGAGTCCAAAGTATCAAGTGC 1000
QY 783 GATAGTCTTAAGTATGAGTAAATCAATCTGATGAGTCACTCTTAAGTATGCTTAATGC 842
DB 1001 GATAGTCTTAAGTATGAGTAAATCAAGCTGATGAGTCACTCTTAAGTATGCTTAATGC 1060
QY 843 AACTGTGACAACT---ACCAAAATGCAATGCTCTCAAGTATTAATTTTACTCTTA 899
DB 1061 GAGCTGTGACAACTTAATTAATGCAAAATGCAATGCTCTCAAGTATTAATTTTACTCTTA 1120
QY 900 TTAATTAATTAATGCTTAATCTTGTGATGCTTAATTTGAAGATTCATA 945
DB 1121 TTAATTAATTAATGCTTAATCTTGTGATGCTTAATTTGAAGATTCATA 1166
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RESULT 8
US-08-501-253A-1

Sequence 1, Application US/08501253A

Patent No. 6146628

GENERAL INFORMATION:

APPLICANT: Uckun, Fatih

APPLICANT: Tumer, Nilgun

TITLE OF INVENTION: Biotechnological Agents Comprising

TITLE OF INVENTION: Recombinant PAP and PAP Mutants

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: Merchant & Gould

STREET: 90 South 7th Street, 3100 No. 6146628west Center

CITY: Minneapolis

STATE: MN

COUNTRY: US

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/501,253A

FILING DATE: 11-JUL-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kettleberger, Denise M.

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 600.323US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 225..1163

US-08-501-253A-1

Query Match 66.8%; Score 630.8; DB 3; Length 1379;
Best Local Similarity 79.9%; Pred. No. 1.1e-167;
Matches 756; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

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QY 3 GAAGGTATGCTTGTAGTGTGACCTTAATAGCGGTGCTCAATGCTGACCAACTTC 62
DB 221 GAAGATGAATGCAATGCTTGTGTGACCAATATCAATATGCTCATCTTGACCAACTTC 280
QY 63 AACTTGTCCATAATATGCAATCACTTTGATGCTGGAATGCCAATTAACAATATGC 122
DB 281 AACTTGTGGCTGTGAATCAATCACTTACATGATGTTGGAATGCCAATTAACAATATGC 340
QY 123 CACCTTATGGAATCTTGTGTATCAAGGAAAGATCCAAACTAAATGCTATGCAAT 182
DB 341 CACTTTTCTGAATGATCTTGTATGAGGAAAGATCCAAAGTTAAATGCTATGCAAT 400
QY 183 ACCAATGCTAAGTATCTTAATTCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGC 242
DB 401 ACCAATGCTGCCAATCAATCAATATCAATCCAAAGTACGTGTGTTGAGTCCAAAGTTC 460
QY 243 AAACCTTAAAAACCTTACATAATGCTGAGACGAATATTAATTAATGCTGATGGCTATTC 302
DB 461 AAATTAATAAAACCATCACTCACTAAATGCTGAGACGAATCAATTTGATGATGAGGTTATTC 520
QY 303 TGATCCCTTCAATGGAATATAGTGTGTTACCATATATTAATGAATTAACAACCA 362
DB 521 TGATCCCTTGAACCAATTAATATGCTTACCAATCTTAAATGATATCTCAAGTATGCA 580
QY 363 ACCGATGATGAGATATCTTGTGCTCAAGTCTAGTCTGATGCTCAATGCTCAT 422
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Db	581	ACGCCAAGATGTAGAGACTACTCTTGGCCAAATGCCAAATCTCGTGTAGTAAAAAAT	640
Oy	423	TAACATACATAGCTTATATTCGACCATGGAAAAAGAACAGAAATTAATCTCAAGAAATCA	482
Db	641	AAACTGTATGTGCATATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAATCA	700
Oy	483	AGTCCAAATTGGGAATTCAAATPACTAGCAGTACATTTGGAAAAAATCTCGAGTGAATTC	542
Db	701	GGTCCAACTGGGAATTCAAATPCTGCACAGTAAATTTGGAAAGATTTCTGGAGTATGTC	760
Oy	543	ATTCCCTGTAAAACTGAAGCTTTTTTTCTACTGTAAGCAATCCAAATGTGTTCAAGAGC	602
Db	761	ATTCACTGAAAAAACCAGCGCAATTCCTATGTGTAGCATAAATGGTATCGAAGC	820
Oy	603	AGCGGATTCAGATCATAGAGAACCAAGTCAGATTAATTTAATPAGCATTTCAACC	662
Db	821	AGCAAGATTCAAGTCAATAGAGAAATCAAGTGAAATTAATTTAACAAGCATTCACCC	880
Oy	663	TGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTGTGAGCAATTCACAA	722
Db	881	TAATCCCAAGTACTTAATTTTGCAAGAACATGGGGTAAAGATTTCACAGCAATTCATGA	940
Oy	723	TGCCAAGATGGGGCTTATACCAAAACCACTTGAGCTAGTGAATGCCAAAGGATCCAAATG	782
Db	941	TGCCAAGAAATGAGATTTTTACCAAAACCTCTGAGCTAGTGAATGCCATGGGCCAAATG	1000
Oy	783	GATAGTCTTAGAGATGATGAATCAATCGTGAATGGCACTCCTTAAGTACGTAAATGG	842
Db	1001	GATAGTGTGAGAGATGATGAATCAACCGTGAATGACACTTTAAACTACGTGGTGGG	1060
Oy	843	AACTGTCAACAATT--ACCAAAATGCCATGTTCTCTCAAGTAAATATTTCTACTTA	899
Db	1061	GAGCTGTCAACAATTATTAACCAAAATGCCATGTTCTCTCAACTTAATATGTACTTA	1120
Oy	900	TTATATATATATGTCTAATCTTGATGATCTAATTTGAAGAATTTCTAA	945
Db	1121	TTATATATTAACATGGTTAATCTTGGAGATCTAATTTGAAGAATTTCTGA	1166

RESULT 9
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniowski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co.
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-07-865-163-2

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Query Match	66.64;	Score 629.2;	DB 3;	Length 1379;
Best Local Similarity	79.84;	Pred. No. 3.1e-167;		
Matches 755; Conservative	0;	Mismatches 186;	Indels 3;	Gaps 1;

OY	3	GAAGTATGCTTGAATGGTGGAGCGTTAATAGCGGGCTCAATGCTGACCAACTTC	62
Db	221	GAAGTGAAGTCATGCTTGTGGTGCAATATCAATATGCTCATTTCTTGACCACTTC	280
OY	63	AACCTGGCCATAATACGATCACTTGTGATGCTGGAATGCGACCATTAACAATATGC	122
Db	281	AACCTGGGCTGTGAATCAATCATCTCAATGTTGGAAAGTACCACTTACCAATATGCG	340
OY	123	CACCTTATGGAATCTCTTGTAATCAAGCAAAAGATCCAAACTAAATGCTATGGCAT	182
Db	341	CACCTTCGGAATATCTTCGTATGAAGCGAAAGATCCAAAGTTTAAATGCTATGGAAT	400
OY	183	ACCAATGCTACCTGATCTAATTCGACCCCTAACTACTTATTTGGTTAAAGTCCAAAGTGC	242
Db	401	ACCAATGCTGCCAATCAATCAAAATCCAAAGCAGTGTGGTGGAGCTCCAAAGTTC	460
OY	243	AAACCTTAAAAACATTAACAATAGTCTGAGACGAATAATCACTTAACGATAGGGCTATTC	302
Db	461	AAATTAATAAAACCATCACTAATAGTCTGAGACGAACAAATTTGATGTGATGGTTATTC	520
OY	303	TGATCCCTTCATGGCAATTAAGTGTGCTTACCATATATTTAATGATATTTACAACACCGA	362
Db	521	TGATCCCTTTGAAACCAATTAATGCTGTACCATATCTTTAATGATATCTCAGTAACGA	580
OY	363	ACGACATGATGTGAGAAATCTCTTCTGCTCAAGTCTAAGTTCGCTGTGCAATGTCAT	422
Db	581	ACGCGAAGATGTAGACTACTCTTGTCCCAAAATGCCAAATTCGTGTGTAGTAAAAAT	640
OY	423	TAACTACAATAGCTTAATATCCGACCATGGAAGAAAGACGAAGTAATCAAGAAATCA	482
Db	641	AAACTTTGATAGTGCATATCCAACTTGGATTCAAAACGGAGTAAATTCAGAAATCA	700
OY	483	AGTCCAAATGGGAATTCAAATACTCAGACAGTGAATTTGAAAAATCTCTGAGTTGATTC	542
Db	701	GGTCAACTGGGAATTCAAATATCTCGACAGTAATATTTGAAAAAGATTTCTGGAGTATGTC	760
OY	543	ATTCCCTGTAAAACTGAGGCTTTTTTTCTAAGTGTGACCATCCAAATGCTTCAAGAGC	602
Db	761	ATTACTGAGAAAAACCAAGCCGAATTCCTAATGGTGGCCATTAATAATGGTATCAGAGC	820
OY	603	AGCGCAATCAAGTACATAGAGAACCAAGTCAAGACTTAATTTAATGAGCAATCTACCC	662
Db	821	AGCAAGATTCAGATGACTAGAGAAATCAGGTGAAACCTAATTTTACGAGAGCATTCACCC	880
OY	663	TGATCCCAAGTATTAATTTGAGAGAAATGGGGCAAAATCTCTGAGGCAATTCACA	722
Db	881	TAAATCCAAAGTACTTAATTTTGCAAGAGCATGGGGTAAAGTTTCAACACAGCAATTCATGA	940
OY	723	TGCCAAGATGGGGCTTACCCCAACCATTTGAGCTAATGAGATGCCAAAGGTACCAAGTG	782
Db	941	TGCCAAGAAATGAGTTTACCCCAAACTCTCGAGCTGTGAGATGCCAGTGGTCCAAAGTG	1000
OY	783	GATGATCTTAAGTGTGATGAATCAATCGATATGGGCACTCCTTAATGAATACGTTAATGG	842
Db	1001	GATGATCTTGAAGTGTGATGAATCAAGCCGTGATGACACTCTTAACATCACTGTGGTG	1060
OY	843	AACCTGTCAACAACCTT---ACCAAAATGCGATGTTCTCAAGTTAATATTTCTACTTA	899
Db	1061	GAGCTGTCAAGCAACTATATACCAAAATGCAATGCTTTCTCAACTTAATATGTCTACTTA	1120
OY	900	TTAATATTAATATGCTTAATCTTGGTGATCTAATTTGAAGATTTCTAA 945	

CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 57.5%; Score 543.8; DB 2; Length 918;
Best Local Similarity 77.4%; Pred. No. 3.1e-143;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

8 TGATGCTTGTAGTGTGAGCGTTAATAGCGGCTCATTCGCGCAACTTCAACT 67
2 TGAAGTGTGATGCTTGTGAGCAATTCAGTATGCTCATCTTTCGCAACCACTCACT 61
68 GTGCGCAATTAATGATCACTTGTGAGTGTGAAATGCCACATTAACAATATGCCACT 127
62 GGGCCGGAATATCATCATCTACCAATGTTGAAATGACCACTTAAGAACTATGCAACT 121
128 TTAGGAATCTCTTGTGATCAAGCGAAAGATCCAAATGCTATGCGATACCA 187
122 TTGGATA---CTTCGTACTGAAGGCGAAGATCC--AGTTATGTCTATGGAATACCA 175
188 TGCTACTGATTAATTAATGACCCCTAAGTACTTATGTTAGTCCAGAGTCAAC 247
176 TGTGCTCCCAATATGATCAATCCAAATACATATGTTGAGCTCCAGGTTCAATG 235
248 TAAAAACAATTACACTAATGCTGAGAAGAAATTAATTAATGATGAGGCTATTCGATC 307
236 AAGAAAGCATCACTAATGCTAAGCAAGAAATTAATTAATGATGAGGCTATTCGATC 295
308 CTTTCATGCGCATTAAGTGTGCTTACATTAATTAATTAATTAATTAATTAATTAATTA 367
296 CTTACAA---CAATAGGTGTGCTTTCATCTCTTAAAGGCTATCAAGTATGAAACGCG 352
368 CTGATGTGAGAAATCTCTTGTGCTCAAGTCTAGTTCGTGTGCAATGTCATTAAC 427
353 AAGATTAAGACTACTCTTGTGCTCAAGTCCAGATTCCTGTTGTGTAATAACATAACT 412
428 ACAATAGCTTAATTCGACCATGAGAAAGAAAGCAAGTAATCTCAAGAAATCAAGTCC 487
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488 AATTGGGAATTCAAATATCTCAGCATGACATTTGAAAAAATCTCTGAGTTGATTCAATCC 547

473 AACTGGGAATTCGAATCTCGACAGTGGCATTTGGAAGATTTCTGAGTGCACGTCATTC 532
548 CTGTAAAAAAGTGAAGCTTTTCTTCTACTGTACCAATCCAAATGTTTCAGAGCGACGC 607
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608 GATTCAAGTACATAGAGAACCAAGTCAAGTAAATTTAATTAAGATTCCTACCTGATC 667
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668 CCAAGTAATTAATTTGAGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCC 727
653 CCAAGTAATTAATTTGAGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCC 712
728 AGATGGGCTTAAACCAACCACTGAGTATGATGATGCAAGGATCAAGTATGATG 787
713 GGAATGAGTTTAAACCAACCACTGAGTATGATGATGCAAGGATCAAGTATGATG 772
788 TTCTTAGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATG 847
773 TGTTAGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATG 832
848 GTGAGACACTT---ACCAATATGCAATGTTCTCTCAAGTTAATTAATTTCTAATTA 904
833 GCCAGAGAACTTAAACCAAAATGCAATGTTCTCTCAAGTTAATTAATTTCTAATTA 892
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RESULT 12

US-08-319-622A-1

; Sequence 1, Application US/08319622A

; Patent No. 5656466

; GENERAL INFORMATION:

; APPLICANT: Moon, Young-Ho

; APPLICANT: Choi, Kyu-Whan

; APPLICANT: Jeon, Hong-Seob

; APPLICANT: Kim, Chul-Hwan

; APPLICANT: Kim, Man-Keun

; TITLE OF INVENTION: Process for Preparing Virus-Resistant

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Darby & Darby PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: US

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/319,622A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, S. Peter

; REGISTRATION NUMBER: 25,351

; REFERENCE/DOCKET NUMBER: 0136/04445

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7700

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 918 base pairs

; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Query Match 57.5%; Score 543.8; DB 2; Length 918;
Best Local Similarity 77.4%; Pred. No. 3.1e-143;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

QY 8 TGAATCTGTGATGTTGGTGAAGCTTAATAGCGTGGCTCATTTGCTGACCAACTTCAACTT 67
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QY 68 GTGCGAATTAATAGATGACCTTGAATGCTGGAATGCAACCTTAATCAATATGCAACT 127
DB 62 GGGCGGTGAATACATCATCTACATGTTGGAAGTACACATTAAGAACTATGCAACTT 121
QY 128 TTATGGAATCTCTTGGTATCAAGCGAAAGATCCAAATCTAAATGCTATGCAATCA 187
DB 122 TTGATA-----CTTGGTACTGAAAGCGAAGATCC--AAGTTATGTGTATGAAATACCA 175
QY 188 TGTCTACCTGATTAATTTGACCCCTTAAGTACTTATTTGTTAAAGCTTCAAGTGAACC 247
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QY 248 TAAAAACATTAATCACTAATGCTGAGAGCAATTAATCTATGCGATGAGGCTATTTGATC 307
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DB 353 AAGATGTAGAGACTACTCTTGTCCCAATGCCAATCTCGTGTGTTAAATACATTAATCT 412
QY 428 ACAATGCTTAATCCGACATGAGAAAGAAAGCAAGAACTCAAGAAATCAAGTCC 487
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DB 593 GATTCAAGTACATGAGAAAGCAAGTCAAGTCAATTTAATGAGCAATTTACCTGATC 652
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QY 788 TTCTTGAAGTGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 847
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QY 848 GTGAGCAACTT--ACCAAAATGCAATGTTCTCAAGTTAATTAATTTCTAATTAAT 904

DB 833 GCCAGAGAACTATATACCAAAAGCAATGTTTCTCACTAATATGCTACTTATATA 892
QY 905 ATTATATGCTAATCTTGTGAT 927
DB 893 ATTACATGCTAATCTTGGAT 915

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kwan-Ho
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326el Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 57.5%; Score 543.8; DB 2; Length 918;
Best Local Similarity 77.4%; Pred. No. 3.1e-143;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

QY 8 TGAATCTGTGATGTTGGTGAAGCTTAATAGCGTGGCTCATTTGCTGACCAACTTCAACTT 67
DB 2 TGAATGTGATGCTTGGTGAAGCTTAATAGCGTGGCTCATTTGCTGACCAACTTCAACTT 61

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Db 296 CTTACAA---CAATAGGTGTGCTTCTTCAATCTCTTAAGGCTATCTAGGTAAGCAACGG 352
Qy 368 CTGATGTGAGAAATCTCTTGTGCTCAAGTTCTAGTTCTGTTGCAATGTCATTAAC 427
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Qy 428 ACAATAGCTTAATCCGACCATGGAAGAAAGCAAGTAATCAAGTAATCAAGTCC 487
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Db 893 ATTACATGCTATCTTGTGAT 915

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/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: SEED AND BERRY LLP
/ STREET: 701 Fifth Avenue, 6300 Columbia Center
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/356,161
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/356,161
/ FILING DATE: 13-APR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 591672cendburg, Carol
/ REGISTRATION NUMBER: 39,317
/ REFERENCE/DOCKET NUMBER: 760100.404US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEO ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 804 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..804
/ NAME/KEY: misc feature
/ LOCATION: 1..804
/ OTHER INFORMATION: /note="Nucleotide sequence
/ OTHER INFORMATION: corresponding to the clone M13 mp18-G7 in Example 1.B.2."
/ FEATURE:
/ NAME/KEY: mat peptide
/ LOCATION: 46..804
/ OTHER INFORMATION: /product="Saporin"
/ US-08-356-161-6

Query Match 9.4%; Score 88.4; DB 2; Length 804;
Best Local Similarity 49.3%; Pred. No. 6, 6e-15;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

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QY      701 AATCTCTGAGGCAATTCAC---AATGCCAAGATGCGGCTTTTACCCAAACCTTGAG 757
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RESULT 15

US-08-356-161-7

Sequence 7, Application US/08356161

Patent No. 5916772

GENERAL INFORMATION:

APPLICANT: Iapeli, Douglas A.

APPLICANT: Barthelemy, Isabel

APPLICANT: Baird, J. Andrew

APPLICANT: Soanowaki, Barbara A.

TITLE OF INVENTION: RECOMBINANT PRODUCTION OF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

STREET: 701 Fifth Avenue, 6300 Columbia Center

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/356,161

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/356,161

FILING DATE: 13-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: No. 5916772tendury, Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 760100.404US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 804 base pairs

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?      TYPE: nucleic acid
?      STRANDEDNESS: double
?      TOPOLOGY: unknown
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 1..804
?      NAME/KEY: misc_feature
?      LOCATION: 1..804
?      OTHER INFORMATION: /note= "Nucleotide sequence
?      OTHER INFORMATION: corresponding to the clone M13 mp18-69 in Example 1.B.2."
?      NAME/KEY: mac_peptide
?      LOCATION: 46..804
?      OTHER INFORMATION: /product= "Saporin"
?      US-08-356-161-7

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Query Match 9.4%; Score 88.4; DB 2; Length 804;
 Best Local Similarity 49.3%; Pred. No. 6.6e-15;
 Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

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QY      47 TTGCTGACCAACTTCACTTGTCCTAATAATGATCACCTTGATGCTGAAATGCA 106
Db      20 TTTCAGCTTGAGCAACAAGTGAATGCGGTCAATCAATCACTTATGATTAATCCGA 79
QY      107 CCATTAACAATATGCACTTATGGAATCTCTGTAATCAAGCAAAAGATCAAAAC 166
Db      80 CCGGGGTCAATATCTCATCTTTGTGATTAATCCGAAACAAAGTAAAGATCAAAAC 139
QY      167 TAAATGCTATGCGATACCAATGC---TACCTGATCAATATGCAAGCCCTTAAGTAT 223
Db      140 TGAATACGGTGTGATACCAATAGCCGTATAGGCCCACTTTAAAGAAATTCCTTA 199
QY      224 TGGTTAAGCTCAAGGTGCAAACTTAATAAACAATTAATAGCTGAGAGCAATTAAT 283
Db      200 GAATTAATTTCCAAAGTTC---CCAGAGAGCGGTCTCACTTGGCTTAAGCGGATTA 256
QY      284 TATACGATGCGGTATTTCTGATCCCTTCAATGCAATTAAGTCTGTTACATATTA 343
Db      257 TGTATGTGTCGGGTATCTTGAATGATTAACAGATGTTAATCGGGCATATTAATCA 316
QY      344 ATGATATTAACAAGACGGAACGACATGATGAGAAATCACTTTGTCAAGTTCTAGT 403
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QY      404 CTCGTGTGCAATGTCATTAATCAATAGCTTAATATCCAGCCATGAGAAAGAAAGAG 463
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QY      581 CCATCCAAATGTTTTCAGAGGCGGAGTTCAGTACATAGAGAACCAATCAGACTA 640
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QY      641 ATTTAATAGAGCATTTCTACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCA 700
Db      614 ACTTCCCAACAAGTTCACTCGGAAAACAAAGTGAATCAAGTTGAGTTAACTGAAAA 673
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Db      734 TCGGGTTTGAAAAGTGAAGCGGTGAAGACTTGCAAAATGG 775

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Mon Apr 10 07:26:45 2006

us-09-978-274a-1.rn1

Page 14

Search completed: April 8, 2006, 09:49:00
Job time : 331.047 secs

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QY 781 TGGATAGTCTTGAAGTGAATCAATCGATGTGGCACTCTTAACTAGTCAAT 840
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Db 901 TATATATATATGCTAATCTTGTGATCTATTTGAAGATCTTAA 945

RESULT 2
US-09-978-274A-3
; Sequence 3, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-3

Query Match 83.2%; Score 786.4; DB 3; Length 792;
Best Local Similarity 99.9%; Pred. No. 4,7e-211;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 193 CCTGATCTAATTTGCAAGCTTAAATGATCTTATGTTAGCTCAAGGTCGAACCTTAA 252
Db 124 CCTGATCTAATTTGCAAGCTTAAATGATCTTATGTTAGCTCAAGGTCGAACCTTAA 183
QY 253 ACCATTACCTAATGCTGAGAGAAATTAATTAATGATGAGGCTATTTCTGATCCCTTC 312
Db 184 ACCATTACCTAATGCTGAGAGAAATTAATTAATGATGAGGCTATTTCTGATCCCTTC 243
QY 313 AATGCAATTAATGCTGATACCAATATTTAATGATATTAACAAGCAGGAGCACTGAT 372
Db 244 AATGCAATTAATGCTGATACCAATATTTAATGATATTAACAAGCAGGAGCACTGAT 303
QY 373 GTGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAATCAAT 432
Db 304 GTGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAATCAAT 363
QY 433 AGCTATATCCGACCATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
Db 364 AGCTATATCCGACCATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 493 GGAATCAATATCTCAGCAGTGAATTTGGAATATCTCTGAGTGTATCTATTTCTCTGTA 552
Db 424 GGAATCAATATCTCAGCAGTGAATTTGGAATATCTCTGAGTGTATCTATTTCTCTGTA 483
QY 553 AAAACGAGGCTTTTCTTCTAGTGAAGCATCAAAATGTTTCAAGAGCAGGCGATTC 612
Db 484 AAAACGAGGCTTTTCTTCTAGTGAAGCATCAAAATGTTTCAAGAGCAGGCGATTC 543
QY 613 AAGTACATGAGAACCAAGTCAAGTAAATTTAATAGCATTTCACTGATCCCA 672
Db 544 AAGTACATGAGAACCAAGTCAAGTAAATTTAATAGCATTTCACTGATCCCA 603
QY 673 GTAATTAATTTGAG 732
Db 604 GTAATTAATTTGAG 663
QY 733 GGGGCTTTTACCCAAACCACTTGAGCTAGTGAATGCCAAGGTAAGTATGTTCTT 792
Db 664 GGGGCTTTTACCCAAACCACTTGAGCTAGTGAATGCCAAGGTAAGTATGTTCTT 723
QY 793 AGAGTGAATGAATCAATGATGATGAGCACTCTTAAGTACGTTAATGAACTGTGAG 852
Db 724 AGAGTGAATGAATCAATGATGATGAGCACTCTTAAGTACGTTAATGAACTGTGAG 783
QY 853 ACAACTTA 860
Db 784 ACAACTTA 791

RESULT 3
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32

Db 1001 GAATGAGTTGAGAGTGGATGATAATCAAGCCTGATGTGACACTCTTAACCTACCTGGTGG 1060
Qy 843 AACCTGTGAGACAACTT---ACCAAAATGCCAGTTCTCAAGTTATATTTCTACTTA 899
Db 1061 GAGCTGTGACAACTTATATACCAAAATGCCAGTTCTTCCATCTTAATATGTTCTACTTA 1120
Qy 900 TTATAATTATATGTCTAATCTTGTGTGATCTTAATTTGAAGATTCTAA 945
Db 1121 TTATAATTACATGTGTATCTTGTGTATCTTATTTGAAGATTCTGA 1166

RESULT 5
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 66.9%; Score 632.4; DB 10; Length 1379;
Best Local Similarity 80.0%; Pred. No. 1.9e-167; Indels 3; Gaps 1;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
Qy 3 GAAGTGTAGTCTGTAGTGTGTGACGTTAATAGCGTGCCTATTGCTGCACCAACTTC 62
Db 221 GAAGATGAAGTGCATGCTGTGTGTGACAAATATGATGCTATTCTTGCACCAACTTC 280
Qy 63 AACTTGTGCATTAATACATACCTTTGATGCTGGAATGCAACCTTAACCAATATGC 122
Db 281 AACTTGTGTGTAATACATATCTTAACAATGTTGGAAGTACCACTTAAGCAAAATACGC 340
Qy 123 CACCTTATGGAATCTCTGTATCAAGGAAAGATCCAAACTAAATGCTAATGGCAT 182
Db 341 CACTTTCGTAGATCTTGTGTATGAGAAAGATCCAAAGTTTAAATGCTATGGAAT 400
Qy 183 ACCAATGCTACTGATATCTAATTCGACCCCTAAGTACTTAATGTTAAGTCCAGAGTGC 242
Db 401 ACCAATGCTGCCCAATACCAATCAATCAATGCAAGTACGTTGAGTCCAGAGTTC 460
Qy 243 AAAACCTAAACCAATTAACATAATGCTGAGACAAATTAATTAATGCTGAGTATTC 302
Db 461 AAATATAAAAAACCATCACTAATATGCTGAGACAAATTAATGCTGAGTATTC 520
Qy 303 TGATCCCTTCAATGGAATATAGTGTGTTACCATATATTAATGATATTAAGACGCCA 362
Db 521 TGATCCCTTTGAAACCAATTAATATGCTTAACATATCTTAATGATATCTCAAGTACTGA 580
Qy 363 AGCACTGATGAGAAATATCTTGTGCTCAAGTTCTGATGCTGCTGCTGCAATGTCAT 422
Db 581 AGCCCAAGATGATGAGACTACTCTTGTGCCCAATGCAATTCGCTGATTAAGTAAAAAT 640
Qy 423 TAACTAACAATAGCTTATATCCAGCATGAAAAAGAAAGCAAGAACTCAAGAAATCA 482

Db 641 AAACCTTGTATAGTCGATATTCACCAATGGAAATCAAAAGGGAGTAAATCAAGAACTCA 700
Qy 483 AGTCCAAATGGGAAATTCAAATCTCAGCAGTGA CATTTGAAAAATCTCGAGAGTTGATTC 542
Db 701 GGTCCAACTGGGAAATTCAAATCTCAGCAGTGA CATTTGAAAAATCTCGAGAGTTGATTC 760
Qy 543 ATTCCCTGTAAAACTAGAGGCTTTTCTTCTAATGCTGAGCAATGCAATGATTTCAAGAGC 602
Db 761 ATTCACTGAGAAAAAGCAAGCCGAATTTCTTAATGCTGAGCAATGCAATGATTTCAAGAGC 820
Qy 603 AGCCGATTCAGTACATGAGAACCAAGTCAAGACTAATTTAATGAGCAATTTCAACC 662
Db 821 AGCAAGATTCAGTACATGAGAACCAAGTCAAGACTAATTTAATGAGCAATTTCAACC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGAGAGAGGGCAAAATCTCGAGAGCAATTCACAA 722
Db 881 TAATCCCAAGTAACTTAATTTGAGAGAGAGGGTGAAGATTTCAACAGCAATTCATGA 940
Qy 723 TGCCAAAGAAATGGGCTTTTACCACCACTGAGTGTGATGCAAGTACCAAGTACCAAGT 782
Db 941 TGCCAAAGAAATGGGCTTTTACCACCACTGAGTGTGATGCAAGTACCAAGTACCAAGT 1000
Qy 783 GATAGTCTTAAAGTGTGAGAAATCAATGTGATGTGCACTCTTAAGTACGTTAATG 842
Db 1001 GATAGTGTGAGAGTGTGAGAAATCAAGCTGATGATGCACTCTTAAGTACGTTGATG 1060
Qy 843 AACCTGTGAGACAACTT---ACCAAAATGCCAGTTCTCAAGTTATATTTCTACTTA 899
Db 1061 GAGCTGTGACAACTTATATACCAAAATGCCAGTTCTTCCATCTTAATATGTTCTACTTA 1120
Qy 900 TTATAATTATATGTCTAATCTTGTGTATCTAATTTGAAGATTCTAA 945
Db 1121 TTATAATTACATGTGTATCTTGTGTATCTTATTTGAAGATTCTGA 1166

RESULT 6
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-31

Query Match 66.6%; Score 629.2; DB 3; Length 1368;
Best Local Similarity 79.8%; Pred. No. 1.5e-166; Indels 3; Gaps 1;
Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
Qy 3 GAAGTGTAGTCTGTAGTGTGTGACGTTAATAGCGTGCCTATTGCTGCACCAACTTC 62
Db 221 GAAGATGAAGTCAATGCTGTGTGTGACAAATATATATGCTCATTTCTGCAACCACTTC 280
Qy 63 AACTTGTGCATTAATACATACCTTTGATGCTGGAATGCAACCTTAACCAATATATGC 122
Db 281 AACTTGTGTGTAATACATATCTTAACAATGTTGGAATATACCACTTAAGCAATATACGC 340
Qy 123 CACCTTATGGAATCTCTGTATCAGCGAAAGATCCAAACTAAATGCTAATGGCAT 182

Db 341 CACTTTTGGAAATGATCTGTAATGAAGCAAGATCAAGTTAAATGCTATGGAAT 400
QY 183 ACCAATGCTACGTATCTAATTTGACCCCAATGCTATGCTTAAAGTCCCAAGTGC 242
Db 401 ACCAATGCTCCCAATCAATATCAATATCCAAAGCAGTGTGTGATGCTCCAAAGTTC 460
QY 243 AAAAATAAAAAACAATGCTAATGCTGAGACGAATTAATTAATGCTGATGCTATTC 302
Db 461 AAAAATAAAAAACAATGCTAATGCTGAGACGAATTAATTAATGCTGATGCTATTC 520
QY 303 TGATCCCTTCAATGCGCAATAGTGTGCTTACATATATTTATGATATTAACAGACCGA 362
Db 521 TGATCCCTTCAATGCGCAATAGTGTGCTTACATATATTTATGATATTAACAGACCGA 580
QY 363 ACCGATGATGAGGAATGCTTGTGCTAAGTTCAGTGTGCTGCTGCTGCTGCTGCTGCT 422
Db 581 ACCGATGATGAGGAATGCTTGTGCTAAGTTCAGTGTGCTGCTGCTGCTGCTGCTGCT 640
QY 423 TAACTAATGCTTATATCCGACCATGGAAGAAAGCAAGAACTTAATCAAGAAATCA 482
Db 641 AAATCTTGATATGCTATATCAATGGAATCAAAAGCGGAGTAAATCAAGAAATCA 700
QY 483 AGTCCAAATGGGAATTAATTAATGCTGAGAGTGAATGGAATTAATGCTGAGTTC 542
Db 701 GGTCCAACTGGGAATTAATTAATGCTGAGAGTGAATGGAATTAATGCTGAGTTC 760
QY 543 ATTCCCTGTAAGAACTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
Db 761 ATTCACTGAGAAACCGAAGCCGAAATTCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
QY 603 AGCGCATTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 662
Db 821 AGCAAGTTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 880
QY 663 TGATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 722
Db 881 TAATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 940
QY 723 TGCAGAAATGGGGCTTAAACCAACCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Db 941 TGCAGAAATGGGGCTTAAACCAACCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
QY 783 GATAGTCTTGAAGTGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 842
Db 1001 GATAGTCTTGAAGTGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1060
QY 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db 1061 GAGCTGTGAGCAACTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1120
QY 900 TTATTAATTAATGCTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 945
Db 1121 TTATTAATTAATGCTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1166

RESULT 7

US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3 4-076
; CURRENT APPLICATION NUMBER: US/10/467, 009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: *Phytolacca americana*

FEATURE:
; NAME/KEY: CDS
; LOCATION: (225) .. (1160)
US-10-467-009-1

Query Match 65.4%; Score 618; DB 8; Length 1376;
Best Local Similarity 79.8%; Pred. No. 2,2e-163;
Matches 755; Conservative 0; Mismatches 185; Indels 6; Gaps 2;

QY 3 GAAAGTATGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62
Db 221 GAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280
QY 63 AACCTGTGAGCAACTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
Db 281 AACCTGTGAGCAACTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340
QY 123 CACCTTATGGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Db 341 CACTTTTCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
QY 183 ACCAATGCTACGTATCTAATTTGACCCCAATGCTTATGCTTAAAGTCCCAAGTGC 242
Db 401 ACCAATGCTCCCAATCAATATCAATATCCAAAGCAGTGTGTGATGCTCCAAAGTTC 460
QY 243 AAAAATAAAAAACAATGCTAATGCTGAGAGAAAGTGAATTAATTAATGCTGAGTTC 302
Db 461 AAAAATAAAAAACAATGCTAATGCTGAGAGAAAGTGAATTAATTAATGCTGAGTTC 520
QY 303 TGATCCCTTCAATGCGCAATAGTGTGCTTACATATATTTATGATATTAACAGACCGA 362
Db 521 TGATCCCTTCAATGCGCAATAGTGTGCTTACATATATTTATGATATTAACAGACCGA 580
QY 363 AGCAAGTTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 422
Db 581 AGCAAGTTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 637
QY 423 TAATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 482
Db 638 TAATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 697
QY 483 AGTCCAAATGGGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 542
Db 698 AGTCCAAATGGGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 757
QY 543 ATTCCCTGTAAGAACTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
Db 758 ATTCCCTGTAAGAACTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
QY 603 AGCGCATTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 662
Db 818 AGCGCATTCAGTACATAGAGAACCAAGTCAAGATTAATTAATGAGCAATTCATCC 877
QY 663 TGATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 722
Db 878 TGATCCCAAGTAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 937
QY 723 TGCAGAAATGGGGCTTAAACCAACCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Db 938 TGCAGAAATGGGGCTTAAACCAACCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
QY 783 GATAGTCTTGAAGTGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 842
Db 998 GATAGTCTTGAAGTGAATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1057
QY 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db 1058 GAGCTGTGAGCAACTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1117
QY 900 TTATTAATTAATGCTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 945
Db 1118 TTATTAATTAATGCTTATTAATTAATGAGAGAAAGTGGGCAAAATCTGAGCAATTCATCA 1163

Db 67 GCTTCTCAACATA-----GTGTTGACGTTGGAAGTCCACACAGAACTTAC 117
Qy 121 GCCACCTTATGATCTCTGTAATCAAGCAAGATCCAAACTAAATGATGAC 180
Db 118 TCTAATTTTCTGACTAGTTGCGAGAGCTGTGAAGCAAGAAATTCATGCAATG 177
Qy 181 ATACCAATGCTACTGATTAATTCAGACCCCTTAAGTACTTATGTTTACCTCAAGT 240
Db 178 ATGATTAATGCGCAACACCTCAGAACACCAAGATGTTGTTGATGACTCAAAATTC 237
Qy 241 GCAACCTTAACCAATTCATGCTAATGCTGAGAAATTAATTAATGATGATGATG 300
Db 238 GGAATCTGGAATTC---ACATTAAGCAATCAAGAGGAACTTAATTAATGAGGCTAT 294
Qy 301 TCTGATCCCTTCAATGCAATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 295 TCTGATCCCTTCAATGCAATGATGATGATGATGATGATGATGATGATGATGATG 339
Qy 361 GAACGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 340 TCAGAAATCCGATGCGCAAGACCGTTTGGCCCGGGGCAAAAGCAAGCTGCACTG 399
Qy 421 ATTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 400 AATTAATTCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 459
Qy 481 CAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 460 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 519
Qy 541 TCA-----TTCCCTGTAACAACTGAGCTTTTCTTCTGATGATGATGATG 588
Db 520 GCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 579
Qy 589 ATGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 648
Db 580 ATGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
Qy 649 -----AGACATTCCTGATGATGATGATGATGATGATGATGATGATGATG 702
Db 640 GATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 699
Qy 703 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 762
Db 700 GTTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 759
Qy 763 GATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
Db 760 GATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 819
Qy 823 CTCCTTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
Db 820 GATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 879
Qy 883 GTTATAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 926
Db 880 ATTAATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 923

RESULT 11
US-11-106-187-3
; Sequence 3, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NISGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301

; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent Ver. 3.3
; SEQ ID NO 3
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(75)
; FEATURE:
; NAME/KEY: mac_peptide
; LOCATION: (76)..(930)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-11-106-187-3

Query Match 11.7%; Score 110.8; DB 10; Length 934;
Best Local Similarity 50.0%; Pred. No. 3e-20;
Matches 472; Conservative 0; Mismatches 427; Indels 45; Gaps 6;

Qy 1 ATGAAGGTGATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 60
Db 7 ATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 66
Qy 61 TCAATGTTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 67 GCTTCTCAACATA-----GTGTTGACGTTGGAAGTCCACACAGAACTTAC 117
Qy 121 GCCACCTTATGATCTCTGTAATCAAGCAAGATCCAAACTAAATGATGAC 180
Db 118 TCTAATTTTCTGACTAGTTGCGAGAGCTGTGAAGCAAGAAATTCATGCAATG 177
Qy 181 ATACCAATGCTACTGATTAATTCAGACCCCTTAAGTACTTATGTTTACCTCAAGT 240
Db 178 ATGATTAATGCGCAACACCTCAGAACACCAAGATGTTGTTGATGACTCAAAATTC 237
Qy 241 GCAACCTTAACCAATTCATGCTAATGCTGAGAAATTAATTAATGATGATGATG 300
Db 238 GGAATCTGGAATTC---ACATTAAGCAATCAAGAGGAACTTAATTAATGAGGCTAT 294
Qy 301 TCTGATCCCTTCAATGCAATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 295 TCTGATCCCTTCAATGCAATGATGATGATGATGATGATGATGATGATGATGATG 339
Qy 361 GAACGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 340 TCAGAAATCCGATGCGCAAGACCGTTTGGCCCGGGGCAAAAGCAAGCTGCACTG 399
Qy 421 ATTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 400 AATTAATTCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 459
Qy 481 CAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 460 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 519
Qy 541 TCA-----TTCCCTGTAACAACTGAGCTTTTCTTCTGATGATGATGATG 588
Db 520 GCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 579
Qy 589 ATGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 648
Db 580 ATGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
Qy 649 -----AGACATTCCTGATGATGATGATGATGATGATGATGATGATGATG 702
Db 640 GATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 699
Qy 703 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 762

Db 700 GTTCTAAGGTCAATGCAAAAGTTGGCACTCCGGTATAGTACTGTACTTAACTGGA 759
Qy 763 GATGCCAAAGGTACAAGTGGATAGTCTTAAAGTGAATGAATCATCGTGAATGGCA 822
Db 760 GACCTTAAAGATAGAAATTAATTAACCTTGGACTACGGCCACATGAACGACTTGAAC 819
Qy 823 CTCCTTAAGTACCTTAATGGAACCTGTGACAACTTACCAAAATGCGATGTTCTCA 882
Db 820 GACATTATGGCACTCCCTAACCCAGTTACTGGCAAGTTAAAGTTCCATGTTCCCTGA 879
Qy 883 GTTATATTTCTACTATTATTAATTAATGCTTAATCTTGGTGA 926
Db 880 ATTATGTCCTATTATTAATGAGTACTGATTAATGAACCTTGTGA 923

RESULT 12

US-11-106-187-20
; Sequence 20, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TURNER, NILGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(855)
US-11-106-187-20

Query Match 11.1%; Score 104.6; DB 10; Length 855;
Best Local Similarity 49.8%; Pred. No. 1.6e-18;
Matches 427; Conservative 0; Mismatches 394; Indels 36; Gaps 5;

Qy 88 TTTGATGCTGGAATGCCACCATTAACAATATGCCACCTTATGGAATCTCTGTAAT 147
Db 10 TTTGAGTTGAGAAATGCCACCAAGAACTTACTTAATTTCTGACTAGTTGGCGAA 69
Qy 148 CAAGCGAAAGATCCAAATCTAAATGTATGTCATACCAATGCTACTGATTAATG 207
Db 70 GCTGTAAAGACAAAGAAATGACATGCAATGATATATATGCGCAACCTCCTACTGA 129
Qy 208 ACCCTTAAGTACTTATTTGGTAAAGTCAAGGTGCAAACTTAATAACCTTACATA 267
Db 130 CAACCAATATATGTGTGTGACCTCAAAATTCGATCTGGAACATTC--ACATTTGCA 186
Qy 268 CTGAGACGAATTAATCTTAATGCTGATGGCTATTTGATCCCTCAATGGCAATTA 327
Db 187 ATCAGAAAGGGAACCTTAATTTGGAGGCTATTTGACATTTTACATGG--AAATGT 243
Qy 328 CATTACCAATATTTAATATATTAACAAGACCGAAGCACTGATGTGAGAAATCTTT 387
Db 244 CGTTATCGATCTTCAAGATTCAGATCC-----GATGCCCAAGGACCGTT 291
Qy 388 TCTCAAGTTCTAGTCTCGTGTGCAATGTCCATTAATCAATAGCTTAATCCGACC 447
Db 292 TGGCCCGGGGACAAAGCAAGCTGGCACTCAGAAATTAATTCCTCATGAAAGAGTTAC 351
Qy 448 ATGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCAATGGGAATTCAAATATCTC 507

Db 352 AAAGGATGGAATCAAAAGGTGGGGCTTAGAACTAATTAAGGGTTAGAAAGATTAACATC 411
Qy 508 AGAGTGACATTTGAAAAAATCTCTGAGTTGATTAATCTCCGT-----AAAA 555
Db 412 AAGAGTCGAATGGTTAAATCTACCGCAAGATGCAAGGATCAAGAGATTAACAAA 471
Qy 556 ACTGAGCTTTTCTTCTACTGTGAGCATCAAAATGTTTACAGAGGACGGCATTTCAAG 615
Db 472 AATGAGCTGAATTTCTTCTTATAGCCGTTCAAAATGTTTACTGAGGCATCAAGTTCAA 531
Qy 616 TACATAGAAACCAAGTCAAGACTAATTTTATAGCA-----TTTACCTGATCCC 669
Db 532 TACATAGAAACCAAGTCAAGCTAATTTTATGATGCAATGGTATCAGCAGATCTT 591
Qy 670 AAGTAATTAATTTGGAGGAAAGTGGGCAAAATCTCTGAGCATTCACATGCAAG 729
Db 592 AAGCTAATTTCCCTAGAGAAAATTTGGACAGTGTTCATAGGTCAATTCAAAAGTTGAC 651
Qy 730 AATGGGCTTTTACCCCAACCACTTGAGCTAGTGAATGCCAAAGTACCAAGTGAATGT 789
Db 652 ACCTCGGTGATAGTACTGTACTTTACTGAGACCTTAAGATGAAATTAATTAACCT 711
Qy 790 CTTAGAGTGAATGAATCAATGATGTGCACTTCCTTAAGTACGTTAATGGAACCTGT 849
Db 712 TGGACTACGGCCACATGAACGACCTTAAGAACGATTAATGCACTCTCAACCCAGTT 771
Qy 850 CAGACCACTTACCAAAATGCAATGTTCTCTCAAGTTAATTAATTTCTATTAATTAAT 909
Db 772 ACTTGAAGTTAAAGTTCATGTTCCCTGAATTAATGTCTTATTAATTAATGACTAGT 831
Qy 910 AATGCTAATCTTGTGTA 926
Db 832 ATTATGAACCTTGTGTA 848

RESULT 13

US-10-919-750-4
; Sequence 4, Application US/10919750
; Publication No. US20050120414A1
; GENERAL INFORMATION:
; APPLICANT: Diamond, Paul
; TITLE OF INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
; FILE REFERENCE: PT100-4US
; CURRENT APPLICATION NUMBER: US/10/919,750
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US 10/644,288
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 10/354,903
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/352,705
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 4
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Saponaria officinalis
US-10-919-750-4

Query Match 10.2%; Score 96; DB 9; Length 935;
Best Local Similarity 49.3%; Pred. No. 4.5e-16;
Matches 398; Conservative 0; Mismatches 395; Indels 15; Gaps 5;

Qy 1 ATGAAGGTATGCTGTGATTTGTGTGACGTTAATTAAGCGTCACTTGTCTGACCAACT 60
Db 85 ATGAAGATTAATGTTGTATGACCAATTAAGCATGATCTCTTCAATTTCACTTGGACA 144
Qy 61 TCAACTGTGCAATTAATAGATCACTTGAATGCTGGAATGCCAATTAACAAATAT 120
Db 145 ACAATGATGCGGTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 204
Qy 121 GCCACTTTATGAATCTCTTGTATTAACAGGAAAGATCAAACTAAATGCTATGGC 180

```

Db      205  TCAATCTTTGTGATAAATCCGAAACAAAGTAAAGATCCAAACTCGAATTAAGGTGCT 265
QY      181  ATACCAAT---GCTACCTGATACTAATTGCAACCCCTAAGTACTTATTGGTTAACTCCAA 237
Db      265  ACCGACATGACCGCTGATAGGCCACCTCTTAAAGAAAAATTCCTTAGAATTAATTCCAA 322
QY      238  GGTGCAACCTTAAAAACAATTACATATGCTGACAGCAATATACCTATACGTGATGGC 297
Db      325  AGTTCT---CCGAGAAACGGCTCACTTGGCTTAAACGCAATTAATTGTATGGTGGC 381
QY      298  TATTCTGATCCCTTCAATGCGCAATTAAGTGTGCTTACATATATTATTATGATATACAGC 357
Db      382  TATCTTGCAATGATATACAGATGTTAATCCGGCATTTACTTCAATCAGAAATTACT 441
QY      358  ACCGAAACGCACTGATGTGAGAAATCTCTTGTCTCAAGTTCTAGTTCTGTGTTCAATG 417
Db      442  TCCGCGAGTCAACCCCTTTTCCAGAGGCCAACACTCAATCAGAAAGCTTTGAA 501
QY      418  TCCATTAACTACATAGTCTTATATCCGACCATATGAAAAAGAAAGCAAGTAACTCA--- 477
Db      502  TACACAGAGATTTATCACTGATTTAAAGAAATGCCAGATTAACAAAGAGATCAAAGT 561
QY      475  AGAAATCAAGTCCAAATTGGGAATTTCAAAATPACTAGCAGTGAACATTGGAAAAATCTCGA 538
Db      562  AGAAAGAAATCGGGTGTGGGATTTGACTTACTTCAACGTCCATGAGACGTGAACAAG 621
QY      535  GTTGATTCATTCCTGTAAAACTGAAGCTTTTCTTACTGTGAGCCATCCAAATGTT 594
Db      622  AAGG---CACGTGTGTTAAAGACGAAGTCAAGTCTCTTATTCGTATTCAGATACG 678
QY      595  TCAGAGGCGACCGCGATTCAGATCATAGAGACCAAGTCAAGACTAATTTTAATAGCA 654
Db      679  GCTGAGGCGACCGGATTTAGTACATACAAACTTGTGTATCAAGAACTTTCCACAAG 738
QY      655  TTCTACCCCTGATCCCAAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTCTGAGCA 714
Db      739  TTCAACTCGGAAAAACAAGTATTCAGTTTGAAGTTTACTGGAATAAAAAATTTCTAGCGCA 798
QY      715  ATTCACT---AATGCCAAGATGGGGCTTTAACCCAAACACTTGAAGTAGTGAATGCCAA 771
Db      799  AATATCGGGGAATGCCAAAAACGGCGTTTAATTAAGATTAATGTTCCGGTTTGGAAA 858
QY      772  GGTACCAAGTGAATAGTCTTAGATGG 799
Db      859  GTTAGCGAGGTGAAGACTTGCAAAATGG 886

RESULT 14
US-09-861-257-37
; Sequence 37, Application US/09861257
; Publication No. US20030040496A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Pierce, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; NUMBER OF INVENTIONS: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

1  APPLICATION NUMBER: US//09/861,257
2  FILING DATE: 17-MAY-2001
3
4  CLASSIFICATION:
5
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Christiansen Ph.D., William T.
8  REGISTRATION NUMBER: 44,614
9  REFERENCE/DOCKET NUMBER: 760100.423C1
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (206) 622-4900
12 TELEFAX: (206) 682-6031
13 INFORMATION FOR SEQ ID NO: 37:
14 SEQUENCE CHARACTERISTICS:
15     LENGTH: 804 base pairs
16     TYPE: nucleic acid
17     STRANDEDNESS: double
18     TOPOLOGY: unknown
19     MOLECULE TYPE: cDNA
20     FEATURE:
21     NAME/KEY: CDS
22     LOCATION: 1..804
23     FEATURE:
24     NAME/KEY: misc.feature
25     LOCATION: 1..804
26     OTHER INFORMATION: /note= "Nucleotide sequence
27     OTHER INFORMATION: corresponding to the clone M13 mp18-G7"
28     FEATURE:
29     NAME/KEY: mat.peptide
30     LOCATION: 46..804
31     OTHER INFORMATION: /product= "Saporin"
32
33 US-09-861-257-37

```

Query Match	9.4%;	Score 88.4;	DB 3;	Length 804;
Best Local Similarity	49.3%;	Pred. No. 5,86-14;		
Matches	376;	Conservative	0;	Mismatches 371; Indels 15; Gaps 5
Qy	47	TTGCTGCACCACTTCAACTGTTGCCAATTAATGATCACCCTTGATGCTGAATAATGCCA	106	
Db	20	TTTCAGCTTGGACAAACAATGATATCGGTCACATCAATCACTATGATATAGTAATTCGGA	79	
Qy	107	CCATTAACAATATATAGCCACCTTTATGGAATCTCTTCGTAATCAAGCGAAATCCAAAC	166	
Db	80	CCGGGGGTCACTACTCACTTTTGTGGATTAATTCGAAACAAGTAAGATCCAAACC	139	
Qy	167	TAAATATCTATGGCATACCAATGC---TACCTGTACTAATTTGCAACCCCTTAAGTACTTAT	223	
Db	140	TGAATATCGGTGTACCGACATACCCGTGATAGGCCACCTTTAAAGAAATATCTTGA	199	
Qy	224	TGCTTAAGCTCCAAAGGTGCAAACTTAATAAACATTACATAATGTGAGAGAAATAACT	283	
Db	200	GAATTAATTTTCCAAAGTTC---CCGAGAAAGGTCTCACTTGGCTTAATAAGCGCAATAC	256	
Qy	284	TATACGTATGAGGCTATTTCTGATCCCTTCATAGGCAATATAGTGTGTTACCATATATTTA	343	
Db	257	TGTATGTGTGTGGCTATCTTGCAATGATATACAGAAATGTTAATGTGGCATATTACTTCA	316	
Qy	344	ATGATATTTACAGACCGGAACGCACTGATGTGGAAATACTCTTTTGCTCAAGTTCTAGTT	403	
Db	317	GATCAGAAATTTACTTCGCCGAGTTAACCGCCCTTTTCCAGAGGCCACCACTCCAAATC	376	
Qy	404	CTCGTGTTCGAATATTCATTAACTACACATATAGCTTATATCCGACCATGAAATGAAGAGAG	463	
Db	377	AGAAAGCTTTAGATATACAGAAATATTTACGTGATCGAAAGAAATGCCAGATTAACAC	436	
Qy	464	AAGTA---AATCTCAAGAAATCAAGTCCAAATTGGGAATTCAAATATCTCAGCAGTACATGG	520	
Db	437	AGGAGATATTAATCAAGAAAGAAATCTCGGTTGGGAGATCGACTTACTTTTGACGTCAATGG	496	
Qy	521	GAATAATCTCTGGAGTTGATTTCAATTCCTGTAAATAATCGAGGCTTTTTCCTACGTGATG	580	
Db	497	AAGCAGTGAACAGAA---AGGCACGTGTGTGTTAAACAGAACTAGATTTCTTTTATCG	553	
Qy	581	CCATCCAAATGTGTTTCAGAGCAGCGGATTCAGATCATAGAGAACCAATCAAGACTA	640	

Db 554 CTTATGATGACGCTGAGGCAAGCATTTAGTACATACAAAAGCTGGTATCATAGA 613
QY 641 ATTTAATAGAGCATTTCTACCTTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCA 700
Db 614 ACTTCCCAACAGATTCACCTCGGAAACAAAGTATTCAGTTAGGTTAACTGGAAAA 673
QY 701 AATCTCTGAGCAATTCAC--AATGCCAAGATGGGGCTTTACCAAAACCACTTGAGC 757
Db 674 AATTTCTACGGCAATATACGGGGATGCCAAAAACGGCGTGTAAATTAAGATTAATGATT 733
QY 758 TAGTGATGCCAAGGTACCAAGTATAGTTCTTAGAGTGG 799
Db 734 TCGGGTTGGAAAAGTACGAGGAGGTGAGGACTTGCAAAATGG 775

RESULT 15
US-09-861-257-38
; Sequence 38, Application US/09861257
; Publication No. US20030040496A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Pierce, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christensen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100,423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..804
OTHER INFORMATION: /notes= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-C9"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-09-861-257-38

Query Match 9.4%; Score 88.4; DB 3; Length 804;
Best Local Similarity 49.3%; Pred. No. 5.8e-14;

Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;
QY 47 TTGCTGACCAACTTCAACTGTGACATTAATAGATGACCTTGTAGTGGAAATGCCA 106
Db 20 TTTGAGCTTGACACAACTGATGCGGTCAATCAATTCATTAATGATCTGATTAATCCGA 79
QY 107 CCATTAACAAATATGCACTTATGAAATCTCTTGATATCAAGGAAAGATCCAAAC 166
Db 80 CCGCGGGTCAATGATCATCTTTTGTGATTAATTCGAAACAAAGTAAGATCCAAAC 139
QY 167 TAAATGCTATGACATACCAATGC--TACGTATATCTAATTTGACCCCTTAAGTACTTAT 223
Db 140 TGAATATACGGTGTATACCAATAGCCGTATAGGCCACCTCTTAAGAAATTCCTTA 199
QY 224 TGGTAAAGCTCCAAAGGTGCAAACTTAACCACTTACATTAATGCTGAGCAAGAAATACT 283
Db 200 GAATTAATTTCCAAAGTTC--CCAGGAACGGTCTCACTTGGCTTAAGCGGATACCT 256
QY 284 TATACGTATGAGCTATTTCTGATCCCTCAATGGCAATTAAGTGTGTTACATATATTTA 343
Db 257 TGTATGTGGTCGGGTATCTTGCAATGATTAACGAAATGTTAATGGGATATTAATCTCA 316
QY 344 ATGATTTTCAAGCACCGCAACGCACTGATGTGAATATCTTTGCTCAAGTTCTAGTT 403
Db 317 GATCAGAAATTACTTCCGCCAGTTAACGCCCTTTTCCAGAGGCCAACATGCAAAATC 376
QY 404 CTGCTGTGCAATGTCATTAATCAATAGCTTATATCCGACCAATGAAAAGAAAGCAG 463
Db 377 AGAAAGCTTGAATACAGAAAGATTAATCAATGATTAATTAAGAAATGCCATATACAC 436
QY 464 AAGTAAACTCA--AGAAATCAAGTCCAAATGGGAATTCAAATPACTCAGACGATGATG 520
Db 437 AAGGAGATCAAGTGAAGAAAGAACTCGGTTGGGATGATCACTTCAAGTCATG 496
QY 521 GAAAAATCTCTGAGATGTTCAATTCCTCTGTAATAAATGAGCTTTTCTTACTGTGAG 580
Db 497 AAGCAAGTGAACAAGA--AGGCAAGTGTGTAAAGACAAACCTAGATTCCTTCTATG 553
QY 581 CCATCCAAATGTTTCAGAGGACGAGCGATTCAGATACATAGAAACCAAGTCAAGACTA 640
Db 554 CTTTCAATGACGCTGAGGCAAGCGGATTTAGTACATCAAAACCTTGGTATACAGA 613
QY 641 ATTTAATAGACATTTCACTCTGATCCCAAGTAAATTAATTTGAGGAAAGTGGGCA 700
Db 614 ACTTCCCAACAGATTCACCTCGGAAACAAAGTATTCAGTTGAGTTAATCTGAAAA 673
QY 701 AATCTCTGAGCAATTCAC--AATGCCAAGATGGGGCTTTACCAAAACCACTTGAGC 757
Db 674 AATTTCTACGGCAATATACGGGGATGCCAAAAACGGCGTGTAAATTAAGATTAATGATT 733
QY 758 TAGTGATGCCAAGGTACCAAGTATAGTTCTTAGAGTGG 799
Db 734 TCGGGTTGGAAAAGTACGAGGAGGTGAGGACTTGCAAAATGG 775

Search completed: April 9, 2006, 01:44:59
Job time : 1094.88 secs


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QY 188 TGGTACCTGATCTAATTCGACCCCTAAGTACTTATGTTAGTTCGAAAGTGGCAACC 247
   |||
Db 388 TGGTACCTGATCTAATTCGACCCCTAAGTACTTATGTTAGTTCGAAAGTGGCAACC 247
   |||
QY 248 TAAAAACCTAATGCTGAGAGCAATTAATCTATACGTGATGGGCTATTTGATC 307
   |||
Db 448 AAAAAACCTAATGCTGAGAGCAATTAATCTATACGTGATGGGCTATTTGATC 307
   |||
QY 308 CCTTCATGGCAATTAAGTGTGTTACCATATATTAATTAATTAACAAGACGCAACGCA 367
   |||
Db 508 CCTTCATGGCAATTAAGTGTGTTACCATATATTAATTAATTAACAAGACGCAACGCA 367
   |||
QY 368 CTGATGTGAGAACTCTCTTCTCTCAAGTCTAGTCTGCTGTGCAATGTCCATTAAT 427
   |||
Db 568 AAGATGTAGAGTCTCTCTTCTCTCAAGTCTAGTCTGCTGTGCAATGTCCATTAAT 427
   |||
QY 428 ACAATGCTATATCCGACCATGAAAGAAAGCAAGAACTCAAGAAATCAAGTCC 487
   |||
Db 628 TTGATGTGCAATTCGAATTCGAAATCAAGAGGAGGAGAAATCAAGAAATCAAGTCC 487
   |||
QY 488 AATTGGGAATTCGAATTCGAGAGTGAATGGAATTAATCTGAGAGTGAATTCGCA 547
   |||
Db 688 AACTGGGAATTCGAATTCGAGAGTGAATGGAATTAATCTGAGAGTGAATTCGCA 547
   |||
QY 548 CTGTAAAACTGAGGCTTTTCTCTCTGAGTGAATTCGCAATGTGTTCAAGGCAAGCC 607
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Db 748 CTGAGAAACCGAAGCCGAAATTCCTATGTTAGTCCATCAATGTGTTCAAGGCAAGCC 607
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QY 608 GATTCAAGTATAGAGAACTCAAGTCAAGTCAATTAATTAATTAAGTTCATCCGATC 667
   |||
Db 808 GATTCAAGTATAGAGAACTCAAGTCAAGTCAATTAATTAATTAAGTTCATCCGATC 667
   |||
QY 668 CCAAGATTAATTAATGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAAATGCCA 727
   |||
Db 868 CCAAGATTAATTAATGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAAATGCCA 727
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QY 728 AGAATGGGCTTTAACCAGCACTGAGTATGATGTCGAAAGTATCCAGTGTGATG 787
   |||
Db 928 AGAATGGGCTTTAACCAGCACTGAGTATGATGTCGAAAGTATCCAGTGTGATG 787
   |||
QY 788 TTCTTAGAGTGAATGAATCGATGATGTCACCTTAAGTACGTTAATGGAACCT 847
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Db 988 TTCTTAGAGTGAATGAATCGATGATGTCACCTTAAGTACGTTAATGGAACCT 847
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QY 848 GTGAGCAACTT---ACCAAAATGCAATGTTCTCTCAAGTATTAATTTCTACTTATTA 904
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Db 1048 GTGAGCAACTTATTAACCAAAATGCAATGTTCTCTCAAGTATTAATTTCTACTTATTA 904
   |||
QY 905 ATTATATGCTTAATCTTGTGATCTAATTTGAAGGATTTCTAA 945
   |||
Db 1108 ATTATATGCTTAATCTTGTGATCTAATTTGAAGGATTTCTGA 1148
   |||

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RESULT 2

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US-11-010-795-21
; Sequence 21, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING I3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 21
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-11-010-795-21

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Query Match 11.7%; Score 110.8; DB 14; Length 934;
Best Local Similarity 50.0%; Pred. No. 3.8e-18;
Matches 472; Conservative 0; Mismatches 427; Indels 45; Gaps 6;

```

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QY 1 ATGAGGTGATGCTGTAGTGTGAGGAGTTAATGCGGGCTCATTTGCTGACCAACT 60
   |||
Db 7 ATGAGGTGATGCTGTAGTGTGAGGAGTTAATGCGGGCTCATTTGCTGACCAACT 66
   |||
QY 61 TCACTTGTGCAATTAATGATCACTTTGATGCTGAAATGCCAATTAATTAATTAAT 120
   |||
Db 67 GCTTCTTAAAGATA-----GTTTGAAGTTGAGAAATGCCACACCAAGAACTTAC 117
   |||
QY 121 GCCACCTTATGGAATCTCTGTAATCAAGCAAGATTCGAATTAATTAATTAAT 180
   |||
Db 118 TCTAATTTTCTGACTAGTTTGCAGAGAGCTGTGAAAGCAAGAAATTTGACATCCATGGA 177
   |||
QY 181 ATACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATGTTAGTTCGCAAGT 240
   |||
Db 178 ATGATATGCGCAACCACTCTGACGAAACAACCAAGTATGTTGCTGACCTCAATTC 237
   |||
QY 241 GCAACCTTAATAACCTTACACTAATGCTGAGAGCAATTAATTAATTAATTAAT 300
   |||
Db 238 GATCTGGAACATTC---ACATTAGCAATCAAGAGGGAACCTTAATTTGAGGGCTAT 294
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QY 301 TCTGATCCCTTCAATGCAATTAATGCTGTTACATATATTAATTAATTAATTAAT 360
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Db 295 TCTGATTTTCAATG---AAATGTCTTATCGGATCTTCAAGAT----- 339
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QY 361 GAAGCACTGATGATGAGAAATCTTTGCTCAAGTTCATGTTCTGCTGTGCAATGTC 420
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Db 340 TCAAGATCCGATGCCAAGAGACCTTTCCTGCGGAGCAAAAGCAAGCTTGCATTCAG 399
   |||
QY 421 ATTATCAATATGCTTATATCCGACATGAGAAAGAAAGCAAGTAAATCAAGAAAT 480
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Db 400 AATATATCCCTATGAAAGAAAGTTACAAAGGATGGAATCAAGGGTGGGCTTAACA 459
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QY 481 CAAGTCAATTTGGGAATTCGAATCTGAGAGTGAATGGAATTAATTTCTGAGTGTAT 540
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Db 460 AAATTGGGTTTGAAGAAATTAACCTCAAGAGTCAATGGAATTAATTTCAAGCAAGAT 519
   |||
QY 541 TCA-----TTCCCTGTAATACTGAGGCTTTTCTCTGATGAGGATCCAA 588
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Db 520 GCAACGATTCAGAGCAATGATCAAAAGAAATGAGGCTGAATTTCTTATAGCGTTCAA 579
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QY 589 ATGCTTCAAGAGCAGCGGATTCAGATCATAGAGAACCAAGTCAAGTAAATTTTAAT 648
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Db 580 ATGCTTCAAGAGCAGCGGATTCAGATCATAGAGAACCAAGTCAAGTAAATTTTAAT 639
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QY 649 -----AGAGCACTTCACTGATCCCAAGTAATTAATTTGAGAGAGAAATGGGCAAA 702
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Db 640 GATGCCAATGGGATATGAGCAGATCTTAAGATTTCCCTGAGAGAAATTTGGGACAGT 699
   |||
QY 703 ATCTGAGGCAATTCAGAAATGCAAGATGAGGAGCTTTACCCCAACCACTGAGCTAGT 762
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Db 700 GTTTCATAGGCTCATGCAAAAGTTGGCACCTCCGATGATGATGTTACTTAACTGGA 759
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QY 763 GATGCCAAGTATCAAGATGATGATTTCTTAAAGTGAATGAATCAATGATGATGGA 822
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Db 760 GACCTAAAGATGAGAAATTAATACTTGAATGAGGCAACATGAAACACTTAAAGAC 819
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QY 823 CTCTTAAGTATGATGAACCTGACAGCACTTACCAAAATGCCAATGTTCTCTCA 882
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Db 820 GACATTTATGCACTCTTAACCAAGTATCTTGAAGTAAAGTTCCAGTTCCTCTGA 879
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QY 883 GTTATATTTCTACTATTAATTAATTAATGATGATGATGATGATGATGATGATG 926
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Db 880 ATTATGCTCTTATTAATTAATGAGCTAGTATTAATGATGATGATGATGATGATG 923
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RESULT 3
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Query Match 6.7%; Score 63; DB 8; Length 1623;
Best Local Similarity 54.0%; Pred. No. 7.7e-06;
Matches 15; Conservative 0; Mismatches 125; Indels 6; Gaps 1;
QY 555 AACTGAGCTTTTCTTCTAGTGGCCATCAAAATGGTTTCAAGGCGCGCATTCAA 614
DB 486 AACTGAGCTTTTCTTCTAGTGGCCATCAAAATGGTTTCAAGGCGCGCATTCAA 545
QY 615 GTACATGAGAACCAACTCAAGACTAATTT-----AATAGACATTTCACTGATCC 668
DB 546 ATATATTGAGGAGAAATGCGGACAGAAATTAAGTACACCGAGATCTGCACCAATCC 605
QY 669 CAAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAGGCAATTCAGATGCCAA 728
DB 606 TAGGTATTAATCACTTGAAGTAAGTGGGGAGACTTCCACTCAATTCAGAGCTTAA 665
QY 729 GAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCAAGGTACCAAGTGAATGT 788
DB 666 CCAAGGAGCTTTGCTAGTCCAATTCAGATGCAAGAGATGTTCCAAATTCAGTGT 725
QY 789 TCTTAGTGTGAGTAATCAATGATGTGATGGCACTCTTAAGTA 833
DB 726 GTAGATGTGATATTAATCCCTATCATAGCTCTCATGTGT 770

RESULT 4
US-10-893-584-83
; Sequence 83, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752

PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-268 insert
US-10-893-584-83

Query Match 6.6%; Score 62.4; DB 8; Length 1855;
Best Local Similarity 50.0%; Pred. No. 1.2e-05;
Matches 187; Conservative 0; Mismatches 181; Indels 6; Gaps 1;
QY 555 AACTGAGCTTTTCTTCTAGTGGCCATCAAAATGGTTTCAAGGCGCGCATTCAA 614
DB 597 AACTGAGCTTTTCTTCTAGTGGCCATCAAAATGGTTTCAAGGCGCGCATTCAA 656
QY 615 GTACATGAGAACCAACTCAAGACTAATTT-----AATAGACATTTCACTGATCC 668
DB 657 ATATATTGAGGAGAAATGCGGACAGAAATTAAGTACACCGAGATCTGCACCAATCC 716
QY 669 CAAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAGGCAATTCAGATGCCAA 728
DB 717 TAGGTATTAATCACTTGAAGTAAGTGGGGAGACTTCCACTCAATTCAGAGCTTAA 776
QY 729 GAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCAAGGTACCAAGTGAATGT 788
DB 777 CCAAGGAGCTTTGCTAGTCCAATTCAGATGCAAGAGATGTTCCAAATTCAGTGT 836
QY 789 TCTTAGTGTGAGTAATCAATGATGTGATGGCACTCTTAAGTAAGTGAATGT 848
DB 837 GTAGATGTGATATTAATCCCTATCATAGCTCTCATAGTGTATGATGCCACCTCC 896
QY 849 TCAGAACCTTACCAAAATGCCAATGTTCTCAAGTTAATTTCAATTAATTAATTA 908
DB 897 ACCATGCTCAAGTTTAAGGGGTGAGATGCTTAGGCCCAATACGCTTATGCTGATGT 956
QY 909 TATGCTAATCTTG 922
DB 957 TTGTATGATCTTG 970

RESULT 5
US-10-893-584-266
; Sequence 266, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-266

Query Match 6.6%; Score 62.2; DB 8; Length 1837;
Best Local Similarity 52.0%; Pred. No. 1.3e-05;
Matches 167; Conservative 0; Mismatches 148; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCAAATGGTTTCAGAGCGCGGATTCAA 614
DB 597 AACTGAGGCTCGTTCCTTATTAATTTGCAATCCAAATGATTTCCAGAGCGCGGATTCCA 656
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCAATTCACCTGATCC 668
DB 657 ATATATTAGGAGGAATATGGCGACGAAATTAGTACACCGAGATCTGCACCAATCC 716
QY 669 CAAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAATGCCAA 728
DB 717 TAGCGTAATTAACATCTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 729 GAATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 777 CCAGAGAGCTTTGCTAGTCCAAATTCGAAAGACGTAAATGTTCCAAATTCAGTGT 836
QY 789 TCTTAGTGATGATGAATCAATCGTATGTCGACTCCTTAAGTACGTTAATGAAACCTG 848
DB 837 GTACGATGTGAGATATTAATCCCTATCATAGCTCTCATGTGTATATAGATCGGAGCGG 896
QY 849 TCAGACAACTTACCAAAATGC 869
DB 897 GACTCACCGCAAGAAATGC 917

RESULT 6
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, KONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
; ORGANISM: *Ricinus communis*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

Query Match 6.5%; Score 61.4; DB 14; Length 807;
Best Local Similarity 53.7%; Pred. No. 1.5e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCAAATGGTTTCAGAGCGCGGATTCAA 614
DB 489 AACTGAGGCTCGTTCCTTATTAATTTGCAATCCAAATGATTTCCAGAGCGCGGATTCCA 548
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCAATTCACCTGATCC 668
DB 549 ATATATTAGGAGGAATATGGCGACGAAATTAGTACACCGAGATCTGCACCAATCC 608
QY 669 CAAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAATGCCAA 728
DB 609 TAGCGTAATTAACATCTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 668
QY 729 GAATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788

DB 669 CCAGAGAGCTTTGCTAGTCCAAATTCAGTCAAGAGCGTAATGTTCCAAATTCAGTGT 728
QY 789 TCTTAGAGTGATGAATCAATCGTATGTCGACTCCTTAAGTA 833
DB 729 GTACGATGTGAGATATTAATCCCTATCATAGCTCTCATAGGTGTA 773

RESULT 7
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: *E. coli*
US-10-893-584-196

Query Match 6.5%; Score 61.4; DB 8; Length 1807;
Best Local Similarity 53.7%; Pred. No. 2.1e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCAAATGGTTTCAGAGCGCGGATTCAA 614
DB 597 AACTGAGGCTCGTTCCTTATTAATTTGCAATCCAAATGATTTCCAGAGCGCGGATTCCA 656
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCAATTCACCTGATCC 668
DB 657 ATATATTAGGAGGAATATGGCGACGAAATTAGTACACCGAGATCTGCACCAATCC 716
QY 669 CAAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAATGCCAA 728
DB 717 TAGCGTAATTAACATCTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 729 GAATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 777 CCAGAGAGCTTTGCTAGTCCAAATTCGAAAGACGTAAATGTTCCAAATTCAGTGT 836
QY 789 TCTTAGTGATGATGAATCAATCGTATGTCGACTCCTTAAGTA 833
DB 837 GTACGATGTGAGATATTAATCCCTATCATAGCTCTCATAGGTGTA 881

RESULT 8
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584

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/ CURRENT FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 168
/
/ LENGTH: 1810
/
/ TYPE: DNA
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/ ORGANISM: B. coli
US-10-893-584-168

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Query Match	6.5%;	Score 61.4;	DB 8;	Length 1610;
Best Local Similarity	53.7%;	Pred. No. 2.1e-05;		
Matches 153;	Conservative	0;	Mismatches 126;	Indels 6;
				Gaps 1;

Qy	555	AACGAGGCGCTTTTCTTCTACGTGGTGGCCATCCAAATGTGTTTCAGAGGCGCGGATTCAA	614
Dy	597	AACCTGGCTCGTTCCTTTATTAATTGGATCCAAATGATTTGAGAGGCAAGAAATTC	656
Qy	615	GTACTATGAGAACCAAGTCACAGCTAATTTT-----AATAGGCAATTCCTCGATCC	668
Dy	657	ATATATTTAGGAGGAGAAATGCGCACAGAAATTGGTACCAACCGAGATCTGCACCAAGATCC	716
Qy	669	CAAGTATATTAATTGGAGAGCAAGTGGGGCAAAATCTGTGAGGCAATTCAATGCGCAA	728
Dy	717	TAGCGTATTTACCTTGGAAATGATGTTGGGGGAGACTTTCACCTGCATTCGAAAGCTTAA	776
Qy	729	GAATGGGCGCTTACCACAACCACTTGAGCTAGTGAGTCAAAGTAGCCAAAGTAGTAGT	788
Dy	777	CCAAAGGAGCCCTTGGTAGTCCCAATTCACCTGCAAGAAGCGTATNGTTCCAAATTCGTGT	836
Qy	789	TCTTAGAGTGATGAATCAATCGATGATGTGCACTCCCTTAAGTA	833
Dy	837	GTACAGATGTAGTATTAATTCCTATCATACCTCTTCATGTGGTGA	881

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RESULT 9
US-10-093-584-245
: Sequence 245, Application US/10893584
: Publication No. US20050272048A1
: GENERAL INFORMATION:
: APPLICANT: Borgford, Thor
: APPLICANT: Braun, Curtis
: APPLICANT: Pirac, Adam
: APPLICANT: Stoll, Dominik
: TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer
: TITLE OF INVENTION: Viral or Parasitic Infections
: INVENTOR:

```

Query Match	6.5%	Score 61.4;	DB 8;	Length 1813;
Best Local Similarity	53.7%;	Pred. No. 2.1e-05;		
Matches 153;	Conservative 0;	Mismatches 126;	Indels 6;	Gaps 1

555 AACTGAGCGTTTTTCTACTGCTGACCATCCAAATGTTTTCAAGAGGAGCGGCATTCAA 614

Accession	Sequence	Position
Db	AACTCGGCTCGTCCCTTATTAATTTGATCCAAATGATTTCCAGACGACGAAGTTCCA	556
Dy	GTACATAGAGAAACCAAGTCAGACTAATTT-----AATAGACATTCTACCTGATCC	668
Db	ATATATTGAGGAGAAATGCGACACGAATTAAGGTACCAACGGAGATCTGCACCAAGTCC	716
Dy	CAAGTAAATTAATTTGGAGAGAAAGTGGGGCAAAATCTGTGAGGCATTCACATGCGAA	728
Db	TACGGTAATTAACACTTGAGAAATAGTTGGGGAGACTTTCACCTGCATTCAGAGGTAA	776
Dy	GAATGGGGCTTTACCCAAACCACTTGAGCTGATGAGATGCCAAAGATGCAAGTGATGT	788
Db	CCAGAGAGCCTTGTCTAGTCCAAATTCACATGCCAAAGACGTAAATGTCTCCAAATTCAGTGT	836
Dy	TCTTAGATGAGATGAAATCATCATCGATGATGGCACTCCTTAAGTA	833
Db	GTACAGATGTGATATTAATTAATCCCATCATGACTCTCATAGGTGTA	881

```

RESULT 10
US-10-893--584-238
: Sequence 238, Application US/10893584
: Publication No. US20050272048A1
: GENERAL INFORMATION:
: APPLICANT: Borgford, Thor
: APPLICANT: Braun, Curtis
: APPLICANT: Purac, Adamir
: APPLICANT: Stoll, Dominik
: TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer
: TITLE OF INVENTION: Viral or Parasitic Infections
: FILE REFERENCE: 10447-025
: CURRENT APPLICATION NUMBER: US/10/893,584
: CURRENT FILING DATE: 2004-07-19
: PRIOR APPLICATION NUMBER: US 09/551,151
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: US 09/403,752
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 10/089,058
: PRIOR FILING DATE: 2000-10-04
: NUMBER OF SEQ ID NOS: 274
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 238
: LENGTH: 1819
: TYPE: DNA
: ORGANISM: E. coli
: US-10-893--584-238

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Query Match	6.5%;	Score 61.4;	DB 8;	Length 1819;
Best Local Similarity	53.7%;	Pred. NO. 2.1e-05;		
Matches 153; Conservative	0;	Mismatches 126;	Indels 6;	Gaps 1.

QY	555	AACTGAGGCTTTTTTTCTACTGGTGGCATCCAAATGGTTTCAAGGAGCGCATTCAA	612
Db	597	AACCTCGGCTCGTTCCTTTATTTGATTCACAAATATGTTTCAGAGCAGCAAGATTC	656
QY	615	GTAACATAGAAACCAAGTCACACTAATTTT-----AATGACATTTACCTGATCC	668
Db	657	ATATATTGAGGAGAAATCGCAGCAAGATTAGGTACAAACGAGATCTGCACAGATCC	718
QY	669	CAAACTAATTAATTGGAGAGAAATGGGGGCAAAATCTGTAGGCATTTCAATGGCAA	728
Db	717	TACGGTAATTAACCTTGAAATAGTTGGGGAGACTTTTCCACTGCAAATTCMAAGGTAA	776
QY	729	GAATGGGCTTTACCCAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGTAGT	788
Db	777	CCAAGAGCCTTTGTGATGCCAATTCACATCGCAAAAGCTAATGGTTCCAAATTCAGTGT	838
QY	789	TCTTGAAGTGAATGAATCAATCGATGATGTGGCACTCCTTAAGTA	833
Db	837	GTAAGATGTGAATATTAATCCCTATCATAGCTCTCAATGGTGTGA	881

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, **using frame p2n model**

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -ALIGN=15 -MODE=LOCAL
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1352	83.6	792	6	AX427704 Sequence

4	1332	82.4	786	15	AB071855	AB071855 PhytoIacc
5	1307	80.8	1092	6	AX427720	AX427720 Sequence
6	1241.5	76.8	942	15	AY572976	AY572976 PhytoIacc
7	1235.5	76.4	942	15	AY547315	AY547315 PhytoIacc
8	1235.5	76.4	1164	15	PAPAP	X55383 P.americana
9	1235.5	76.4	1195	6	AA2103	AA2103 Sequence 1
10	1235.5	76.4	1195	6	I43835	I43835 Sequence 1
11	1235.5	76.4	1195	6	I55866	I55866 Sequence 1
12	1235.5	76.4	1379	6	AR009535	AR009535 Sequence 1
13	1235.5	76.4	1379	6	AR136704	AR136704 Sequence
14	1235.5	76.4	1379	6	AX427731	AX427731 Sequence
15	1232.5	76.2	1379	6	AR141172	AR141172 Sequence
16	1231.5	76.2	1164	15	AY049785	AY049785 PhytoIacc
17	1229.5	75.0	1195	6	A36639	A36639 Sequence 1
18	1227.5	75.9	1378	6	AX427732	AX427732 Sequence
19	1227.5	75.9	1379	6	AR136705	AR136705 Sequence
20	1225	75.8	939	15	AY327475	AY327475 PhytoIacc
21	1216.5	75.2	1114	15	AF533515	AF533515 PhytoIacc
22	1172.5	72.5	2472	6	B05033	B05033 DNA encodin
23	1172.5	72.5	2472	15	PTC8AP	D10600 P. american
24	1166.5	72.1	1052	15	AY137202	AY137202 PhytoIacc
25	1157.5	71.6	882	6	A67183	A67183 Sequence 1
26	1147.5	71.0	2369	15	AF141331	AF141331 PhytoIacc
27	1147.5	71.0	1133	15	AY071928	AY071928 PhytoIacc
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45	464	28.7	1180	15	MCU80072	UC80072 Mesembryant

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
CAMBRIDGE
FEATURES
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AX427702 945 bp DNA linear PAT 20-JUN-2002
Sequence 1 from Patent WO0233107.
AX427702.1 GI:21537815
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Phytolacca americana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1
Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
Plant cell death system
Patent: WO 0233107-A.1 25-APR-2002;
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/organism="Phytolacca americana"
/mol_type="unassembled DNA"
/db_xref="taxon:3527"
1. 24
/note="Binding site for primer PPS1BF"
complement(735..776)
/note="Binding site for primer PSXDR"
736..777


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variation                               /note="Binding site for primer PSXP"
750..759                                /note="Sequence replacing removed XbaI site"
misc_feature                             complement(922..945)
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Score:          1617.00        Matches:      314
Percent Similarity: 100.0%      Conservative: 0
Beet Local Similarity: 100.0%    Mismatches: 0
Query Match:    100.0%         Indels:      0
DB:             Gaps:          0

US-09-978-274a-2 (1-314) x AK427702 (1-945)

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QY      21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
        |||
Db       61 TCACTTGGCCATTAATACGATCAGCTTGATGCTGGAATGCAACCATTAACAATAT 120

QY      41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyGly 60
        |||
Db       121 GCCACCTTATGGAATCTCTCGTAATCAAGCGAAGATCCAAACCTAAATCTATGCG 180

QY      61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
        |||
Db       181 ATACCAATGCTACTGATTAATTCGACCCCAAGACTTATTTGGTTAAGCTCCAAAGT 240

QY      81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyValMetGlyTy 100
        |||
Db       241 GCACACTTAAACCACTTACACTTAATGCTAGAGCAAAATACCTTAACGATGGCTAT 300

QY      101 SerAspProPheAsnGlyAsnLysCysArgTyRHisIlePheAsnAspIleThrSerThr 120
        |||
Db       301 TCTGATCCCTTCATAGGCATTAAGTGTGCTTACCATATATTATTAATTAACAAGACC 360

QY      121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
        |||
Db       361 GAACGACATGATGTGAGATATACCTTTGCTCAAGTCTCTGCTGTGCAATGTC 420

QY      141 IleAsnTyAsnSerLeuTyProThrMetGluLysValGluValAsnSerArgAsn 160
        |||
Db       421 ATTAACTACATAGCTTATATCCGACCATGGAAGAAAGAACAGATTAACCTCAAGAAAT 480

QY      161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
        |||
Db       481 CAAGTCAATGGGAATTCAAATATCTCAGCAGTGACATTTGGAATAATCTTGAGATTGAT 540

QY      181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
        |||
Db       541 TCATTCCTCGTAAAACTGAGGCTTTTCTCTGCTGATGCCATCCAAAGGTTTCAGAG 600

QY      201 AlaAlaArgPheLysTyIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
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Db       601 GCAAGCGGATTCAGATACATAGAAACCAAGTCAAGCTTAATTTTAATAGCAATTCAC 660

QY      221 ProAspProLysValIleAsnLeuGluGluLysTyIleGlyLysIleSerGluAlaIleAs 240
        |||
Db       661 CCGATCCCAAGATTAATTTGAGAGGAAGTGGGGCAAAATCTCTGAGCAATTCAC 720

QY      241 AsnAlaLysAsnGlyValLeuProLysProLeuGluLeuValAspAlaLysGlyThrLys 260
        |||
Db       721 AATGCGCAAGATGGGGCTTTACCCCAACCACTTGAGTGTGATGCCAAAGGTACCAAG 780

QY      261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
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Db       781 TGGATTCCTTCTTGAAGTGAAGAAATCAATCGATGTGCACTCTTAAGTACGTTAAT 840

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QY      281 GlyThrCysGlnThrThrTyGlnAsnAlaMetPheSerGlnValIleIleSerThrTy 300
        |||
Db       841 GGAACCTGCAGCAACTTATCCAAATGCCAATGCTTCTCAACTTATTAATTTCTACTTAT 900

QY      301 TyrAsnTyMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
        |||
Db       901 TATATTAATATATGCTTAATCTTGATGATCTATTGGAAGATTC 942

RESULT 2
PAPASRIP      1249 bp      mRNA      linear      PLN 18-APR-2005
LOCUS         P.americana mRNA for pokeweed antiviral protein.
DEFINITION    X98079
VERSION       X98079.1 GI:1707648
KEYWORDS      PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating
SOURCE        Phytolacca americana (American pokeweed)
ORGANISM      Phytolacca americana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolacaceae; Phytolacca.
REFERENCE     1
AUTHORS      Poyet,J.L. and Hoeveler,A.
TITLE        cDNA cloning and expression of pokeweed antiviral protein from
             seeds in Escherichia coli and its inhibition of protein synthesis
             in vitro
JOURNAL       FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED       9109394
REFERENCE     2 (bases 1 to 1249)
AUTHORS      Poyet,J.L.
TITLE        Direct Submission
JOURNAL       Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
             Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16
             route de Gray, 25030 Besancon Cedex, FRANCE
REMARK        Revised by author 20-SEP-1996
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              QVQLGILISDGIKSGVDSPTKTEAFILVALIOMVSEARFXYIEQVKTNPRA
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              178..1047
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              /product="unnamed"
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              /gene="PAP-S"
              1235
              /gene="PAP-S"
ORIGIN
Alignment Scores:
Pred. No.:      1,84e-126      Length:      1249
Score:          1617.00        Matches:      314

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Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 DB: 15
 Gaps: 0

US-09-978-274A-2 (1-314) x PAPABSRIP (1-1249)

QY 1 MetIyValMetIeuValValValThreIleAlaTrpLeuIleAlaIleProThr 20
 DB 106 ATGAAGGTGATGCTTGTAGTGTGTGTGATGCTTAATAGGTGGCTCATTTGGCCACCACT 165
 QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThr 40
 DB 166 TCACCTGTGCGCAATTAATACATCACTTGTATCTGTGAATGCGACCATTAACAAATAT 225
 QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
 DB 226 GCCACCTTTATGAAATCTTCTGTAACTACCGGAAAGATCCAAATCTAAATGCTATGGC 285
 QY 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
 DB 286 ATACCAATGCTACCTGATTAATTTCCAGCCCTTAAGTACTTATTTGGTTAAGCTCCAGGT 345
 QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuLysValMetGlyThr 100
 DB 346 GCAAACTTAATAAACATTACATCACTATGCTGAGAGAAATACTTATACGTATGGCTAT 405
 QY 101 SerAspProPheAsnGlnLysLeuLysCysArgThrIlePheAsnAspIleThrSerThr 120
 DB 406 TCGATCTCTTCAATGCGCAATAGTGTGCTGATCACTAATTAATTAATTAATTAACAGACC 465
 QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSer 140
 DB 466 GAACGCACTGATGAGGAATACCTTTGGCTCAAGTTCTAGTTCTCGTTGGCAATGCC 525
 QY 141 IleAsnThrAsnSerLeuLysProThrMetGluLysLysValGluValAsnSerArgAsn 160
 DB 526 ATTAACCTACATAGCTTATATCCAGCATGAGAAAGAGAGCAAGATTAATCAAGAAAT 585
 QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
 DB 586 CAAATCCAAATTTGGAAATTCAAATATCTAGCAGTACATTTGAAAAATCTCTGGAGTTGAT 645
 QY 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 DB 646 TCATTCCTCTGTAATAAAGCTGAGGCTTTTCTTCTAGCTGATCCAAATGGTTTCAGAG 705
 QY 201 AlaAlaArgPheLysThrIleGlnLysGlnValLysThrAsnPheAsnArgAlaPheThr 220
 DB 706 GCAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGAGCATTTCTAC 765
 QY 221 ProAspProLysValIleAsnLeuGlnGluLysProLysIleSerGlnAlaIleHis 240
 DB 766 CCGATCTCCAAAGTAATTAATTTGGAGAGAGAGGGGCAAAATCTCTGAGGCAATTCAC 825
 QY 241 AsnAlaLysAsnGlnAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
 DB 826 AATGCCAAGATGGGGCTTTTACCAAACTCTAGAGCTTAGGATGCCAAAGGTACAG 885
 QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysThrValAsn 280
 DB 886 TGGATGTCTTGAAGTGAATGAATCAATCGTATGGGCACTCTTAAGTACGTTAAT 945
 QY 281 GlyThrCysGlnThrThrThrArgIleAsnAlaMetPheSerGlnValIleIleSerThrThr 300
 DB 946 GGAACCTGTGACAACTTACCAAAATGCTTCTCAAGTTAATTAATTTCTACTAT 1005
 QY 301 TyrAsnThrMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
 DB 1006 TATATATATATATGCTAATCTTGGTATCTAATTTGAAGAGATTC 1047

RESULT 3
 AX427704

LOCUS AX427704 792 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 3 from Patent WO023107.
 ACCSSION AX427704
 VERSION AX427704.1 GI:21537816
 KEYWORDS

SOURCE
 ORGANISM
 Phytolacca americana (American pokeweed)

Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
 1 Neelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.
 Plant cell death system
 Patent: WO 023107-A 3 25-APR-2002;
 CAMBRIDGE ADVANCED TECH (GB)

FEATURES
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 location/qualifiers
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misc_feature
 1..3
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misc_feature
 complement(436..462)
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misc_feature
 463..492
 /note="Binding site for primer P82BP"

variation
 612
 /note="Nucleotide change from published sequence"

variation
 681..686
 /note="Sequence replacing removed XbaI site"

misc_feature
 complement(765..792)
 /note="Binding site for primer P82SR"

misc_feature
 790..792
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ORIGIN
 Alignment Scores:
 Pred. No.: 1.96e-104 Length: 792
 Score: 1352.00 Matches: 262
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 83.6% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-2 (1-314) x AX427704 (1-792)
 QY 25 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThrAlaThrPheMet 44
 DB 4 ATTAATTCATACCTTTGATGCTGGAATGCCAACATTAACAAATATGCACTTTATG 63
 QY 45 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysArgThrIlePheMetLeu 64
 DB 64 GAATCTCTGTAATCAAGGAGAAATCCAAATCTAATAGCTATGCGCATACCAATGCTA 123
 QY 65 ProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGlnValAlaAsnLeuLys 84
 DB 124 CCGATCTCAATTAATTCAGCCCTTAAGTACTTATTTGATGCTCAAGGTGCAAACTTAAA 193
 QY 85 ThrIleThrLeuMetLeuArgArgAsnLeuLysValMetGlyThrSerThrGluArgThrAsp 104
 DB 184 ACCATTAACCTAATGCTGAGACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 243
 QY 105 AsnGlyAsnLysCysArgThrIlePheAsnAspIleThrSerThrGluArgThrAsp 124
 DB 244 AATGCCAATTAAGTGTGTTACCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 303
 QY 125 ValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSerIleAsnThrAsn 144
 DB 304 GTGAGAAATACCTTTGCTCAAGTTCTAGTTCTCGTTGCAATGTCATTAATCAAT 363
 QY 145 SerLeuThrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 164

Db 364 AGTTTATATCCGACCAAGAAAAGAGCAAGTAATCAAGAAATCAAGTCCAAATTG 423
165 GYIIEGIIIEIIEUSEISERASPIIEGIYLYEIIIESEGIYVAIAASERPEHPEVIA 184
Db 424 GGAATTCATATCTGACGACATGACATTCGAAAATCTCTGAGATTGATTCATCTCTGTA 483
QY 185 LYETHRGIIUALAPHHELEUVAIAIAIEGIMETVAISERGIIUALAIAARGPHE 204
Db 484 AAAACGAGGCTTTTCTACTGTGTAGCCATCCAAATGGTTTCAGAGGACGGCGCATTC 543
QY 205 LYETRTIEGIUEGIIIVALLYETTHAAPHASNAARGIAAPHEIYTRPAAEPPOLYS 224
Db 544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATGACATTCACCTGTATCCCAA 603
QY 225 VALIEASNUGIIUGIULYSTPGLIYLYEIIIESEGIUALAIEHIIASNAIALYASNA 244
Db 604 GTAAATTAATCTTGAGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 663
QY 245 GIYALALEUPROLYSPROLEUGIULEUVAIAASPIALALYSGIYTHLYSTPIIEVALLIU 264
Db 664 GGGGCTTACCCAAACCACTTGAAGCTAGTGAGATGCCAAAGSTACCAAGTGAGTATGTTCTT 723
QY 265 ARGVALASPGIUIIEASNAARGAPVALAIALEULEULYSTYRTVALAENGIIYTHCYSGIN 284
Db 724 AGAGTGAGTGAATCAATCGTATGTGCACTCCTTAAGTACGTTAATGGAACCTGTCTAG 783
QY 285 ThrThr 286
Db 784 ACAACT 789
RESULT 4
LOCUS AB071855 786 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paps2 gene for PAP-S2, partial cde.
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Honjo,E. and Watanabe,K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 786)
AUTHORS Watanabe,K. and Honjo,E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail:watakei@cc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)
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ORIGIN
Alignment Scores:
Pred. No.: 9.3e-103 Length: 786
Score: 1332.00 Matches: 257
Percent Similarity: 99.2% Conservative: 3
Best Local Similarity: 98.1% Mismatches: 2
Query Match: 82.4% Indels: 0
DB: 15 Gaps: 0
US-09-978-274A-2 (1-314) x AB071855 (1-786)
QY 25 IIEASNTHRIETHRPEASAPALAGIYAENALAEHIIIESEGIYVAIAASERPEHPE 44
Db 1 ATCAATTAATCTTCACTTTTGAATGCTGGAATTCACCAATTAACAAATATGCCACCTTATG 60
QY 45 GIUSERIEUARANGIUALALYASAPROLYSLEULYSEYTRGIIYIIEPROMETLEU 64
Db 61 GAATCTCTGTATATCAAGAGAAAGATCCAAACTAAATGCTATGGCATACCAATGCTTA 120
QY 65 PROASPTHASNERTHPROLYSTYRLLEUVAIIYLSLEUGINGIIYALASNULYS 84
Db 121 CCGAATTAATTAATTCGACCCCTTAAGTACTTAATGTTAAGTCCAAAGTGCAAACTTAAAA 180
QY 85 THRIETHREUWETLEUARARGAANAENLEUTYVAIMEGIYTYRSEARPPROPE 104
Db 181 ACCATTAATCAATATGCTGAGAGCAAAATTAATTAATGCTATGAGGCTATTTCTGATCCCTTC 240
QY 105 AENGIYASNUYSEYARGTYRHAIEIIEASNAEPIIETHSERTHGIIUARGTHRAAP 124
Db 241 AATGCAATTAAGTGTGTTACCATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
QY 125 VALGIUANETHRIEUCYSESERSESERSESERSESERSESERSESERSESERSE 144
Db 301 GTGGAATAATACCTTTTGTCTCAAGTTCTAGTTCGGTGGCAATGCCATTAATCAATCA 360
QY 145 SERLEUTYRPROTHMETGIIULYSTYLSAIIAGIUALAASERARGAENGIIVALGII 164
Db 361 AGCTTATATCCGACCTTGAGAAAAGAGCAAGATTAATCTCAAGAGTCAATGCCAATTTG 420
QY 165 GYIIEGIIIEIIEUSEISERASPIIEGIYLYEIIIESEGIYVAIAASERPEHPEVIA 184
Db 421 GGAATTCATATCTGACGACATGACATTTGAAAAAATCTCTGAGATTGATTCATTCCTCTGTA 480
QY 185 LYETHRGIIUALAPHHELEUVAIAIAIEGIMETVAISERGIIUALAIAARGPHE 204
Db 481 AAAACGAGGCTTTTCTACTGTGTAGCCATCCAAATGGTTTCAGAGGACGGCGCATTC 540
QY 205 LYETRTIEGIUEGIIIVALLYETTHAAPHASNAARGIAAPHEIYTRPAAEPPOLYS 224
Db 541 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATGAGCAATTCACCTGTATCCCAA 600
QY 225 VALIEASNUGIIUGIULYSTPGLIYLYEIIIESEGIUALAIEHIIASNAIALYASNA 244
Db 601 GTAAATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACCAATGCCAAGAT 660
QY 245 GIYALALEUPROLYSPROLEUGIULEUVAIAASPIALALYSGIYTHLYSTPIIEVALLIU 264
Db 661 GGGGCTTACCCAAACCACTTGAAGCTAGTGAGATGCCAAAGGATCAAGAGGATAGTTCTT 720
QY 265 ARGVALASPGIUIIEASNAARGAPVALAIALEULEULYSTYRTVALAENGIIYTHCYSGIN 284
Db 721 AGAGTGAGTGAATCAATCGTATGTGCACTCCTTAAGTACGTTAATGGAACCTGTCTAG 780
QY 285 ThrThr 286
Db 781 GCCACT 786
RESULT 5
LOCUS AX427720 1092 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 19 from Patent WO0233107.
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Neelam, A., Atkinson, H. J., Mcpherson, M. J. and Thomas, C. J. R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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complement(742. .786)
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misc_feature
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misc_feature
complement(1066. .1092)
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ORIGIN
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Score: 1307.00 Matches: 254
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 80.8% Indels: 0
DB: Gaps: 0
US-09-978-274a-2 (1-314) x AX427720 (1-1092)
QY 25 ILEASNTHRIETHPHEAPALAGLYASNALATHRIEASNLYSTYRALATHRPHMET 44
DB 4 ATAAATACGATCACTTGATGCTGAATGCCACCTTAACAAATATGCCACCTTATG 63
QY 45 GUSERTLEUARGANGIALYASPPROLYLEULYSCYRTGYLLEPROMETLEU 64
DB 64 GAATCTCTTGATATCAAGCAAGAAATCAAACTAAATGCTATGCGATACCAATGCTA 123
QY 65 PROASPTHRANSETHRPROLYSTYRLEULEUVALYLEUNGNGLYALAAENLEULY 84
DB 124 CCGATACACTAATTCAGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCAACCTTAAA 183
QY 85 THRIETHEULEULEUARGASNAASNLTYRVALMETGYLYRSEARPPROPH 104
DB 184 ACCATTACACTAATTCAGACCAAAATACCTTAAGTGGCTATTTCTGATCCCTTC 243
QY 105 AENGLYASNLYSCYARATGYTHGILEPHASNAAPLLETHRSETHRGUARGTHA 124
DB 244 AAATGGCAATAGTGTCTTACCATATATTTAATATTTCAAGCACGAAACGACATGAT 303
QY 125 VALGLUASANTHREUCYSSERSESSERSESSERSESSERSESSERSESSERSE 144
DB 304 GTGGAGATATCTCTTGCTCAAGTTCATGTTCTCGTGTTCATCAATGTCATTAACTA 363
QY 145 SERLEUTYRPROTHMETGLUTYLYALAGLYVALASNAERARGAENGIVALGLN 164
DB 364 AGCTTATATCCGACCAATGAAAAGAAAGAAAGTAATCAAGAAATCAAGTCCAT 423
QY 165 GLYILEGLINLEUSERSESSERAPLLEGLYLYSILESERGLYVALASPPH 184
DB 424 GGAATTCAAATACTCAGCAAGTGAATTTGAAATATCTCTGAGTTGATTCATCCCTGTA 483

QY 185 LYETHRGUVALPHEPHELEULEUVALALILEGLMETVALSERGIUALAALARGPHE 204
DB 484 AAACTAGAGGCTTTTCTTACTGCTGAGCCATCCAAATGGTTTCAGGCGAGCTTC 543
QY 205 LYETRYLLEGLUNANGIVALYSTHRASPHASNAARGALAPHETYRPROASP 224
DB 544 AAGTACATATAGAACCAAGTCAGACATTAATTTTATATGACATTTTCCATCCAAA 603
QY 225 VALLEASNLEUGLUGLUTYTPGILYSELISERGIUALAILEHISASNAALYAS 244
DB 604 GTAAATTAATCTTGAGGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCA 663
QY 245 GLVALALEUPROLYSPROLEUGLULEUVALASPALYASGLYTHRYSTPPILE 264
DB 664 GGGGCTTTACCAACCACTTGAAGCTATGAGAGCCAAAGATACCAAGTGAATGTTCTT 723
QY 265 ARGVALASPGULILEASNAARGAPVALALALEULEULYSTYR 278
DB 724 AGAGTGAATGAATCAATCGTATGTCGACCTCTTAAGTAC 765

RESULT 6
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS
DEFINITION Phytolectra americana antiviral protein (PAP) mRNA, complete cds.
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE
ORGANISM
Phytolectra americana (American pokeweed)
Phytolectra americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolectraceae; Phytolectra.
1 (bases 1 to 942)
Xiao, Z. A. and Jiang, Y.
A gene encoding the pokeweed antiviral protein in the leaf of
Phytolectra americana
Unpublished
2 (bases 1 to 942)
Xiao, Z. A.

REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
University, No. 19 Xijiekouwai Street, Haidian District, Beijing
100875, China
location/Qualifiers

FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 4.55e-95 Length: 942
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Percent Similarity: 86.7% Conservative: 33
Best Local Similarity: 76.2% Mismatches: 39
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US-09-978-274A-2 (1-314) X AY572976 (1-942)

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Db	1	ATGAAGGTGATCTGTGGTGACAAATCAAT-----TGGCTCATTTCTGGACCAACT	54
Oy	21	SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyr	40
Db	55	TCAACTGGGGCTGTGAATACATCATCTCAATGTTGGAAGTACCAACCATTAGCAATAAC	114
Oy	41	AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProLysLeuLysCysTyrGly	60
Db	115	GGCAGCTTTCTGAATGATCTTCGTATGAAAGCAAAAGATCCAAATTAAATCTATGGA	174
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Db	175	ATACCAATCTCTCCCAATACAAATCAAAATCCAAAGTACGTGTGGTTGAGCTCCAGGT	234
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Db	235	TCAATATAAAAAACCATCACATCAATAGCTGAGCGAAACAATTGTATGTATGGGGTTAT	294
Oy	101	SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr	120
Db	295	TCTGATCCCTTGGAAACCATAAATGTCGTTCCAAATCTTATATGATATCTCAAGTACT	354
Oy	121	GluArgThrAspValGluAsnThrLeuLysSerSerSerSerSerArgValAlaMetSer	140
Db	335	GAAGCCCAAGATGTAGAGCTACTCTTTGGCCAAATGCCAAATCTGTGTAGTAAAAAC	414
Oy	141	IleAsnTyrAsnSerLeuTyrProThrMetGluLysLeuAlaGluValAsnSerArgAsn	160
Db	415	ATTAACCTTGATATGTCGATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAGT	474
Oy	161	GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp	180
Db	475	CAAGTCCAACTGGGAATTCAAATACTCGCAGATTAATTTGGAAAGATTTCTGAGATGATG	534
Oy	181	SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu	200
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Oy	261	TyrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn	280
Db	775	TGGATATGTTGAGATGTGATGAATCAAGCCGTGATGTGACCTCTTAAACTACGTTGGT	834
Oy	281	GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr	299
Db	835	GGGAGCTGTCAACAACCTATATACCAAAATGCGCATGTTCTTCACCTTATATATGTCACT	894
Oy	300	TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe	314
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SOURCE
ORGANISM

Phytolacca americana (American pokeweed)
Phytolacca americana

1

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL

Zhao, Y., Wang, X., Zhou, G. and Li, H. A pokeweed antiviral protein gene in roots of *Phytolacca americana* *Acta Virol.* 48 (2), 131-132 (2004)

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

15462289
2 (bases 1 to 942)
Zhao, Y., Wang, X. and Li, H.
Direct Submission
Submitted (11-FEB-2004) Plant Virology, Institute of Plant

FEATURES
SOURCE
mRNA

Protection CAAS, No.2 Yuanmingyuan Road west, Beijing 100094, P.R China

Location/Qualifiers

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CDS

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ORIGIN
Alignment
Pred. No.:
Score:
Percent Si
Best Local
Query Matc
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US-09-978-

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Dy	241	AaaAlaLYsaenGIYALaleuProLYsProlEugIuLeuVaIAspaIalySGlyThrLYs	260
Dy	715	GATGCCAAGAATGGAGATTTCACCACCTCTTGACCTAGTGATGCCAGTGGTCCAAG	774
Dy	261	ThrlIeValIleuarXVaIAspGIuIleaaaAgAspVaIAleuLeuLYstrYrValAsn	280
Dy	775	TGGATAGTGTGAGAGGTGATAAACAAGCCTGATGTAGCATCTTAAACTACGTTGGT	834
Dy	281	GIYTrCySGLInThrThrTYR---GlnaenAlaMetPheserGIuVallIleIleSerThr	299
Dy	835	GGGAGCTGTCAACAATTATTAACCAAATGCCATITTTCTCAACTTATTAATGTCTACT	894
Dy	300	TYrTYraSnTYrMetSerasnLeuGIyaSPLeuPhueGIuGIYPhe	314
Dy	895	TATTATTAATTACATGGTTAATCTTGSTGATCTATTGAAAGGATTC	939
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LOCUS	AY547315	942 bp	DNA linear PLN 13-JUL-200
DEFINITION	Phytolacca americana antiviral protein gene, complete cds.		
ACCESSION	AY547315		
VERSION	AY547315.1	GI:44889055	
KEYWORDS	.		

Qy
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Qy
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Db
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Db
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Db

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 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerArgIleGlyIleSerGlyValAsp 180
 DB 475 CAGGTCCAACTGGGAATTCAAATCTGACAGTAAATGGAAAGATTCTGAGGTAGT 534
 QY 181 SerPheProValYrThrGlnAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
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 QY 201 AlaAlaArgPheLeuYrIleGluAsnGlnValYrThrAsnPheAsnArgAlaPheTyr 220
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 QY 221 ProAspProValYrIleAsnLeuGluGluYrTrpGlyIleSerGluAlaIleHis 240
 DB 655 CCTAATCCCAAGTAACTTAATTTGCAAGACATGGGGTAAAGATTTCACAGCAATTCAT 714
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 DB 775 TGAATAGTGTGAGAGTGAAGTGAATCAAGCTGATGACCTTTAACTACGTTGCT 834
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 DB 835 GGGAGCGTCTGACCAACTTATTAACCAAAATGCCATGTTCTCTCACTTATTAATGCTACT 894
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RESULT 8
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 DEFINITION X55383
 ACCESSION X55383.1 GI:20421
 VERSION anti-viral protein; cell wall protein; PAP gene; ribosome
 KEYWORDS inactivating protein.
 SOURCE Phytotholacca americana (American pokeweed)
 ORGANISM Phytotholacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.
 1 (bases 1 to 1164)
 Lin, Q., Chen, Z. C., Antoniw, J. F. and White, R. F.
 Isolation and characterization of a cDNA clone encoding the
 anti-viral protein from Phytotholacca americana
 Plant Mol. Biol. 17 (4), 609-614 (1991)
 1912488

JOURNAL 2 (bases 1 to 1164)
 Antoniw, J. F.
 DIRECT SUBMISSION
 TITLE Direct Submission
 AUTHORS Submitted (05-NOV-1990) Antoniw, J. F., AFRC Inst of Arable Crops
 RESEARCHER, Dept. of Plant Pathology, Rothamsted Experimental
 STATION, Harpenden, Hert, AL5 2JQ, UK
 LOCATION/Qualifiers

FEATURES
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 CDS

Alignment Scores:
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 Query Match: 76.4% Indels: 3
 DB: 15 Gaps: 2

US-09-978-274a-2 (1-314) x PAPAP (1-1164)

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 DB 56 TCAACTGGCGCTGATACATCAATCATCTCAATGTTGAAGTACCAACCATTTAGCAATAC 115
 QY 41 AlaThrPheMetCysLeuSerLeuArgGlnAlaYrAspProValYrGly 60
 DB 116 GCCACTTCTCTGATGATCTTCTGTAATGAGCCAAAGATCCAAAGTTTAAATCTTAATGGA 175
 QY 61 IleProMetLeuProAspThrAsnSerThrProValYrLeuValYrLeuGlnGly 80
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 QY 81 AlaAsnLeuYrThrIleThrLeuMetLeuArgArgAsnAsnLeuYrValMetGlyYr 100
 DB 236 TCAATTAATAAAACCATCAACATCAATGCGAGCGAAACATTTGATGATGGGTAT 295
 QY 101 SerAspProPheAsnGlyAsnYrCysArgYrHisIlePheAsnAspIleThrSerThr 120
 DB 296 TCTGATCCCTTTCAAAACCAATAAATGCTTACCATATCTTATATGATATCTCAGGTA 355
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LOCUS   A42103 1195 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION  A42103.1 GI:2297595
KEYWORDS
SOURCE  PhytoIaccas americana (American pokeweed)
ORGANISM
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          Caryophyllales; Phytolaccaceae; Phytolacca.
          1 (bases 1 to 1195)
REFERENCE
AUTHORS  Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, W.
TITLES   A novel expression vector for phytoIaccas antiviral protein
          Patent: EP 0637591-A 1 08-FEB-1995;
          JINRO LIMITED (KR)
COMMENT  Other publication AU 662844 950914
          Other publication JP 7067660 950314
          Other publication CA 2102859 950103
          Other publication AU 5064293 950119.
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Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2

US-09-978-274A-2 (1-314) x A42103 (1-1195)
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      87 TCAACTTGGGCTGTGATCAATCATCATCATGTTGGAGTGCACCACTTATGCAAAATAC 146
      41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyGly 60
      147 GCACATTTCTCTGAATGATCTTCTGTAATGAAGCGAAAGATCCAAATTTAAATGCTATGA 206
      61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
      207 ATAACCAATCTGCGCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 266
      81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyValMetGlyTy 100
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      121 G1uArgThrAspValGluAsnThrLeuCysSerSerSerSerSerTyValAlaMetSer 140
      387 GAACGCCAAGATGTAAAGACTCTTGTGCCAAAGCCAAATCTGTGTGTGATAAAAC 446
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      161 GlnValGlnLeuGlyTleGlnIleLeuSerSerSerAspIleGlyLysIleSerGlyValAsp 180
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      281 G1YthrCyeGlnThrThrTy---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
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RESULT 10
LOCUS   I43835 1195 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5633155.
ACCESSION I43835
VERSION  I43835.1 GI:2468933
KEYWORDS
SOURCE  Unknown.
ORGANISM
          Unclassified.
          1 (bases 1 to 1195)
REFERENCE
AUTHORS  Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.
          and Jeon, H.-S.
          Expression vector for phytoIaccas antiviral protein and process for
          preparing transgenic plant transformed therewith
          Patent: US 5633155-A 1 27-MAY-1997
JOURNAL
TITLES   Location/Qualifiers
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1.9e-94 Length: 1195
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2

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US-09-978-274A-2 (1-314) x 143835 (1-1195)

Qy 1 MetIyValMetLeuValValValThreulealATPleuilealAaProthr 20
Db 33 ATGAAAGTCAGTGGTGGTGAACAATATCAATA-----TGGCTCATCTTGGACCAACT 86
Qy 21 SerThrCysAlaIleAenThrIleThrPheAspIleGlyAsnAlaThrIleAsnLysThr 40
Db 87 TCAACTGGGCTGGTGAATACATCACTACATGTTGAGAGTACCACTTGAAGCAATAC 146
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
Db 147 GCCACTTTCTGATATGATCTTGGTAATGAGCGAAAGTCCAACTTTAAATGCTATGGA 206
Qy 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuValLysLeuGlnGly 80
Db 207 ATACCAATGCTGCCCAATACAAATACCAATCCAAATGACGTGGTGGTGAAGCTCAAGT 266
Qy 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuThrValMetGlyThr 100
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Db 387 GAACGCCAAGATGAGAGACTACTCTTGGCCCAATGCCAATCTCGTGGTGAATAAAC 446
Qy 141 IleAsnThrAsnSerLeuThrProThrMetGluLysValGluValAsnSerArgAsn 160
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Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db 507 CAAGTCCAACTGGGAATTCAAATATCTGACAGTAAATTTGGAAGAATTTCTGAGTATG 566
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RESULT 11

LOCUS 155866 1195 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5648234.
ACCESSION 155866
VERSION 155866.1 GI:2476660

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1195)

AUTHORS

Moon, Y.-H., Jeon, H.-S., Choi, K.-W., Lee, K.-H. and Kim, M.-K.

TITLE

Expression vector for *Phytolacca* antiviral protein

JOURNAL

Patent: US 5648234-A 1 15-JUL-1997;

FEATURES

Location/Qualifiers
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ORIGIN

Alignment Scores:

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Score:	1.9e-94	1195	239	33	40	2
Percent Similarity:	86.3%					
Best Local Similarity:	75.9%					
Query Match:	76.4%					
DB:	6					

US-09-978-274A-2 (1-314) x 155866 (1-1195)

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Qy 21 SerThrCysAlaIleAenThrIleThrPheAspIleGlyAsnAlaThrIleAsnLysThr 40
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Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
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Qy 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuValLysLeuGlnGly 80
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Qy 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuThrValMetGlyThr 100
Db 267 TCAATTAATAAAACCAATCACTAATGCTGAGACCAATTTGATGATGGATAT 326
Qy 101 SerAspProPheAsnGlyAsnLysCysArgThrHisIlePheAsnAspIleThrSerThr 120
Db 327 TCTGATCCCTTGAACCAATTAATGCTTACCATATCTTTATGATATCTCAGTACT 386
Qy 121 GluArgThrAspValGluAenThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db 387 GAACGCCAAGATGAGAGACTACTCTTGGCCAAATGCCAATCTCGTGGTGAATAAAC 446
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Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db 507 CAAGTCCAACTGGGAATTCAAATATCTGACAGTAAATTTGGAAGAATTTCTGAGTATG 566
Qy 181 SerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
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Db 687 CTTAATCCCAAGATCTTAATTTGCAAGAGACATGGGTTAAGATTTTCAACAGCAATTCAT 746
Qy 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLys 260

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Db	807	TGGATAGTGTGAGAGTGGATGAATCAAGCCTATGTAGCACTTTAACTACCTGGT	866
Cy	281	GIYThCyGInThrThrTyr---GlnAsnAlaMetPheSerGlnValIleSerThr	299
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Db	867	GAGAGCTCAGACAACTTATTAACCAAAATGCGATGTTCCCTCAACTTATATAGTCTACT	926
Cy	300	TyrTYraenyIrmEseAsnLengIlyAspLeuPheGluGlyPhe	314
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Alignment Scores:	
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Gaps:	2

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Qy 41 AAlaThrPheMetGluSerLeuArgAsnGlnAlaValAspProlyLeuLeuGlyCysTyrGly 60
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Qy 61 IleProMetLeuProAspThrAsnSerThrProlyTyrLeuLeuValIleLeuGlnGly 80
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Qy 81 AAlaAsnLeuValThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
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Qy 101 SerAspProPheAsnGlyAsnLeuGlyCysArgTyrHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTGAACCAATTAATGCTTACCTTAATCTTAATGATATCTCAAGTACT 578
Qy 121 GluArgThrAspValGluAsnThrLeuGlySerSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAAGCGCCAAAGATGAGAGACTACTCTTGGCCAAATGCGCAATTCGTGTTAGTAAATAC 638
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Db 639 ATAAACTTGTATGATGATCATATCCAAATGGAATCAAAAGCGGAGTAAATCAAGAGT 698
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Qy 181 SerPheProValIlySerThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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Qy 201 AAlaAlaArgPheLeuTyrIleGlnAsnGlnValIlySerThrAsnPheAsnArgAlaPheTyr 220
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Qy 221 ProAspProPheValIleAsnLeuGlnGluIlySerThrGlyValIleSerGlyValAlaIleHis 240
Db 879 CTTAATCCCAAGATCTTAATTTTCAGAGACATGAGGTAAAGATTTCACAGCAATTCAT 938
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RESULT 14

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LOCUS AX427731
DEFINITION Sequence 30 from Patent WO20233107.
ACCESSION AX427731
VERSION AX427731.1 GI:21537838
KEYWORDS
SOURCE
ORGANISM

Phytolacca americana (American pokeweed)

Phytolacca americana

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
AUTHORS
TITLE Plant cell death system

JOURNAL Patent: WO 0233107-A 30 25-APR-2002;

FEATURES CAMBRIDGE ADVANCED TECH (GB)

Location/Qualifiers

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/mol_type="unassigned DNA"

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ORIGIN

Alignment Scores:

Pred. No.:	2,24e-94	Length:	1379
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	6	Gaps:	2

US-09-978-274A-2 (1-314) x AX427731 (1-1379)

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Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyr 40
Db 279 TCAACTGGGCTGATGATCATATCTACATGTTGGAAGTACCACTTACCAATATC 338
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Qy 61 IleProMetLeuProAspThrAsnSerThrProlyTyrLeuLeuValIleGlnGly 80
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Qy 81 AAlaAsnLeuValThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
Db 459 TCAATAAATAAAACCATCATCACTTAATCTCAGAGCAAACTTTGATGATGAGTTAT 518
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Db 999 TGAATAGTGTGAGAGTGATGAATATCAAGCTGATGACCTTAACTTAACTGTTGCT 1058
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LOCUS AR141172 Sequence 1 from patent US 6146628.
DEFINITION AR141172
ACCESSION AR141172
VERSION AR141172.1 GI:15106689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Uekun,F.M. and Turner,N.B.
TITLE Biotherapeutic agents comprising recombinant PAP and PAP mutants
JOURNAL Patent: US 6146628-A 14-NOV-2000;
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Percent Similarity: 86.3% Conservative: 34
Best Local Similarity: 75.6% Mismatches: 40
Query Match: 76.2% Indels: 3
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Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTy 40
Db 279 TCAACTTGGGCTGTGAATCAATCATCTACATCTTGAAGTACCACTTACCAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlyseuLeuTyCysTy 60
Db 339 GCCACTTCTGATGATGATCTTCTGTAATGAAGCGAAAGATCCAAATTAAATGCTATGA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProlyseuLeuValLeuGlnGly 80
Db 399 ATACCAATGCTGCCCAATACAAATCAAAATGACGTGGTGAAGCTCCAAAGT 458
Qy 81 AlaAsnLeuTyThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
Db 459 TCAAAATRAAAAAACCATCAACATATGCTGAGAGAAACAAATTTGTATGTGATGGTAT 518
Qy 101 SerAspProPheAsnGlyAsnLeuTyCysArgTyHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTGAAAACCAATTAATGCTTACCATATCTTTAATGATATCTCAGGTA 578
Qy 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCACAGATGAGAGACTACTCTTGGCCAAATGCCAATTCCTGTTAGTAAAC 638
Qy 141 IleAsnTyraAsnSerLeuTyProThrMetGluLeuValIleValIleAsnSerArgAsn 160
Db 639 ATTAACCTTGTGATGTGATATCCACATCTGGAATCAAAACGGAGATTAATATCAAGAGT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLeuIleSerGlyValAsp 180

Db 699 CAGGTCCAACTGGGAATTCAAAATCTGACAGATTAATTTGAAAGATTTCTGGAGTGATG 758
Qy 181 SerPheProValTyThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCAATCACTGAGAAAACCCAAAGCGAATTCCTAATGGATGCCATACAAATGATACAG 818
Qy 201 AlaAlaArgPheLeuTyTrileGluAsnGlnValIleThrAsnPheAsnArgAlaPheTy 220
Db 819 GCAGCAAGATTCAGATACATAGAGATCAGTGAAAACCTAATTTTAAACAGACATTCAC 878
Qy 221 ProAspProlyseuValIleAsnLeuGluGlyLeuTyTrileGlyValIleSerGlnAlaIleHis 240
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Qy 241 AsnAlaIleAsnGlnValAlaLeuProlyseuLeuValAspAlaIleValIleSerGly 260
Db 939 GATGCCAAGATGATGATTTTACCCAAACCTCTGACCTAGTGGATGCCAGTGGCCAG 998
Qy 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuTyTyValAsn 280
Db 999 TGAATAGTGTGAGAGTGATGAATCAAGCTGATGACACTTTAAACTACGTTGCT 1058
Qy 281 G|YThrCysGlnThrThrTyrr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
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Search completed: April 9, 2006, 07:31:28
Job time : 7173.98 secs


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XX      Thomas CR, Mcpherson MJ, Atkinson MJ, Neelam A,
XX      WPI; 2002-489891/52.
XX      P-PSDB; AAE25918.
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XX      Inducing necrotic effect in specific cells of plant by transforming plant
XX      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      which acts in response to application of specific stimulus to plant.
XX
XX      Claim 24; Page 73-74; 87pp; English.
XX
XX      The invention relates to a method of inducing a necrotic effect in
XX      specific cells of a plant. The method involves transforming the plant
XX      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX      in response to the application of a specific stimulus to the plant so as
XX      to facilitate expression of the pokeweed antiviral protein in specific
XX      cells of the plant. The method is useful for inducing a necrotic effect
XX      in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
XX      protein encoding DNA
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Score:      1617.00      Matches:      314
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Best Local Similarity:      100.0%      Mismatches:      0
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Db      121 GCCACCTTATAGAAATCTCTTCGTAAATCAAGCAAAAGATCCAAACTTAAATCTCTATGGC 180
Oy      61 IleProMetLeuProAspThrAsnSerThrProLysTyrIleLeuValLysLeuGlnGly 80
Db      181 ATACCAATGCTACTACTAATTAATTCGACCCCTTAAGTACTTATTTGTTAAGCTCAAGGT 240
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Oy      161 GlnValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db      481 CAAGTCCAATGGGAATTCAAATATCTCAGACAGTCAATGGGAAAAATCTCTGAGATTGAT 540
Oy      181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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XX      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX      Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX      WPI; 2002-469891/52.
XX      P-PSDB; AAE25919.
XX
XX      Inducing necrotic effect in specific cells of plant by transforming plant
XX      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      which acts in response to application of specific stimulus to plant.
XX
XX      Claim 2; Page 76; 87pp; English.
XX
XX      The invention relates to a method of inducing a necrotic effect in
XX      specific cells of a plant. The method involves transforming the plant
XX      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      PAP', PARI and PAP-S, where the gene(s) comprises a promoter which acts
XX      in response to the application of a specific stimulus to the plant so as
XX      to facilitate expression of the pokeweed antiviral protein in specific
XX      cells of the plant. The method is useful for inducing a necrotic effect
XX      in specific cells of a plant. The present sequence is pokeweed mature PAP
XX      -S protein encoding DNA
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SQ      Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;

Alignment Scores:
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Score:          1352.00      Matches:      262
Percent Similarity: 100.0%      Conservative: 0
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US-09-978-274A-2 (1-314) x AAD42716 (1-792)
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DB      64 GAATCTTCTTGATCAAGGAGAAAGATCAAAATCAAAATGCTAATGCAATCAATCTA 123
QY      65 ProAspThrAsnSerThrProlyTyrleuValIlyleuGlnGlyAlaAsnleuLys 84
DB      124 CCGATGACTAATTCGACCCCTTAAGTACTAATGTGTTAAGTCCCAAGTGCACCACTAAA 183
QY      85 ThrilleThrleuMetleuArgAsnAsnleuTyrValMetGlyTyrSerAspProphe 104
DB      184 ACCATTACACTAATGCTGAGACGAAATTAATTAATGAGTGGCTATTCTGATCCCTTC 243
QY      105 AsnGlyAsnLysCysAsgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 124
DB      244 AATGGCAATAGTGTCTTACCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 303
QY      125 ValGluAsnThrleuValCysSerSerSerSerSerSerValAlaMetSerIleAsnTyrAsn 144
DB      304 GTGGAGAAATACCTCTTCTCAAGTTCTAGTTCTGCTTTCGATGCAATTAATTAATTA 363
QY      145 SerleuTyrProthrmMetGluValGlyValAlaMetSerArgAsnGlnValGlnleu 164
DB      364 AGCTAATATCGACCAATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTTC 423

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QY      165 GlyIleGlnIleleuSerSerAspIleGlyIleValIleSerGlyValAspSerPheProVal 184
DB      424 GAATTCAAATTAATCAAGACATGACATTTGGAATAATCTGAGTGAATTCATTCCTCGTA 483
QY      185 LythrGluAlaPhePheleuValAlaIleGlnMetValSerGluAlaAArgPhe 204
DB      484 AAAACGAGGCTTTTTCCTACTGTAAGTACCAATTAATTAATTAATTAATTAATTAATTA 543
QY      205 LyThrIleGluValGlnValIlyThrAsnPhaAsnArgAlaPheTyrProAspProlys 224
DB      544 AAGTACATAGAGAACCAAGTCAAGACTTAATTTAATGACATTCCTCCGATCCGAAA 603
QY      225 ValIleAsnleuGlnGluValTyrGlyIleValIleSerGluAlaIleHisAsnAlaValAsn 244
DB      604 GTAAATTAATCTTGAGGAGAAAGTGGCAAAATCTGAGGCAATTCACAAATGCCAAGAAAT 663
QY      245 GlyAlaLeuProlyAspProleuGluLeuValAspAlaLysGlyThrIlyStrIleValIleu 264
DB      664 GGGGCTTTACCAACCACTTGAAGTATGATGATGCCAAAGTACCAAGTGAATGTTCTT 723
QY      265 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 284
DB      724 AGAGTGATGAATCAATCGTATGTCGACCTCTTAAGTACGTTAATGGAACCTGTACAG 783
QY      285 ThrThr 286
DB      784 ACAACT 789

RESULT 3
AAD42729
ID      AAD42729 standard; DNA; 1092 BP.
XX
XX      AAD42729;
XX
XX      29-AUG-2003 (revised)
DT      15-NOV-2002 (first entry)
XX
DB      Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
XX      Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX      chimeric; rice; cystatin delta D86; Nta protease cleavage site; PCS; ds.
XX
XX      Phytolacca americana.
OS      Oryza sativa.
OS      Tobacco; Etch virus.
OS      Chimeric.
XX
XX      Key
XX      Location/Qualifiers
FT      primer_bind      1..29
FT      /*tag= a
FT      /bound_molecly= "Primer PS1BP"
FT      misc_feature      681..686
FT      /*tag= b
FT      /note= "Modified XbaI site"
FT      primer_bind      complement(742..786)
FT      /*tag= c
FT      /bound_molecly= "Primer PCS-PAPSR"
FT      primer_bind      766..806
FT      /*tag= d
FT      /bound_molecly= "Primer PCS-Delta86P"
FT      misc_feature      766..786
FT      /*tag= e
FT      /note= "TEV Nta protease cleavage site"
FT      /*tag= f
FT      complement(1066..1092)
FT      /*tag= f
FT      /bound_molecly= "Primer SYNPOrtelDelta86R"
XX
XX      WO200233107-A2.
XX
XX      25-APR-2002.
XX
XX      15-OCT-2001; 2001WO-GB004593.

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XX 14-OCT-2000; 2000GB-00025217.
 PR (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 PA Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
 PI WPI; 2002-469891/52.
 DR
 XX
 XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 XX Disclosure; Page 83; 87pp; English.
 PS
 XX The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAP-I and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is a fusion DNA. This
 CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
 CC and Tobacco Etch Virus (TEV) N1a protease cleavage site (PCS). (Updated
 CC on 29-AUG-2003 to standardise OS field)
 CC
 XX
 XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 3,86e-128 Length: 1092
 Score: 1307.00 Matches: 254
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 80.8% Indels: 0
 DB: Gaps: 0
 US-09-978-274a-2 (1-314) x AAD42729 (1-1092)
 QY 25 ILeaSnThrlEThrPheAPAlAGLYaSnAlaThrlEaSnLySTrYalATnRrPheMet 44
 DB 4 ATAAATACGATCACTTGTGATGCTGGAATATGCCACTTAAACAAATATGACACCTTTATG 63
 QY 45 GluSerLeuArgAngInAlaLyAspProLyLeuLyCySTyrgLyIleProMetLeu 64
 DB 64 GAATCTCTCGTATACAGCGAAAGATCCAAATCTAAATAGTATGCAATCAACCAATGCTA 123
 QY 65 ProAspThrAsnSerThrProLySTyrlEuleuVallyLeuGlnGlyAlaAenLeuLyS 84
 DB 124 CCGAATACCTAATTCGACCCCTTAAGTACTTAATGCTTCAAGGTGCAAACTTAAAA 183
 QY 85 ThrIleThrLeuMetLeuArgArGaAsnAsnLeuTyrlValMetGlyTyrlSerAspProPhe 104
 DB 184 ACCATTACACTAATGCTGAGACGAATTAACCTTAAGCTATGAGGCTATTTGATCCCTTC 243
 QY 105 AenGlyAsnLyCySaArgTyrlHisIlePheAsnAspIleThrSerThrgIuArgThrAsp 124
 DB 244 AATGGCAATTAAGTGTGATACCATATATTATTAATGATTTCAAGACCGAAGCCACATGAT 303
 QY 125 ValIGuaSnThrLeuCySerSerSerSerSerSerArgValAlaMetSerIleAenTyrlAsn 144
 DB 304 GGGAGAAATACCTTTTGCTCAAGTCTAGTCTCGGTGCAATGTCCTAATTACTCAAT 363
 QY 145 SerLeuTyrlProThrMetGluLySlyAlaGlyAlaAsnSerArgAngInValGlnLeu 164
 DB 364 AGCTTATATCCGACCAATGAAAAGAAAGCAAGATTAACCTCAAGAAATCAAGTCCATTTG 423
 QY 165 GlyIleGlnIleLeuSerSerAspIleGlyLySlyIleSerGlyValAspSerPheProVal 184
 DB 424 GGAATTCAAATACTCGACAGTGCATTTGAAAATCTCTCGAATTTGATTCATTCCTCGTA 483
 QY 185 lyeThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 204

DB 484 AAAACTGAGGCTTTTTTCTACTGTAGCCATCCAAATGGTTCAAGAGCAGCGCATTC 543
 QY 205 lyeTyrlIleGluAenGlnVallySThrAsnPhaAsnArgAlaPheTyrlProAspProLyS 224
 DB 544 AAGTACATGAGAACCAAGCAAGACTTAATTTAATGAGCAATTCACCTGATCCCAA 603
 QY 225 ValIleAsnLeuGluGluLySTPGLyLySlyIleSerGluAlaIleHisAenAlaLyAsn 244
 DB 604 GTAAATTAACCTTGAGAGAGAAAGTGGCCAAATCTCTGAGCAATTCACATGCCAAGAT 663
 QY 245 GlyAlaLeuProLySProLeuGluLeuValAlaAspAlaLySlyThrylSTPILleValLeu 264
 DB 664 GGGGCTTTACCAACCAACTTGTAGTGCAGTCCAAAGTACCAAGTGAATGATGTTCTT 723
 QY 265 ArgValAspGluIleAsnArgAspValAlaLeuLeuLySTyr 278
 DB 724 AGAGTGAATGAAATCAATCGTATGTGGCACTCTTAAGTAC 765
 RESULT 4
 AAZ45197
 ID AAZ45197 standard; DNA; 1379 BP.
 XX
 AC AAZ45197;
 DT 29-FEB-2000 (first entry)
 XX
 DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
 XX
 KW Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
 KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
 KW potato virus X; cucumber mosaic virus; CMV; ss;
 KW tomato yellow leaf curl virus.
 XX
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /tag = "PAP"
 FT /product = "PAP"
 FT /note = "Pokeweed antiviral protein"
 XX
 EN WO960843-A1.
 XX
 PD 02-DEC-1999.
 XX
 PP 21-MAY-1999; 99WO-US011301.
 XX
 PR 22-MAY-1998; 98US-0086374P.
 XX
 PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Turner NE, Wang P;
 XX
 PI WPI; 2000-062555/05.
 DR P-PADB; AAY58025.
 XX
 PT New antiviral DNA useful for generating transgenic plants resistant to
 PT viruses and/or fungi.
 PS
 PS Example; Page 4-5; 43pp; English.
 PS
 CC This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
 CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
 CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
 CC catalytically removes a specific adenine residue from a highly conserved
 CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
 CC antiviral protein II (PAP II) protein confers antiviral and/or antifungal
 CC activities to plants. A DNA molecule encoding a PAP II protein with an
 CC intact catalytic active site amino acid residue (R172) is useful for
 CC generating transgenic plants. PAP II DNA is useful for generating
 CC transgenic plants (especially cereal crops) through transforming a
 CC protoplast or introducing the DNA directly into a plant part prior to
 CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal

CC actively thus have increased resistance to viruses and/or fungi. Viruses
 CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
 CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
 CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
 CC other plants pests including insects, bacteria and nematodes. PAP II DNA
 CC is also useful for identifying a PAP II protein having reduced
 CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
 CC unlike PAP transgenic plants which are stunted and sterile, PAP II
 CC transgenic plants have a normal and fertile phenotype

SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,91e-120	Length:	1379
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ5197 (1-1379)

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QY 1 MetlyValMetleuValValValThreulealATpLeuilealAalProthr 20
DB 225 ATGAAGTCGATGCTTGCGTGAACAATCAATA-----TGGCTCATTCCTGCACCACT 278
QY 21 SerThrCysAlaIleAenThrIleThrePheaspIaGlyAaAlaThrIleAaLysThr 40
DB 279 TCAACTGGGCTGGGAATACATCACTACATGTTGGAAATACACCATTAAGCAAAATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
DB 339 GCCACTTTCTCGATGATCTTCGTATGACGAAAGATCCAAAGTTAAATGCTATGCA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCCCAATACCAATCAAAATCAAGTACGTTGCTGACCTCCAAAGT 458
QY 81 AlaAsnLeuLysThrIleThreMetLeuArgAsnAenLysValMetGlyThr 100
DB 459 TCAAAATAAAACCAATCACTACATGCTGAGACGAAACAAATGATGATGATGATAT 518
QY 101 SerAspProPheAsnGlyAsnLysCysArgTyRHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTGAACCAATTAATGCTTACCATATCTTAATGATATCTCAGTACT 578
QY 121 GluArgThrAspValGluAenThrLeuLysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAGAGACTACTCTTGGCCAAATGCCAATCTCGGTAGTAAAAAC 638
QY 141 IleAsnTyRAsnSerLeuLysProThrMetGlnLysAlaGluValAsnSerArgAsn 160
DB 639 ATAAACTTGTATGATCAATATCAATCAATGGAATCAAAAGGGAGTAAATCAAGAGT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCCAATCGGAATTCAAATATCTGACAGATTAATTTGAAAAGATTTTCGAGTATG 758
QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB 759 TCATTTCACTGAGAAACCGAAGCGCAATTCCTATTGAGGCAATCAAAATGATGAGAG 818
QY 201 AlaAlaIlePheLysTyRTrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheThr 220
DB 819 GCGACCAAGATTCAGATCAATGAGAAATCGGTGAAACTAAATTTTAAACAGAGCATTAAC 878
QY 221 ProAspProLysValIleAsnLeuGlnGluLysTrpGlyLysIleSerGluAlaIleHis 240
DB 879 CCTAATCCCAAGTACTTAATTTGCAAGAGCATGGGTAAAGATTTTCAACGCAATTCAT 938
QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLysValAspAlaLysGlyThrLys 260
DB 939 GATGCCAAGATGAGTTTATCCAAACCTCTCGAGCTAGTGGATGCCAGGTGCGCAAG 998
  
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QY 261 ThrIleValleuArgValAspGlnIleAsnArgAspValAlaLeuLysTyRValAsn 280
DB 999 TGGATAGTGTGAGAGATGATGAATATCAAGCTGATAGACTCTTAACCTACGTTGGT 1058
QY 281 GlyThrCysGlnThrThrTyR---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTGTGACACACTTAATTAACCAAAATGCCATGTTCTCTCACTTATATATGCTACT 1118
QY 300 TyRThrAsnTyRMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
DB 1119 TATTATATTAATCAATGATGTTAACTTGATGATCTATTTAAGGATTC 1163
  
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RESULT 5

AAZ59220 ID AAZ59220 standard; cDNA; 1379 BP.
 AAZ59220; AC
 XX 20-APR-2000 (first entry)
 DT
 XX
 DS Pokeweed antiviral protein coding sequence spring leaf form.
 XX
 KW Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 KW resistance; potato virus X; potato virus Y; potato leaf roll virus;
 KW tuber; ss.
 OS
 XX PhytoIacca americana.
 PN
 XX US6015940-A.
 PD 18-JAN-2000.
 XX
 PP 07-APR-1992; 92US-00865169.
 XX
 PR 07-APR-1992; 92US-00865169.
 XX
 PA (MONS) MONSANTO CO.
 PI
 PI Kaniewski WK, Turner NE, Lodge JK;
 XX
 DR WPI; 2000-126326/11.
 XX
 XX
 PT Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 PS
 XX Claim 6; Fig 4; 30pp; English.

CC This is the coding sequence for the spring leaf form of the pokeweed
 CC antiviral protein (PAP) which is used to generate transgenic potato
 CC plants. PAP is able to confer resistance to infection by potato virus X
 CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
 CC potato plant or tuber expressing PAP

SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,91e-120	Length:	1379
Score:	1235.50 <td>Matches:</td> <td>239 </td>	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ59220 (1-1379)

```

QY 1 MetlyValMetleuValValValThreulealATpLeuilealAalProthr 20
DB 225 ATGAAGTCGATGCTTGCGTGAACAATCAATA-----TGGCTCATTCCTGCACCACT 278
QY 21 SerThrCysAlaIleAenThrIleThrePheaspIaGlyAaAlaThrIleAaLysThr 40
DB 279 TCAACTGGGCTGGGAATACATCACTACATGTTGGAAATACACCATTAAGCAAAATAC 338
  
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```

QY 41 AlAtThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLysCysTyrGly 60
DB 339 GCCACTTTTCTGATGATCTTCTGTAATGAGCGGAATATCAAGTTAAATGCTAATGA 338
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCGCAATACAAATACAAATCCAAAGTACGTGTGTTGAGCTCCAGGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
DB 459 TCMAATTAATAAAACCATACACATTAATGCTAAGCGAAACATTTGATGTGATGGTTAT 518
QY 101 SerAspProPheAsnGlnLysAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTTGAACCAATTAATGCTTACCATATCTTTAATGATATCTCAGGTAAT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATTCCTCGTGTAGTAAAAAAC 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysLysValGluValAsnSerArgAsn 160
DB 639 ATTAACCTTGTGATGTGATATCCAACTGGAATCAAAACCGGAGTAAATCAAGAGAT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCAACTGGGAATTCAAATTAATCTGACAGATTAATTTGGAAGANTTTTGGAGTCATG 758
QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB 759 TCATTCCTGAGGAACCGAAGCCGAATTCCTATGTTGATCCCAATGAGTATCAGAG 818
QY 201 AlaAlaArgPheLysTyrIleGlnGlnValLysThrAsnAsnAspAlaPheTyr 220
DB 819 GCAGCAAGATTCAGATGATGAGATTCAGATGGAATCTAATTTTAACAGAGCATTCAC 878
QY 221 ProAspProLysValIleAsnLeuGlnGlyLysTyrGlyLysIleSerGluAlaIleHis 240
DB 879 CTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGTTTCAACAGCATTCAT 938
QY 241 AsnAlaLysAsnGlnLysLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
DB 939 GAGGCCAAGATGAGATTTTAACTCCAAACCTCTGAGCTAGTGAATGCTGCGCAAG 998
QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn 280
DB 999 TGGATAGTGTGAGAGTGAATTCAGCTGATGACACTCTTAACCTAGCTTGGT 1058
QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTGCAGACCACTTAATACCAAAATGCCATGTTTCTCACTTAATATGCTACT 1118
QY 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
DB 1119 TATTAAATTAACATGCTTAATCTTGGTGAATCTAATTGAAGGATTC 1163

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RESULT 6
AADD42738
ID AADD42738 standard; DNA; 1379 BP.

AC AADD42738;
DT 15-NOV-2002 (first entry)
XX Pokeweed PAP' DNA #1.
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; de.
XX Phycolacca americana.
XX Key Location/Qualifiers
FH misc_feature 290..1076
FT

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FT /*tag= a
FT /note= "Mature PAP' sequence"
XX
XX MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB04593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
XX Sequence 1379 BP; 488 A; 233 C; 269 G; 369 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 1,91e-120 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2

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US-09-978-274A-2 (1-314) x AADD42738 (1-1379)
QY 1 MetLeuValMetLeuValValValIleLeuIleAlaTrpLeuIleAlaIleProThr 20
DB 225 ATGAAGTCAATGCTTGTGTGGTGAACATATCAATA-----TGGCTATTTCTTGACCACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyr 40
DB 279 TCAACTTGGGCTGTGAATACATCATCTCAATGTTGGAAGTACCACTTGGCAATAC 338
QY 41 AlAtThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLysCysTyrGly 60
DB 339 GCCACTTTTCTGATGATCTTCTGTAATGAGCGGAATATCAAGTTAAATGCTAATGA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCGCAATACAAATACAAATCCAAAGTACGTGTGTTGAGCTCCAGGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
DB 459 TCMAATTAATAAAACCATACACATTAATGCTAAGCGAAACATTTGATGTGATGGTTAT 518
QY 101 SerAspProPheAsnGlnLysAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTTGAACCAATTAATGCTTACCATATCTTTAATGATATCTCAGGTAAT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATTCCTCGTGTAGTAAAAAAC 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysLysValGluValAsnSerArgAsn 160

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|||||.....|
Db 639 ATAACTTGATGATCATATCCAACTGGAATCAAAAGCGGAGTAAATCAGAGACT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAsp 180
Db 699 CAGGTCCAACTGGGAATTCAAATCTGACAGTAAATATGGAAGAATTTCTGGAGTATG 758
Qy 181 SerPheProValIleThrGlnAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATACAGAG 818
Qy 201 AlaAlaArgPheIleGlyIleGlnValAspGlnValIleThrAsnPheAsnArgAlaPheTyr 220
Db 819 GCAGCAAGATTCAATGATACATGAGATCAAGTGAATCTAATTTTAAACAGAGCATTCAC 878
Qy 221 ProAspProIleValIleAsnLeuGlnGluIleThrGlyIleSerGluAlaIleHis 240
Db 879 CCTAATCCCAAGACTTAATTTGCAAGAGACATGGGGTAAAGATTTCCAAACGCAATTCAT 938
Qy 241 AsnAlaIleAsnGlyAlaLeuProIleProIleGluLeuValAspAlaIleGlyThrIle 260
Db 939 GATGCCAAGATGAGATTTTACCCAACTCTCAGACTAGTGGATGCCAGTGGTCCAG 998
Qy 261 TrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIleTyrValAsn 280
Db 999 TGGATAGTGTGAGAGTGAATGAAATCAAGCCTGATGAGACCTTAAACTGATGGT 1058
Qy 281 GlyThrCysGlnThrIleThrIle---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGGAGCTGTCAAGCAACTTATTAACCAAAATGCCAATGTTCTCTCAACTATTAATGTCTACT 1118
Qy 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATTATTAATTAATCATGTGTTAATCTTGATGATCTATTGAAAGATTC 1163

RESULT 7
AD105787
ID AD105787 standard; DNA; 1379 BP.
XX
AC AD105787;
XX
DT 15-APR-2004 (first entry)
XX
DE DNA encoding the wild-type pokeweed antiviral protein.
XX
KW ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
KW cytosolic; immunosuppressive; agricultural biotechnology; pharmaceuticals;
KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
KW de.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT CDS 225..1166
FT /*tag= a
FT /product= "wild-type pokeweed antiviral protein"
XX
PN MO200262952-A2.
XX
PD 15-AUG-2002.
XX
PF 01-FEB-2002; 2002MO-US0002792.
XX
PR 02-FEB-2001; 2001US-0266396P.
XX
PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE, Hudak KA, Parikh B;
XX
DR WPI; 2003-156656/15.
XX
DR P-PSDB; AD105788.
XX

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PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT type PAP, useful in agricultural biotechnology or in the fields of
PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
PT or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 1; 51pp; English.
XX
CC The invention relates to a novel pokeweed Antiviral Protein (PAP) mutant
CC that is less toxic than wild-type PAP and exhibits ribosome depurination
CC activity, where the mutant is a central domain mutant or N-terminal
CC domain mutant. The PAP mutants have the following activities: antifungal,
CC antiviral, virucide, anti-HIV, cytosolic and immunosuppressive. The PAP
CC mutants are useful in agricultural biotechnology as well as in the fields
CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
CC treating mammals with cancer, AIDS, viral infection or autoimmune
CC diseases associated with proliferations of unwanted T-cells or B-cells.
CC The transgenic plants are useful in exhibiting resistance to a broad
CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC sequence represents the DNA encoding the wild-type pokeweed antiviral
CC protein of the invention.
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,91e-120 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: Gaps: 2

US-09-978-274A-2 (1-314) x AD105787 (1-1379)
Qy 1 MetIleValMetLeuValValValIleThrLeuIleAlaTrpLeuIleAlaIleProThr 20
Db 225 ATGAAGTCAGATGCTTGCTGGTGAACAATATCAATA-----TGGCTCATTTCTTGACACCAACT 278
Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleTyr 40
Db 279 TCAACTGGGCTGTGAATCAATCATCAATCATCAATGTTGAAGTCAACCATTTAGCAAAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProIleLeuIleCysTyrGly 60
Db 339 GCCACTTTCTGATGATGATCTTCTGTAATGAAGCCAAAGATCCAACTTTAAATGCTATGCA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProIleTyrLeuLeuValIleGlnGly 80
Db 399 ATACCAATGCTGCCAATACAAATACAAATCAAAAGTACGTGTGTTGAGCTCCAAAGT 458
Qy 81 AlaAsnLeuIleThrIleThrLeuMetLeuArgArgAsnLeuIleTyrValMetGlyTyr 100
Db 459 TCAAAATTAATAAAACCAATCACTAATGCTGAGACGAAACAAATTTGATGTGATGGGTAT 518
Qy 101 SerAspProPheAsnGlyAsnIleCysArgTyrHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTGAAACCAATTAATGCTGTACCAATCTTTAATGATATCTCAGGACT 578
Qy 121 GluArgThrAspValGluAsnThrIleuGlySerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATGTAGAGACTACTCTTGGCCAAATGCCAAATCTCGTGTAGTAAAAAC 638
Qy 141 IleAsnTyrAsnSerLeuIleProThrMetGluIleValAlaGluValAsnSerArgAsn 160
Db 639 ATAACTTTGATGATATTCATCAATTCAGATTCGAAAGCGGAGTAAATCAAGAGT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAsp 180
Db 699 CAGGTCCAACTGGGAATTCAAATCTGACAGTAAATATGGAAGAATTTCTGGAGTATG 758
Qy 181 SerPheProValIleThrGlnAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATACAGAG 818

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QY 201 AAlaAlarGPhelyleTyrlleGluanglnVallyleThrAnpPheAnaGAlaPheTyR 220
DB 819 GCAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAAACTAATTTTAAACAGACATTCAAC 878
QY 221 ProAspProLyseValilleAnleuGluGluTyRTPGlylyleSerGluAlaileHls 240
DB 879 CCTAATCCCAAGTACTTAATTTTGCAAGAGACATGGGGTAAGATTTCACACGCAATTCAT 938
QY 241 AsnAlaLyseAnGlyAlaLeuProLyseProLeuGluLeuValAspAlaLyseGlyThrLyse 260
DB 939 GATGCCAAGATGAGATTATACCAAACTCTGAGCTAGTGAATGCCAGTGGTCCAG 998
QY 261 TPrlleValleuArGValAspGluilleAnArGAspValAlaLeuLeuTyRValAsn 280
DB 999 TGGATAGTGTGAGAGTGAATCAAGCCCTGATGACCTTAAACTACGTTGCT 1058
QY 281 GlyThrCyseGlnThrThrTyR---GlnAsnAlaMetPheSerGlnValilleleSerThr 299
DB 1059 GGGAGCTGTCAGACACTTAATACCAAAATGCCATGTTCTCTCAACTTAATATGCTACT 1118
QY 300 TyrTyRAsnTyRMetSerAnleuGlyAspLeuPheGluGlyPhe 314
DB 1119 TATTAATTAATTAATGATTGTTATCTTGGTGAATCTATTGGAAGATTTC 1163

RESULT 8

ADG76061

ID ADG76061 standard; DNA; 1378 BP.

XX ADG76061;

XX 11-MAR-2004 (first entry)

XX American pokeweed antiviral protein (PAP) DNA SegID 1.

XX gene; db: pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;

XX nucleoside analogue inhibitor; viral protease inhibitor; viral infection;

XX american pokeweed; retroviral.

XX PhytoIacca americana.

XX WO2003106479-A2.

XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019141.

XX 17-JUN-2002; 2002US-0389649P.

XX (PARK-) PARKER HUGHES INST.

XX Uckun FM;

XX WPI: 2004-082156/08.

XX P-PsDB; ADG76064.

XX Novel modified pokeweed antiviral protein useful for inhibiting viral

XX replication, for inducing depurination of viral RNA, or for treating

XX viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As

CC such, they are useful for inhibiting viral replication and for
CC deactivating viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX

SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:

	3..11e-120	Length:	1378
Pred. No.:	1233..50	Matches:	239
Score:	86.3%	Conservative:	33
Percent Similarity:	75.9%	Mismatches:	40
Best Local Similarity:	76.3%	Indels:	3
Query Match:	12	Gaps:	2

US-09-978-274A-2 (1-314) x ADG76061 (1-1378)

QY 1 MetLyseValMetLeuValValValValMetLeuAlaThrLeuAlaAlaProThr 20
DB 224 ATGAAGTCAGATGTTGGTGTGACCAATATCAATA-----TGGCTCATTTCTTGACCAACT 277
QY 21 SerThrCyAlaAlleAnThrilleThrPheAspAlaGlyAsnAlaThrilleAnTyR 40
DB 278 TCACTTGGGCTGTGAATCAATCATCATCATGTTGGAAGTACCACTTACCAATATC 337
QY 41 AlaThrPheMetGluSerLeuArGAnGlnAlaLyseProLyseLeuTyRtyRgly 60
DB 338 GCACATTTTCTGAATGATCTCTGTATGAAGGAATCCAGTTAAATGCTATGGA 397
QY 61 IleProMetLeuProAspThrAnSerThrProLyTyRLeuLeuVallyleuGlnGly 80
DB 398 ATACCAATGCTGCCCAATCAATCAATCAATCAATGATGTTGGTTCAGCTCCAAAGT 457
QY 81 AlaAnleuTyRThrilleThrleuMetleuArGArGAsnAnleuTyRValMetGlyTyR 100
DB 458 TCAATTAATAAAACCATCACTAATGCTGAACCAAAATTTGTATGTGATGGTTAT 517
QY 101 SerAspProPheAnGlyAnLyseAnTyRtyRillePheAsnAspilleThrSerThr 120
DB 518 TCGATCCCTTGAACCAATTAATGCTTACCAATATCTTAATGATATCTCAGGTAAT 577
QY 121 GluArGThrAspValGluAnThrleuCyseSerSerSerSerArgValAlaMetSer 140
DB 578 GAACGCCAAGATGTGAGACTACTCTTGGCCCAATGCCAATCTCTGTTGTGTAATAAC 637
QY 141 IleAnTyRAsnSerleuTyRProThrMetGluTyRlyAlaGlyValAsnSerArgAn 160
DB 638 ATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
QY 161 GlnValGlnleuGlylleGlnleuSerSerAspilleGlylyleSerGlyValAsp 180
DB 698 CAGTCCCAATGGGAATTCATTAATCTCGACATTAATGGAAGATTTCTGGAATGATG 757
QY 181 SerPheProVallyleThrGluAlaPhePheleuLeuValAlaIleGlnMetValSerGlu 200
DB 758 TCATTCCTGAGAAAAACCAAGCCCAATTCATTTGGTGAATGCAATGATGATGATGATG 817
QY 201 AAlaAlarGPhelyleTyrlleGluanglnVallyleThrAnpPheAnaGAlaPheTyR 220
DB 818 GCAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAAACTAATTTTAAACAGACATTCAAC 877
QY 221 ProAspProLyseValilleAnleuGluGluTyRTPGlylyleSerGluAlaileHls 240
DB 878 CCTAATCCCAAGTACTTAATTTTGCAAGAGACATGGGGTAAGATTTCACACCAATTCAT 937
QY 241 AsnAlaLyseAnGlyAlaLeuProLyseProLeuGluLeuValAspAlaLyseGlyThrLyse 260
DB 938 GATGCCAAGATGAGATTATACCAAACTCTGAGCTAGTGAATGCCAGTGGTCCAG 997
QY 261 TPrlleValleuArGValAspGluilleAnArGAspValAlaLeuLeuTyRValAsn 280
DB 998 TGGATAGTGTGAGAGTGAATCAAGCCCTGATGACCTTAAACTACGTTGCT 1057
QY 281 GlyThrCyseGlnThrThrTyR---GlnAsnAlaMetPheSerGlnValilleleSerThr 299

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DB      1058 GGGAGCGCTGACGACCACTTAAACCAAAATGCCATGTTTCTCTCAACTATATGCTACT 1117
OY      300  TTTTAAATTTTMeTSeRseRnLeuGIyAAspleuPheGluGIyPhe 314
DB      1118 TATTATAATTAATGATGTTAACTTGGATGATCTATTGAAGGATTC 1162

RESULT 9
AAC87929 ID AAC87929 standard; DNA; 1379 BP.
XX
AC      AAC87929;
XX
DT      06-MAR-2001 (first entry)
XX
DB      P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
KM      Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
KM      biotherapeutic; fusion protein; immunconjugate; mutant; cytostatic;
KM      anti-HIV; human immunodeficiency virus; AIDS; leukaemia; lymphoma;
KM      brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; SS.
XX
OS      Phytolacca americana.
XX
FH      Key Location/Qualifiers
FT      CDS 225..1166
FT      /*tag= a
FT      /product= "pokeweed antiviral protein (PAP)"
XX
XX      US6146628-A.
XX
PD      14-NOV-2000.
XX
PF      11-JUL-1995; 95US-00501253.
XX
PR      11-JUL-1995; 95US-00501253.
XX
PA      (MIND) UNIV MINNESOTA & RUTGERS.
PA      (UYNE-) UNIV STATE NEW JERSEY.
XX
PI      Uckun FM, Turner NE;
XX
DR      WPI; 2001-040422/05.
DR      P-PSDB; AAB36500.
XX
PT      Immunconjugates useful for treating cancer and acquired immunodeficiency
PT      syndrome, comprises mutant pokeweed anti-viral protein and a targeting
PT      moiety that binds a cell surface receptor.
XX
PS      Disclosure; Col 47-50; 32pp; English.
XX
CC      The present invention describes a fusion protein or an immunconjugate
CC      (I), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
CC      acid substitution at residue 75, 97 or 176 of native PAP and a targeting
CC      moiety that binds a cell surface receptor. (I) can have cytosolic and
CC      anti-HIV activities, and is an inhibitor of cellular RNA or protein
CC      synthesis. (I) is useful for treating AIDS and cancers including
CC      leukaemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
CC      tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
CC      colon cancer. Immunconjugates prepared using PAP mutants exhibit an
CC      improved therapeutic index over immunconjugates containing either wild-
CC      type PAP or variant PAP. The present sequence encodes the wild-type PAP,
CC      which is given in the exemplification of the present invention
XX
SQ      Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,97e-120 Length: 1379
Score: 1232.50 Matches: 238
Percent Similarity: 86.3% Conservative: 34
Best Local Similarity: 75.6% Mismatches: 40
Query Match: 76.2% Indels: 3
DB: 4 Gaps: 2
```

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US-09-978-274A-2 (1-314) x AAC87929 (1-1379)
OY      1  MellyValMelleuValValValThleuIleAlaTrpleuIleAlaProthr 20
DB      225  ATGAAGCGATGCTTGGTGAGCAATATCAATA-----TGGCTCATTTCTGCACCACT 278
OY      21  SerThrCysAlaIleAenThrIleThrPheAspAlaGlyAenAlaThrIleAenLysThr 40
DB      279  TCAACTTGGGCTGGGAATACATCATCTACAAATGTTGAAGATACACACATTAAGCAATAC 338
OY      41  AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyGly 60
DB      339  GCCACTTTCTGAATGATCTTCGTAATGAAGCGAAGATCCAGTTTAAATGCTATGCA 398
OY      61  IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
DB      399  ATACCAATGCTGCCCAATACAAATACAAATCCAAAGTACCTGTTGAGCTTCCAAAGT 458
OY      81  AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTyTr 100
DB      459  TCAATTAATAAAACATCACACTAATGCTGAGACGAAACAAATTTGATGATGAGGTTAT 518
OY      101  SerAspProPheAsnGlyAsnLysCysArgTyTrHisIlePheAsnAspIleThrSerThr 120
DB      519  TCTGATCCCTTTGAACCAATTAATGCTTACCATATCTTTAATGATATCTCAGTACT 578
OY      121  GluArgThrAspValGluAenThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB      579  GAACGCCAAGATGTAGAGACTACTCTTGGCCAAATCCCAATTCCTCGTTAGTAATAAAC 638
OY      141  IleAsnTyTrAsnSerLeuTyTrProThrMetGluLysLysIleGluValAsnSerArgAsn 160
DB      639  ATAACTTGATGATGTCATATTCACACATTTGAATCAAAAGCGGAGTAATAATCAAGAGT 698
OY      161  GlnValGlnLeuGlnIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB      699  CAGTCCAACTGGGAATTCAAATACCTGCACAGTAATATTTGAAAGATTTCTGAGATGAG 758
OY      181  SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB      759  TCATTCATCGAGAAACCCCAAGCCGAATTCCTATTGCTAGCCATACAAATGATATCAGAG 818
OY      201  AlaAlaArgPheLysTyTrIleGluAenGlnValLysThrAsnPheAsnArgAlaPheTyTr 220
DB      819  GCAGCAAGATTCAGATACATGAGAAATCAGTGAAAACTAATTTTAAACAGACATTTCAAC 878
OY      221  ProAspProLysValIleAsnLeuGluGluTyTrGlyLysIleSerGluAlaIleHis 240
DB      879  CTTAATCCCAAGTACTTAATTTTGCACAGACATGGGGTAAAGATTTTCAACAGCAATTCAT 938
OY      241  AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
DB      939  GATGCCAAGATGAGATTTTAACTCAAACTCTGACCTAGTGATGCCAGTGGGCAAG 998
OY      261  TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
DB      999  TGGATGTGTGTGAGATGATGAAATCAAGCTGATGTGACATCTTAAACATAGTGGT 1058
OY      281  GlyThrCysGlnThrThrTyTr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB      1059  GGGAGCTGTCAGACCACTTAATACCAAAATGCCATTTTCTCTCACTTAATATGCTACT 1118
OY      300  TTTTAAATTTTMeTSeRseRnLeuGIyAAspleuPheGluGIyPhe 314
DB      1119 TATTATAATTAATGATGTTAACTTGGATGATCTATTGAAGGATTC 1163

RESULT 10
ADM74765 ID ADM74765 standard; cDNA; 1164 BP.
XX
AC      ADM74765;
XX
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XX 16-AUG-1992; 92KR-00014895.
 PR (JINR-) JIN RO LTD.
 PA
 PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
 XX WPI; 1994-076002/10.
 DR P-PSDB; AAR48548.
 XX
 PT Expression vector for phytolecta antiviral protein - used for producing
 PT transgenic virus-resistant plants and for producing the antiviral agent.
 XX
 PS Disclosure; Fig 1; 15pp; English.
 CC To isolate PAP gene, total cellular mRNA was purified from leaves of
 CC phytolecta americana L. obd. in Korea. A cDNA library was constructed.
 CC The PAP gene was selected by immunoscreening employing anti-PAP antibody.
 CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
 CC sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,78e-120 Length: 1195
 Score: 1229.50 Matches: 238
 Percent Similarity: 86.0% Conservative: 33
 Best Local Similarity: 75.6% Mismatches: 41
 Query Match: 76.0% Indels: 3
 DB: Gaps: 2
 US-09-978-274A-2 (1-314) x AAQ56672 (1-1195)
 QY 1 MetlytAlmetleuValValThleuileAlaTrpleuileAlaIaProthr 20
 DB 33 ATGAAGTCGATGCTTGTGTGACATATCAATA-----TGGCTCATTTCTTGACCACT 86
 QY 21 SerThrCysAlaIleAnthrIleThrPheAspIaGlyAsnAlaThrIleAsnLysTyr 40
 DB 87 TCAACTTGGCTGTGAATACATATCATACATGTTGAAGTACACCATTTAGCAATATC 146
 QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGly 60
 DB 147 GCCACTTTTCTGAATATCTTTCGTAATGAGCGAAATCCAACTTTAAATGTAATGCA 206
 QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
 DB 207 ATACCAATGCTGCCCAATACAAATCAAAATGACGTGTTGAGTTCACAGGT 266
 QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
 DB 267 TCAAAATTAATAAACCAATACATACATATCTGACGAAACAAATTTGATGAGGTAT 326
 QY 101 SerAspProPheAsnGlyAsnLysCysArgTyrIleIlePheAsnAspIleThrSerThr 120
 DB 327 TCTGATCCCTTTGAAACCACTAATATGCTTACATATCTTATATGATATCTCAAGTACT 386
 QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
 DB 387 GAACGCCAAGATATGAGACTACTCTTGGCCAAATCCCAATTCCTCTGAGCAATAAAC 446
 QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysValGluValAsnSerArgAsn 160
 DB 447 ATTAACCTTATATGTCATATCCAACTTGAATCAAAACCGGAGTAATCAAGAGT 506
 QY 161 GlnValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
 DB 507 CAAGTCCAACTGGGAATTCAAATATCTGACAGTAATATGGAAGATTCTCGAGGTATG 566
 QY 181 SerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
 DB 567 TCATTCAGTGAAGAAACCGAAGCCGAATTCCTATGTGTACCAATAGTATATCAGAG 626

QY 201 AlaIaIaPheLysTyrIleGluAsnGluValLysThrAsnPheAsnArgAlaPheTyr 220
 DB 627 GCAGCAAGATTCAGATCATAGAGATCAGGTGAAACTATATTTAAACAGCAATTCAC 686
 QY 221 ProAspProLysValIleAsnLeuGluGlyLysTyrGlyLysIleSerGluAlaIleHis 240
 DB 687 CCTATCCCAAGACTTATTTTGCAGAGACATGGGGTAAATTTCAACAGCAATTCAT 746
 QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyTyrLys 260
 DB 747 GATGCCAAGATGAGATTTTACCAAACTCTGAGCTAGTGAATGCGAGTGGCCAG 806
 QY 261 ThrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLysTyrValAsn 280
 DB 807 TGGATGATGTTGAGAGTGAAGTAATCAAGCTGATGTACACTTTAACTAGTGGT 866
 QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGluValIleIleSerThr 299
 DB 867 GGGAGCTGTGACAACTTATTAACCAAAATGCCATGTTCTCTCACTTATATATGTACT 926
 QY 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
 DB 927 TATATATATTAACATGTTAATCTGTGATCTATTTGAAGATTC 971
 RESULT 12
 AAD42739
 ID AAD42739 standard; DNA; 1378 BP.
 XX
 AC AAD42739;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DB Pokeweed PAP' DNA #2.
 XX
 OS Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds-
 XX
 PH Phytolecta americana.
 XX
 FT Key Location/Qualifiers
 FT misc_feature 290..1076
 FT /*tag= a
 FT /note= "Mature PAP' sequence"
 XX
 PN W0200233107-A2.
 XX
 XX 25-APR-2002.
 PD
 XX 15-OCT-2001; 2001MO-GB004593.
 PF
 PR 14-OCT-2000; 2000GB-00025217.
 XX
 XX (ADTB-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 PA
 PI Thomas CUR, Mcpherson MJ, Atkinson HU, Neelam A;
 XX WPI; 2002-489891/52.
 DR
 PT Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 PS Claim 5; Page 86-87; 87pp; English.
 CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
 XX

SQ Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,34e-119	Length:	1378
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	6	Gaps:	2

US-09-978-274A-2 (1-314) x AAD42739 (1-1378)

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QY 1 MetLyvAlMeLeuValValValThrLeuIleAlaTrpLeuIleAlaAlaProthr 20
   |||||
DB 225 ATGAAATCAATGCTTGTGGTGAACAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
   |||||

QY 21 SerThrCyAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysrTy 40
   |||||
DB 279 TCAACTTGGGCTGTGAATCAATCATCTACATGTTGGAAGTACCAACCATTTAGCAAAATAC 338
   |||||

QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCy8TyrgLy 60
   |||||
DB 339 GCCACTTTTCGGAATGATCTTCTGTATGAAGCCAAAGATCCAAAGTTTAAATGCTATGA 398
   |||||

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
   |||||
DB 399 ATACCAATGCTGCCAATCAAAATACAAATCCAAAGCAGTGTGGTGGAGCTCCAAAGT 458
   |||||

QY 81 AlaAsnLeuLysrThrIleThrLeuMetLeuArgArgAsnLeuLysrValMetGlyTy 100
   |||||
DB 459 TCAAAATAAAAAACCATCACTAATGCTGAGAGCAAAACATTTGATGTGATGGGTAT 518
   |||||

QY 101 SerAspProPheAsnGlyAsnLysCy8TyrgLyIlePheAsnAspIleThrSerThr 120
   |||||
DB 519 TCTGATCCCTTTGAACCAATATATGTCCTTACCAATCTTTATATGATATCTAGATCT 578
   |||||

QY 121 GluArgThrAspValGluAsnThrLeuCy8SerSerSerSerSerArgValAlaMetSer 140
   |||||
DB 579 GAACGCCAAGATGTATAGACTACTCTTGGCCAAATGCCAAATCTCGTGTATGATAAAG 638
   |||||

QY 141 IleAsnTyAsnSerLeuLysrProThrMetGluLysValGluValAsnSerArgAsn 160
   |||||
DB 639 ATAACTTTGATGTGATATCCAAACATTTGAAATCAAAAGCGGAGCTTAAATCAAGAGT 698
   |||||

QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
   |||||
DB 699 CAGGTCCAATCGGGAATTCAAATACTCGACAGTAATATTTGGAAGATTTCTGAGATGATG 758
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QY 181 SerPheProValLysrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
   |||||
DB 759 TCATTCACCTGAGAAAACCCAAAGCCGAATTCCTATTTGTGTAGCCATACAAATGTGATCAGAG 818
   |||||

QY 201 AlaAlaArgPheLysrThrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
   |||||
DB 819 GCGAGCAAGATTCAGATCAATAGAGATCGAGTAAAACTAATTTTAAACAGAGATTCAC 878
   |||||

QY 221 ProAspProLysValIleAsnLeuGlnGluLysrTyrgLyLysIleSerGluAlaIleHis 240
   |||||
DB 879 CCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTGAAGTTTCAACAGCAATTCAT 938
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QY 241 AsnAlaLysAsnGlyValaLeuProLysrProLeuGlnLeuValAspAlaLysrGlyThrLys 260
   |||||
DB 939 GATGCCAAGATGAGATTTTACCCCAAACTCTCGAGCTAGTGATGCCAGTGGTGCAGAG 998
   |||||

QY 261 TrpIleValLeuArgValaAspGluIleAsnArgAspValAlaLeuLeuLysrTyValAsn 280
   |||||
DB 999 TGAATAGTGTGAGATGTGATGAATCAAGCTCGATGTAGCACTTTAAACATACGTTGGT 1058
   |||||

QY 281 GlyThrCy8GlnThrThrTyrgLyGlnAlaMetPheSerGlnAlaIleIleSerThr 299
   |||||
DB 1059 GGGAGCTGTGACAGCAACTTATACCAAAATGCGATGTTCTTCACTTATATATGTCTACT 1118
   |||||

QY 300 TyrTyAsnTyMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314

```

DB 1119 TATTATATTTACATGCTTAATCTTGTGATCTATTTGAAGATTC 1163

RESULT 13

AAZ59221
ID AAZ59221 standard, cDNA, 1379 BP.

XX
AC AAZ59221,

XX
DT 20-APR-2000 (first entry)

XX Variant pokeweed antiviral protein spring leaf form coding sequence.

XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;

XX resistance; potato virus X; potato virus Y; potato leaf roll virus;

XX tuber; ss.

OS Phytolacca americana.

PN US6015940-A.

XX 18-JAN-2000.

XX 07-APR-1992; 92US-00865169.

XX 07-APR-1992; 92US-00865169.

XX (MONS) MONSANTO CO.

XX Kanlewski WK, Turner NE, Lodge JK;

XX WPI; 2000-126326/11.

XX Production of transgenic potato plants or tubers expressing pokeweed

PT antiviral protein which are resistant to potato virus X or Y.

XX Claim 7; Fig 5; 30pp; English.

XX This is the coding sequence for a variant spring leaf form of the

CC pokeweed antiviral protein (PAP) which is used to generate transgenic

CC potato plants. PAP is able to confer resistance to infection by potato

CC virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in

CC the potato plant or tuber expressing PAP. PAP varies from PAP

CC (AAZ59220) by mutations L20R and Y49H

XX
SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,34e-119	Length:	1379
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ59221 (1-1379)

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QY 21 SerThrCyAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysrTy 40
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DB 279 TCAACTTGGGCTGTGAATCAATCATCTTACATGTTGGAAGTACCAACCATTTAGCAAAATAC 338
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QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCy8TyrgLy 60
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DB 339 GCCACTTTTCGGAATGATCTTCTGTATGAAGCCAAAGATCCAAAGTTTAAATGCTATGA 398
   |||||

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
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DB 399 ATACCAATGCTGCCAATCAAAATACAAATCCAAAGCAGTGTGGTGGAGCTCCAAAGT 458
   |||||

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QY 81 AlaAsnLeuYsrHrIleThrLeuMetLeuArgArgAsnLeuYrValMetGlyTyr 100
 DB 459 TCAAAATAAAAAACCATCACTATGCTGAGACGAAACAATTGTATGATGGTTAT 518
 QY 101 SerAspProPheAsnGlyAsnLeuYrCysArgTyrHisIlePheAsnAspIleThrSerThr 120
 DB 519 TCGATCCCTTTGAAACCAATAAATGTCGTATCAATCTTAAATGATATCTCAGACT 578
 QY 121 GluArgThrAspValGluAsnThrLeuYrSerSerSerSerSerArgValAlaMetSer 140
 DB 579 GAAGCCCAAGATGAGAGACTACTCTTGCCCAATGCAATCTTCGTGTATGAAAAAC 638
 QY 141 IleAsnTyrAsnSerLeuYrProThrMetGluYrValGluValAsnSerArgAsn 160
 DB 639 ATAAACTTGTATGATCATATCCCAATTCAGATCAAAAGCGGAGTAAATCAAGACT 698
 QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyYrIleSerGlyValAsp 180
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 QY 181 SerPheProValYsrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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 DB 819 GCAGCAAGATTCAGATGATCATAGAGATCAGGTGAAACTATTTAAACAGCATTTCAAC 878
 QY 221 ProAspProYrValIleAsnLeuGluGlyYrTyrGlyYrIleSerGlyValAlaIleHis 240
 DB 879 CCAATCCCAAGACTTAAATTTGCAAGACAGATGGGGTAAAGATTTCAACGCAATTCAT 938
 QY 241 AsnAlaIysAsnGlyAlaLeuProYrLeuGlnLeuValAspAlaYrGlyThrLys 260
 DB 939 GATGCCAAGATGAGCTTTTAAACCAACCTCTGAGCTAGAGATGCCAGTGGCCAG 998
 QY 261 TyrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuYrYrValAsn 280
 DB 999 TGGATAGTGTGAGAGTGAATCAAGCTGATGAGATCACTTAACTACGTTGGT 1058
 QY 281 GlyThrCysGlnThrTyr--GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
 DB 1059 GGGAGCTGTCAGCAACTTAAACCAAAATGCCATGTTCTCTCAACTAATATATGCTACT 1118
 QY 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
 DB 1119 TATTATATTAATCAATGCTTAATCTTGATCTATTTGAAAGGATTC 1163
 RESULT 14
 ID AAQ81457 standard; cDNA; 1195 BP.
 AC AAQ81457;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-AUG-1995 (first entry)
 XX
 DB Phytolacca antiviral protein (PAP) cDNA.
 XX
 KM Antiviral protein; vector pMW12; KCCM 10037; PAP; ss.
 XX
 OS Phytolacca americana; L.
 XX
 PN AU9350642-A.
 PD 19-JAN-1995.
 XX
 PF 11-NOV-1993; 93AU-00050642.
 PF 02-JUL-1993; 93KR-00012360.
 PR
 PA (JINR-) JIN RO LTD.
 XX

PI Lee K, Choi K, Jeon H, Kim M, Moon Y;
 XX
 DR WP1; 1995-067518/10.
 XX
 PT Recombinant vector for producing Phytolacca anti-viral protein - and
 PT transformed E. coli useful for making immunconjugates for treatment of
 PT AIDS.
 XX
 PS Claim 1; Fig 1; 27p; English.
 XX
 CC Total cellular mRNA from leaves of *P. americana* was used to produce a
 CC cDNA library and this screened with anti-PAP antibody raised in rabbits
 CC against purified PAP. Inserts were isolated from 2 clones and sequenced
 CC to identify a 1195 ORF (AAQ81457) that encodes a 313 AA PAP including a
 CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
 CC amplification using primers AAQ81458 and AAQ81459. The amplification
 CC product was cut with Hind III and inserted into the commercial FLAG (RTM)
 CC vector cut with the same enzyme to form pMW12. pMW12 is deposited with
 CC the Korean Collection of Culture and Microorganism (KCCM), an
 CC International Depository Authority, on June 30 1993, ad deposition No.
 CC KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7,73e-119 Length: 1195
 Score: 1219.50 Matches: 237
 Percent Similarity: 85.7% Conservative: 33
 Best Local Similarity: 75.2% Mismatches: 42
 Query Match: 75.4% Indels: 3
 DB: Gaps: 2
 US-09-978-274A-2 (1-314) x AAQ81457 (1-1195)
 QY 1 MetLeuValMetLeuValValValIleThrLeuIleAlaTrpLeuIleAlaIleAlaProThr 20
 DB 33 ATGAAGCGATGCTGTGGTGGAGCAATATCAATAT-----TGGTCATTTCTTGACCACT 86
 QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnYrTyr 40
 DB 87 TCAACTGGGCTGTGAATCAATCAATCATCTCAAAATGTGGAGATCCACCATTTACCAATAC 146
 QY 41 AlaThrPheMetGlnSerLeuArgAsnGlnAlaIleAspProYrLeuYrCysTyrGly 60
 DB 147 GCCACTTTTCTGATATGATCTTCTTAATGAAAGCAAAATCACTTAAATCTTATGCA 206
 QY 61 IleProMetLeuProAspThrAsnSerThrProYrTyrLeuLeuValYrLeuGlnGly 80
 DB 207 ATACCAATGCTGCGCAATACCAATACCAATATCCAAAGTACGTGTGGTGAAGTCCAAAGT 266
 QY 81 AlaAsnLeuYsrHrIleThrLeuMetLeuArgArgAsnLeuYrValMetGlyTyr 100
 DB 267 TCAAAATAAAAAACCATCACTATGCTGAGACGAAACAATTGTATGATGGTTAT 326
 QY 101 SerAspProPheAsnGlyAsnLeuYrCysArgTyrHisIlePheAsnAspIleThrSerThr 120
 DB 327 TCTGATCCCTTTGAAACCACTAATATGCTTACCAATATCTTAAATGATATCTCAGACT 386
 QY 121 GluArgThrAspValGluAsnThrLeuYrSerSerSerSerSerArgValAlaMetSer 140
 DB 387 GAAGCCCAAGATGAGAGACTACTCTTGCCCAATGCAATCTTCGTGTATGAAAAAC 446
 QY 141 IleAsnTyrAsnSerLeuYrProThrMetGluYrValGluValAsnSerArgAsn 160
 DB 447 ATAACTTGTATGATCATATCCCAATTCAGATCAAAAGCGGAGTAAATCAAGACT 506
 QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyYrIleSerGlyValAsp 180
 DB 507 CAGGTCCAACTGGGAATTCAAATCTGACAGATATGTGAAAGATTTCTGGAGTATG 566
 QY 181 SerPheProValYsrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 DB 567 TCATTCACGTAGAAACCGAAGCCGAATCTCTATTGGTAGCCATACAAATGATGATCAGAG 626


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Db      1788  AAGTGATAGTGTGAGAGTGAATGATGAACCTGATGTGGAGTCTCTTAAGTATGTT 1847
Qy      280  AsnGlyThrCysGlnThrThrTyGlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db      1848  AATGGGACCTGCCGCGCACTTACCAAGGCCATGTTCCCTCACCCT-ATAATGCTTACT 1906
Qy      300  TyrTyrAsnTyrMetSerAsnLeuGlyAsp-LeuPheGluGlyPhe 314
Db      1907  TATTATTAATTACATGGCTAATCTTGTGACTCTATTGAAGATTTC 1952

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Search completed: April 9, 2006, 02:22:19
 Job time : 842.351 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 5706.88 seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-2

Sequence: 1 MKVWLVVVVTLIAWLAAPF.....VISTYYNYSNGLDFEGF 314

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=p2n -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes07
-USBR=US09978274 @CCN 1.1.9564 @runat_07042006_173034_28424 -NCP=6 -ICPU=3
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EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345.5	21.4	829	7	CN782289 EST00385
2	281.5	17.4	1021	2	BE036639 MP03B03 M
3	266.5	16.5	993	2	BE035039 MM02A03 M
4	263.5	16.3	1033	2	BE036541 MP01B07 M
5	256.5	15.9	816	2	BE035038 MM02A01 M
6	251.5	15.6	639	2	BE037217 MP18B02 M
7	251.5	15.6	903	7	CO103587 GR_EB003

8	248.5	15.4	837	1	AM053634
9	245	15.2	649	6	CA838757
10	245	15.2	649	6	CA839330
11	245	15.2	661	6	CA835532
12	245	15.2	671	6	CA839511
13	245	15.2	689	6	CA833333
14	245	15.2	689	6	CA833383
15	239	14.8	841	7	CO121195
16	225	13.9	639	6	CA835855
17	222	13.9	1038	6	CA835546
18	208.5	12.9	489	2	BE130330
19	198	12.2	662	6	CF227047
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23	176	10.9	698	6	CA838926
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25	154	9.5	671	7	CN846973
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29	149.5	9.2	665	6	CF227084
30	148.5	9.2	603	5	BO590856
31	148	9.2	667	6	CA838446
32	145	9.0	669	7	CN848288
33	144	8.9	644	6	CA838401
34	136	8.4	422	6	CF227044
35	135	8.3	419	6	CF226983
36	135	8.3	659	5	BO584743
37	134	8.3	546	5	BO588856
38	134	8.3	601	6	CA198032
39	132	8.2	621	7	CV052755
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41	126	7.8	420	6	CF227009
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ALIGNMENTS

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LOCUS
DEFINITION
EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.
CN782289
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
Coles,N.D., Coleman,C.E., Christensen,S.A., Jellen,E.N.,
Stevens,M.R., Bonfante,A., Rojas-Beltran,J.A., Fairbanks,D.J. and
Maughan,P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WDR, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig_coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward

TITLE

JOURNAL
COMMENT


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Db 315 CCCCTGACACCGGTACACCGACCGGATCTCCACGATTCGTCTGTGATCTCAAAACA 374
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Db 375 ACCTGGAAAGACATCACTACACCTGCAATGACGTAACACGTCATGTGTGCGCTAC 434
Qy 101 SerapProPheanGlyAsnLysCySarTyRHisIlePheAsnApIleThSerThr 120
Db 435 CGCAGCAAGCTT---GGCGAAAGAACCGTCCAACTTCCTTAGAGATGCTCCACGCTC 491
Qy 121 GluArgThrapValGluAsnThleuCySerSerSerSerSerArgValAlaMeSer 140
Db 492 GCTGG-----AACACCTCTTCAAGGCGCGACGCTTCG-----AAC 530
Qy 141 IleAsnTyraSerleuTyProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
Db 531 ATTCCGTCGAGGAGATTACATACCTTAGAGAAAGCTGCAAG---CAAGGCCAAAT 587
Qy 161 GluValGluLeuGlyIleGlnIleLeuSerSerApIleGlyLysIleSerGlyValAsp 180
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Qy 181 SerPheProVallysrThrgLualaPhePheLeuValAlaIleGlnMetValSerGlu 200
Db 647 CCGATTATGGGCACTGTGAGGCCAAATCTTGCTGATTCATATACAGATGTTCTGAA 706
Qy 201 AlalaArgPheLysTrIleGluAsnGln---VallysrThraPheAsnArgAlaPhe 219
Db 707 GCGACAGCGTTAAGTATTAATTAAGTAAGTACCCAAAGTGGTATATGATGCTGTTCA 766
Qy 220 TyrProAspProLysValIleAsnLeuGluLysTrpGlyLysIleSer---GluAla 238
Db 767 AACCCGACCCGAAAGTCTGAGTTGGAGAAACAATTGGGAAAGATTCCCAAGAAATT 826
Qy 239 IleHisAsnAlaLysaAnglyAlaLeuProLys-----ProLeuGluLeuValAspAla 256
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RESULT 3
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LOCUS
DEFINITION
M002A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION
BE035039
VERSION
BE035039.1 GI:8330048
KEYWORDS
EST.
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alceaceae; Mesembryanthemum.
1 (bases 1 to 993)

REFERENCE
AUTHORS
Bohnert, H.U., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West Room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu

TITLE
JOURNAL
COMMENT
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers
1. 993
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/clone_id="MM"  
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:  
XhoI; Plants stressed 6 weeks in 500mM NaCl"
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ORIGIN

Alignment Scores:
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Score: 266.50 Matches: 67
Percent Similarity: 56.8% Conservative: 25
Best Local Similarity: 41.4% Mismatches: 56
Query Match: 16.5% Indels: 14
DB: 2 Gaps: 3

US-09-978-274a-2 (1-314) x BE035039 (1-993)

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Qy 126 GluAsnThreLeuCySerSerSerSerArg-ValAlaMeSerIleAsnTyraSse 145
Db 746 GAAACCTCTTTAAGGAGCGACCGTTCCAAACATTCATTGGTGTACTACATAC 687
Qy 145 rLeuTyProThrMetGluLysLysAlaGluValAsnSerArgAnGluValGlu 165
Db 686 TCTG-----GAGAAAGCTGCCCGTCAAGACGAAGAAACGATATTGAGTTGG 642
Qy 165 yIleGlnIleLeuSerSerApIleGlyLysIleSerGlyValAspSerPheProVally 185
Db 641 GCTTGCTAAACTAGAGTTGCCATCGATCGATTTATAGTAAAGAAACGATCGATGGAA 582
Qy 185 sThrgLualaPhePheLeuValAlaIleGlnMetValSerGluAlaIArgPheLy 205
Db 581 ACTGAGGCCAAATCTTACTGATTCGATTCGATTCGATTCGATTCGATTCGATTC 522
Qy 205 sTyrlIleGluAsnGlnVal---LysThraPheAsnArgAlaPheTyProAspProLy 224
Db 521 TTATATGAGACCTAAGGTGACCGAAAGTGGATCGATGTTCTTCAACCCGATCCGAA 462
Qy 224 sValIleAsnLeuGluLysTrpGlyLysIleSerGluAlaIleHisAsnAlaLys 244
Db 461 AGTATTAACCTGAGAAACAATGGGAAAGATTTCGATGATGATTAATGATGAT 402
Qy 244 nGlyAlaLeuPro-----LysProLeuGluLeuValAspAlaLy 257
Db 401 GTGGAACACACCTGCTAATTGTACGAACATTTCCCGCATTAATCAATGCTGCA 342
Qy 257 sGlyThrLysTrIleValLeuArgValAspGluIleAsnArgApValAlaLeu 277
Db 341 TGTACACATAGGAAGGTGATTAAGATTGCCACTATTAACCTGACTTGGGATATCA 282
Qy 277 gTyf 278
Db 281 GTTC 278
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RESULT 4
BE036541 1033 bp mRNA linear EST 07-JUN-2000
LOCUS
DEFINITION
M001B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION
BE036541
VERSION
BE036541.1 GI:8331550
KEYWORDS
EST.
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alceaceae; Mesembryanthemum.
1 (bases 1 to 1033)

REFERENCE
AUTHORS
Bohnert, H.U., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)

TITLE
JOURNAL
COMMENT
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Location/Qualifiers
1. 993
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/mol_type="mRNA"

COMMENT

Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu
An open reading frame exists.
location/Qualifiers

FEATURES

source

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 - /db_xref="taxon:3544"
 - /tissue_type="apical meristem and leaf primordia"
 - /dev_stage="6 weeks"
 - /clone_id="MP"
 - /note="3 d 500mm NaCl"

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Pred. No.:	2,58e-21	Length:	1033
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Percent Similarity:	54.1%	Conservative:	36
Best Local Similarity:	35.6%	Mismatches:	68
Query Match:	16.3%	Indels:	21
DG:	2	Gaps:	7

US-09-978-274A-2 (1-314) x BE036541 (1-1033)

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Db          47 AGCGTCATGTCTGTGGCCCTACCGGCACAAGCTT---GGCGAAAAGACCGGCCACTTC 103
Oy          114 PheaaNapllEthrSerThrGlubgThraPvalGluantHrLeuCysSerSer 133
Db          104 CTTAGCCAGTGCTCCACGCGTGCCTAG-----AACCACTCTTCAAGGCGCG 151
Oy          134 SerSerArgValAlMeSerIleantYzanserLeutyPrroThmeGlulylals 153
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Db          203 GCMAAG---CAAAGCCGAATGCATTAGAGTTGGGGTGAAATAACTGAGATTGCCATC 259
Oy          174 GlyLyrlSerGlyValalpserPerhevallyvrrhgualAPhepheleuleuVal 193
Db          260 GAGTCGTTTTTGTGTAAGAACCCCATVATAGGCGACGTTGAGGCCCAATTCTTGCTGATT 319
Oy          194 AlaIleGlmMetValSerGluAlaAlaArGPhelysTYrllegluAenglnVal---lys 212
Db          320 GCTATACACATGGTTCGTGAAGCACGACGAGTTTAATGTAAGAACTGAGTGACCNA 379
Oy          213 ThrAenPheaAnaArgAlaPheTyRProAppProLysValIleAenleugluluyerrp 232
Db          380 AGTGGGTACATGAGTCGTTCACTACCCGACCCGAAGTGCAGATTGGAAGAACATTGG 439
Oy          233 GlyLyrlSerGluAlaIleHisAnaAlaySAenglyAlaleuProlysePro----- 250
Db          440 GGGAAGATTTGCGAAGACATTCATATGACA-----GTTGGCGGCAAACTGCTTGT 490
Oy          251 -----LeugluleuVallepAlalyglYnTrlyerrpleValleu 264
Db          491 ACGAATATTTCACCGCGCATTAACGTTCAMAATGCTGATGTGTCATATGAAACGTGAT 550
Oy          265 ArgValAepGluIleAenArgApValAlaleuleuLytyr 278
Db          551 GATGTTGCCACTATTAACTGATTTGGGGGATATCAACTTC 592
  
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RESULT 5

BR035038 816 bp mRNA linear EST 07-JUN-2000

LOCUS BR035038/c

DEFINITION MM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to antiviral protein, mRNA sequence.

ACCESSION	BE035038
VERSION	BE035038.1 GI:8330047
KEYWORDS	EST.
SOURCE	Mesembryanthemum crystallinum (common iceplant)
ORGANISM	Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons Caryophyllales; Alzooceae; Mesembryanthemum. 1 (bases 1 to 816) Bohnert,H.U., Bohnert,C., Brazille,S., Brooks,J., Eaton,M., Pierres,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R. Functional Genomics of Plant Stress Tolerance Unpublished (2000) Contact: Michalowski,C.B. University of Arizona BIO Sciences West room 513, Tucson, AZ 85721, USA Tel.: 520-621-7982 Fax: 520-621-1697 Email: cbm@u.arizona.edu. Location/Qualifiers 1. 816 /organism="Mesembryanthemum crystallinum" /mol_type="rRNA" /db_xref="taxon:3544" /cell_type="epidermal bladder cells" /dev_stage="12 weeks old" /clone_lib="MM" /note="Vector: Bluescript SK+; Site 1: EcoRI; Site_2: XhoI; Plants stressed 6 weeks in 500mM NaCl"
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Pred. No.:	1,33e-20 Length: 816
Score:	256.50 Matches: 65
Percent Similarity:	54.4% Conservative: 28
Best Local Similarity:	38.0% Mismatch: 59
Query Match:	15.9% Indels: 19
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US-09-978-274A-2 (1-314) x BE035038 (1-816)	
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Dd	786 CAATAATTCCTTAAGCGATGCTTCAACGTGCATAGAAGAACCTTTAAAGGAGCG 727
OY	137 ---ValAlMeSerSerIleAsnTyRasMetSerLeuTyRProThrMetGluValAlaGlu 155
Dd	726 CCCGTTGCCAAAACATTCCCATTTGGTGGTGAATATCATAGTCTGGAGAAACTGCGGT 667
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Dd	666 ---CAAGCGAGAAACAAGTATTGACGTTGGCGCTTGCTAATAGAGCTTGCATGACATCA 610
OY	176 IlSeGlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIle 195
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OY	196 GlnMetValSerGluAlaAlaPhePheTyRTrIleGluWangInVal---LysThrAsn 214
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OY	215 PheAsnArgAlaPheTyRProAspProLysValIleAsnLeuGlnGluIleTyRTrpGlyLys 234
Dd	489 TCACATGTTTCGTTCAAACCAGATCCGAABATGATTAACTTGGAGAACCACTGGGGAAG 430
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Dd	429 ATTTCCGATGAGATTCATATGATCACTTACGTCGTAACCACTGCTAATTGACGACATT 370
OY	249 ---LysProLeuGlnLeuValAspAlaLysGlyThrTyRTrpIleValIleAsnArgValAsp 267
Dd	369 TCCCTTCGATTTACTTAATCATATCTGATGATCACAAATGAAGGTGATGAATGATGCC 310

OY	268	GluIleAsnArgSerValAlaLeuMetLeuTyr	278
Bd	309	ACTATAAACCTGAGCTTGCGGAGTACTCAAGTTC	277
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LOCUS	BE037217		
DEFINITION	MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to ribosome-inactivating protein/antiviral protein, mRNA sequence.		
ACCESSION	BE037217		
VERSION	BE037217.1		
KEYWORDS	GI:8332233		
SOURCE	EST.		
ORGANISM	Mesembryanthemum crystallinum (common iceplant)		
REFERENCE	Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alizaceae; Mesembryanthemum. 1 (bases 1 to 639) Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kamasaki,S., McColough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R. Functional Genomics of Plant Stress Tolerance Unpublished (2000) Contact: Michalowski,C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: chm@u.arizona.edu. Location/Qualifiers		
FEATURES	source		
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Best local Similarity:	36.8%	Mismatches:	71
Query Match:	15.6%	Indels:	22
DB:	2	Gaps:	7
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Db	29	ACGGAAACCTTCTGTGGTGGTGCCTCCAAICGAIGTAATGACGCAAAAACCATACATT	88
OY	89	MetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspPropheAsnGlyAsnLys	108
Db	89	ACTCTCAGAGAAATGCTTTATCTATCTATGATGCGTATATGTACAAGTAA---GATA	145
OY	109	CysArgTyrHisIlePheAsn-----AspIleThrSerThrGluArg	122
Db	146	TGTGGCTACCACTGAGGTTTAGAACCTAAAGATGTAAGCATCTGTGTGATGATGAATCA	205
OY	123	ThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsn	142
Db	206	GCGGACAAAGCTTAGGCTTTGGGAGAAGAAACGAAAGTGAAGAAAGAAATCCC	265
OY	143	TyrAsnSerLeuTyrProThrMetGlnIleValIleGluValAsnSerArgAsnGlnVal	162
Db	266	TACACGTTGCATTTGTGACACTTGAATAAAAAACCTGGCTTGAGCTTAAGGA-----	319
	163	GlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLys---IleSerGlyValAspSer	181
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DB	FEATURES	Source
Db	330 AGAAGAAGAGTCGAATTGATATTAGTAAGCTAATAATAGTTTCATATAAAAAACAGCATATA 379	
Qy	182 PheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 201	
Db	360 ATGAATGAAGAAGCATGAGGCTACATTTCTTCTTACGATTCGATTCAAAGGTTTGAGAGCT 439	
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DEFINITION	COI03587 GR_EB0032EB01.r GR_Eb Gossypium raimondii cDNA clone GR_EB0032EB01 3', mRNA sequence.	
ACCESSION	COI03587	
VERSION	COI03587.1 GI:48902273	
KEYWORDS	EST.	
SOURCE	Gossypium raimondii	
ORGANISM	Gossypium raimondii	
REFERENCE	Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosoids; euphorbia II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 903)	
AUTHORS	Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.	
TITLE	Global assembly of Cotton ESTs	
JOURNAL	Unpublished (2004)	
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: twing@genome.arizona.edu Plate: 0032 row: E column: 01. Location/Qualifiers	
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	/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2: EcoRV; library made by Invitrogen with RNA supplied by Wendle lab. Directional clones into NotI-EV. Clones plated/picked by AGI. More glycerol clones held in -80."	
ALIGNMENT SCORES:		
Score: 251.50	Length: 903	
Percent Similarity: 45.4%	Matches: 80	
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Query Match: 15.6%	Mismatches: 110	
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US-09-978-274A-2 (1-314) x COI03587 (1-903)		

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Qy      30 PheAspAlaGlyAsnAlaThrIleAsnLysThrIleThrPheMetGlySerAspArgAsn 49
Db      187 TTCACCACTGAAGACGACAGCAAGACTTATCTGATGTTATGAAAGATCTGTACAAAT 246
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Qy      126 GluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnThrAsnSer 145
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Qy      166 IleGlnIleLeuSerSerAspIleGlyLysIleSerGlyVal-----AspSer 181
Db      562 ATGATGATGATGACCAACATATTGATACCTGATTAATCAACCTTAATTAATCAAT 621
Qy      182 PheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 201
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Qy      202 AlaArgPheLysThrIleGluAsnGlnVal-----LysThrAsn 214
Db      673 GCCCGATGAGAAACATCCACAAATACTCTGAGTTCAGAGCTTCACGGCGATGA 732
Qy      215 PheAsnArgAlaLysThrProAspProLysValIleAsnLeuGlnGlyLys 234
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Qy      255 ---AspAlaLys 257
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RESULT 8
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DEFINITION NACL treatment Mesembryanthemum crystallinum cDNA clone L30-1401
5', mRNA sequence.
ACCESSION AM053634
VERSION AM053634.1 GI:5916827
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 837)

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AUTHORS Cushman, J. C.
TITLE An expressed sequence tag database for the common ice plant,
JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
Poly(A) tail, 10 nt: 838. .847
PCR PRIMERS
FORWARD: T7
BACKWARD: T3
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Plate: L30-15 row: A column: 5
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High quality sequence stop: 450.
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Alignment Scores:
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Score: 248.50 Matches: 76
Percent Similarity: 52.1% Conservative: 36
Best Local Similarity: 35.3% Mismatches: 84
Query Match: 15.4% Indels: 20
DB: 1 Gaps: 8
US-09-978-274A-2 (1-314) x AM053634 (1-837)
Qy      38 AsnLysThrValaThrPheMetGlySerLeuArgAsnAlaLysAspProLysLeuLys 57
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Qy      58 CysThrGlyIleProMetLeuProAspThrAsnSerThr-----ProLysThr 73
Db      62 TGT-----CAATCCCGCGGACACGGTCAACCGCAGATCTCAACGATTC 109
Qy      74 LeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeuMetLeuArgAsn 93
Db      110 GTCTCTGTGACCTCAAAACACCTCGCAAAAGACCATCACTCGCAATCGACGTGACA 169
Qy      94 AsnLeuThrValMetGlyThrSerAspProPheAsnGlyAsnLysCysArgThrHisIle 113
Db      170 AGCGTCTATGTGCTGCGCTACCGCGACAGCTT---GGCGAABAACCGTCCCACTTC 226
Qy      114 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 133
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Qy      134 SerSerArgValAlaMetSerIleAsnThrAsnSerLeuThrProThrMetGlyLys 153
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Db      326 GCAAAAC---CAAGCCGGAATGCAATAGAGCTTAGAGGCTGAATAACTTAGAGTTGGCATC 382
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Db 383 GAGTCGGTTTGGTAAGAACCCGATTAATGGCAGGTGAGCCAAATTCCTGCTANT 442

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Qy 213 ThrAsnAheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyr 232

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Qy 233 GilyValIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeu 247

Db 562 GGAAGATTCCAGAGATCATAGACAGTTCGGCGCAAAACCGGTG 606

RESULT 9
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LOCUS CA838757
DEFINITION MCT020B02_167445 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5, mRNA sequence.

ACCESSION CA838757 GI:26566522
VERSION CA838757.1 GI:26566522
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukayofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
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/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: SCORI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

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Alignment Scores:
Pred. No.: 2.53e-19 Length: 649
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 15.2% Indels: 14
DB: 6 Gaps: 4

US-09-978-274A-2 (1-314) x CA838757 (1-649)

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Db 25 GAGAAATCTTTTCAATGAGCAACGTTCCGAAACCTTGCTTCAAGGACTTACATCC 84

Qy 146 LeuTyrProThrMetGluLysValGluValAsnSerArgAsnGluValGlnLeuGly 165

Db 85 TTA-----GAGAAATCGCAACCAACGACGAGAGAGCATAGATTAGGG 129

Qy 166 IleGlnIleuSerSerArgIleGlyLysIleSerGlyValAspSerPheProValLys 185

Db 130 GTGATTAACCTAGAGTTTGGATCGAGTCCGTTTATGTGAACATCGAACAGCAGAGA 189

Qy 186 ThrGluAlaPhePheLeuValAlaIleGluMetValSerGluAlaAlaArgPheLys 205

Db 190 AATGAGGCCAAATTTCTTGATTTGCATTCACATACAGATGTTCTGAAGCAGCAAGTTCA 249

Qy 206 TyrIleGluAsnGluValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 223

Db 250 TATATTGAGAGTAAAGTGAAAGCAACAAAGTCGTTAGATTATGATCGTTCTTACCGACCG 309

Qy 224 LysValIleAsnLeuGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 243

Db 310 AAAATGCTGCTTTTGGAGACCAATGGGGAGATTTCGACGAGATTCATGAGAGTCT 369

Qy 244 AsnGlyValAlaLeuPro-----LysProLeuGluValAlaPheLys 257

Db 370 ---GGGGCAACCTGCTGTGTATGAATCTTCACTTCGATTCGTTAAAGAAACCAAT 426

Qy 258 GlyThrLysTyrPheLysValLeuArgValAspGluIleAsnArgAspValAlaLeuLys 277

Db 427 GTGATTCATGACGACGCGTGAATGTTGACACTTATGACTGAATGGGATATCTCAG 486

Qy 278 Tyr 278

Db 487 TTC 489

RESULT 10
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS CA839330
DEFINITION MCT026C11_171755 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5, mRNA sequence.

ACCESSION CA839330 GI:26567095
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukayofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers
1. 649
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Db 438 GGTATCCATGAGCGGTGATGATGACACTATAGACCTGAATGGGATACTCAAG 497
Qy 278 Tyr 278
Db 498 TTC 500

RESULT 15
COL21195
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

COL21195 841 bp mRNA linear EST 16-JUN-2004
GR_EB02E11.f GR_EB Gossypium raimondii cDNA clone GR_EB02E11 5',
mRNA sequence.
COL21195
COL21195.1 GI:48819882
EST.
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 841)
Kim.H., Yu.Y., Kudrna.D., Hatfield.J., Stum.D., Mueller.C.,
Udall.J.A., Rapp.R.A., Wendel.J.F., Rao.K., Soderlund.C. and
Wing.R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu
plate: 02 row: E column: 11.
Location/Qualifiers
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/db_xref="taxon:29730"
/clone="GR_EB02E11"
/issue_type="Floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_id="GR_EB"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; library made by invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Clones
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:
Pred. No.: 2,08e-18 Length: 841
Score: 239.00 Matches: 73
Percent Similarity: 47.0% Conservative: 44
Best Local Similarity: 29.3% Mismatches: 98
Query Match: 14.8% Indels: 34
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US-09-978-274A-2 (1-314) x COL21195 (1-841)

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Qy 45 GluSerLeuArganginalAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 64
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Qy 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100

Db 214 ---GGTTACCAAACTGACATTTAGCCTTGATGCTGAGTAATGNTATATCTTGCGTTAT 270
Qy 101 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
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Qy 141 ILeAsnTyrAsnSerLeuTyrProThrMetGluLysAlaGluValAsnSerArgAsn 160
Db 349 CTACCCCTTACAGGACATATGCGGCTTGAAGGGCTCGCGGAGATGACAGAAAG 408
Qy 161 GluValGluLeuGlyIleGlnIleLeuSerSerSerAspIleGlyLysIleSerGlyVal--- 179
Db 409 GAATATCCCTCTGGAAATGATGAACTACGCCCAATATGTATACCTGAATTCATCAAC 468
Qy 180 -----AspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGln 196
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Qy 197 MetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnVal----- 211
Db 520 ATGATTCCGAGCTGGCGAATGAGAAACATCCAGCAACAAATCTTGACATTGCAGAG 579
Qy 212 -----LysThrAsnPheAsnAlaGlyAlaPheTyrProAspProLysValIleAsnLeuGlu 229
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Qy 230 GluLysThrProGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLys 249
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Qy 250 ProLeuGluLeuVal---AspAlaLys 257
Db 700 GCAGTTGTTTATGATATATGATGCTCA 726

Search completed: April 9, 2006, 06:20:21
Job time: 5710.88 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 342.749 Seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 1617
Sequence: 1 MKWLVVVVTLIAWLIAPF.....VISTYNNYNSLGLDFEGF 314

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 segs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1235.5	76.4	1195	2	US-08-342-786B-1
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5	1235.5	76.4	1379	3	US-07-865-169-1
6	1235.5	76.4	1379	3	US-09-005-273-1
7	1235.5	76.4	1379	6	PCT-US96-11546-1
8	1235.5	76.2	1379	3	US-08-501-253A-1
9	1235.5	75.9	1379	3	US-07-865-169-2

10	1227.5	75.9	1379	3	US-09-005-273-3	Sequence 3, Appl1
11	1031	63.8	918	2	US-08-138-636-1	Sequence 1, Appl1
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15	361.5	22.4	804	3	US-08-718-904-23	Sequence 23, Appl1
16	361.5	22.4	804	6	PCT-US93-05702-7	Sequence 7, Appl1
17	361.5	22.4	804	6	PCT-US95-10973A-7	Sequence 7, Appl1
18	361.5	22.4	804	2	US-08-356-161-4	Sequence 4, Appl1
19	357.5	22.1	804	3	US-08-718-904-20	Sequence 20, Appl1
20	357.5	22.1	804	3	US-09-449-249-20	Sequence 20, Appl1
21	357.5	22.1	804	6	PCT-US93-05702-4	Sequence 4, Appl1
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24	356.5	22.0	804	3	US-08-718-904-22	Sequence 22, Appl1
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37	355.5	22.0	804	6	PCT-US95-10973A-7	Sequence 7, Appl1
38	355.5	22.0	804	6	PCT-US95-10973A-79	Sequence 79, Appl1
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42	347.5	21.5	1557	6	PCT-US95-10973A-78	Sequence 1, Appl1
43	345.5	21.4	879	2	US-08-182-114-1	Sequence 72, Appl1
44	339	21.0	1260	3	US-08-718-904-72	Sequence 72, Appl1
45	339	21.0	1260	3	US-09-449-249-72	Sequence 72, Appl1

ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5631155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoelactase
TITLE OF INVENTION: Antifungal Protein and Process for Preparing Transgenic
TITLE OF INVENTION: Plant Transformed Thereof.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

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Pred. No.:	2,596-139	Length:	1195
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Query Match:	76.4%	Indels:	3
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US-09-978-274a-2 (1-314) x US-08-373-858-1 (1-1195)

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DB 447 ATMAACTTTGATGATGATATCCAACTTGAATCAAAAGCGGAGATTAATMAAAGT 506
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 507 CAAGTCCACTGGGATTTCAAAATCTCGACAGTAATATTTGGAAGATTTCTGAGATGAG 566
QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB 567 TCATTCACCTGAGAAACCGAAGCCGAATCTTATGTGTAGCCATCAAAATGTATCAGAG 626
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DB 627 GCAGCAAGATTCAGATGACATAGAAATCAGGTGAAAACTAATTTTAACAGAGCATTCAC 686
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DB 687 CTTAATCCCAATGACTTAAATTTTGCAGAGACATGGGGTAAAGATTTTCAACAGCAATTCAT 746
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RESULT 2

US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Wan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for Phytolacca
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Phytolacca americana L.

IMMEDIATE SOURCE:

CLONE: PAP
US-08-342-786B-1

Alignment Scores:

Pred. No.:	2.59e-139	Length:	1195
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	2	Gaps:	2

US-09-978-274A-2 (1-314) x US-08-342-786B-1 (1-1195)

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Qy 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
Db 447 ATAACTTTGATGTGATATCCAAATGTGAATCAAAAGGGAGTAAATCAAGAGT 506
Qy 161 GluValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db 507 CAAGTCCAACTGGGAATTCAAATCTCAGACGTAAATTTGGAAGATTTCTGGAGTATG 566
Qy 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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Qy 221 ProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGluAlaIleHis 240
Db 687 CCAATATCCCAAGATCTTAATTTGCAAGACATGCGGTAAAGATTCAACGCAATTCAT 746
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Db 747 GATGCCAAGATGAGCTTTTACCCAAACCTCTCAGCTTAGTGAGTGCAGTGGGCCAG 806
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Db 807 TGGATAGTGTGAGAGTGAATACATCAAGCTGATAGCACTTAAACTAGCTTGTGT 866
Qy 281 GlyThrCysGlnThrThrTyr--GlnAsnAlaMetHesSerGlnValIleIleSerThr 299
Db 867 GGGAGCTGTCAAGCAACTATTAACCAAAATGCCATGTTTCTCAACTAATTAATGTACT 926

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Qy 300 TyrThrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
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RESULT 3
US-08-500-611-1
Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Turner, Nijgun B.
TITLE OF INVENTION: Pokedweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1

Alignment Scores:
Pred. No.: 3.25e-139 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 2 Gaps: 2

US-09-978-274A-2 (1-314) x US-08-500-611-1 (1-1379)

Qy 1 MetlyValMetleuValValValThreuleuLea1aTripleuLea1a1aProthr 20
Db 225 ATGAAGCGATGCTTGTGGTACATATCAATA-----TGGCTCATTTCTTGACCAACT 278
Qy 21 SerThrCysAlaIleuAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThr 40
Db 279 TCAACTTTGGGCTGTGAATACATCATCTACAAATGTTGGAAGTACCACTTACCAATAC 338

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QY 41 A|A|Thr|Phe|Met|Glu|Ser|Leu|Arg|Asn|Gln|Ala|Leu|Asp|Pro|Leu|Leu|Val|Met|Gly| 60
DB 339 GGCACCTTTCTGAATGATCTTGGTAAATGAGCGAAGATCCAGATTAAATCTAATGGA 398
QY 61 I|Le|Pro|Met|Leu|Pro|Asp|Thr|Asn|Ser|Thr|Pro|Leu|Gly|Leu|Val|Leu|Gln|Gly| 80
DB 399 ATAACCAATGCTGCCAATACCAATACCAATGCAAGATCGTTGGTGGTGGATCCCAAGGT 458
QY 81 A|A|Asn|Leu|Leu|Thr|Ile|Thr|Leu|Met|Leu|Arg|Asn|Asn|Leu|Tyr|Val|Met|Gly|Tyr| 100
DB 459 TCMAATTAATAAAACCATTCACACTAATGCTAGACGAAACCAATTTGATGTGATGGGTTAT 518
QY 101 Ser|Asp|Pro|Phe|Asn|Gln|Val|Asn|Val|Ser|Gly|Thr|Ile|Phe|Asn|Asp|Ile|Thr|Ser|Thr| 120
DB 519 TCTGATCCCTTTGAAACCAATTAATGCTGTACCATATCTTTAATGATATCTCAGGTAAT 578
QY 121 Glu|Arg|Thr|Asp|Val|Glu|Asn|Thr|Leu|Cys|Ser|Ser|Ser|Ser|Arg|Val|Ala|Met|Ser| 140
DB 579 GAAAGCCCAAGATGTAGAGACTCTCTTGGCCCAAAATGCCAAATTCGTGTAGTAAAAAC 638
QY 141 I|Le|Asn|Tyr|Asn|Ser|Leu|Tyr|Pro|Thr|Met|Glu|Leu|Val|Val|Glu|Val|Asn|Ser|Arg|Asn| 160
DB 639 ATTAATCTTGTATGTGATATTCGAACATTCGAAATCCAAACCGGAGTAATAATCAGAGAT 698
QY 161 Gln|Val|Gln|Leu|Gly|Ile|Gln|Ile|Leu|Ser|Ser|Asp|Ile|Gly|Val|Ile|Ser|Gly|Val|Asp| 180
DB 699 CAGGTCCAACTGGGAATTCMAATATCTCGACAGTAATATTCGAAAGATTTCTGAGAGTATG 758
QY 181 Ser|Phe|Pro|Val|Leu|Thr|Glu|Ala|Phe|Phe|Leu|Leu|Val|Ala|Ile|Gln|Met|Val|Ser|Glu| 200
DB 759 TCATTTACTGAGAAACCCGAAAGCCGAAATTCCTTATGTTGGTCCCAATACCAATAGGTATCAGAG 818
QY 201 A|A|A|Ala|Arg|Phe|Leu|Tyr|Ile|Glu|Asn|Gln|Val|Val|Thr|Asn|Phe|Asn|Arg|Ala|Phe|Tyr| 220
DB 819 GCGAGCAGATTCAGATGACATGATAGGATCAGGTGAAATCTAATTTTAAACAGACATTCAC 878
QY 221 Pro|Asp|Pro|Leu|Val|Ile|Asn|Leu|Gln|Glu|Val|Tyr|Gly|Val|Ile|Ser|Glu|Ala|Ile|Asn| 240
DB 879 CCTAATCCCAAGTACTTATATTTCGAAGAGACATGGGGTAAATTTCAACAGCAATTCAT 938
QY 241 Asn|Ala|Leu|Asn|Gly|Ala|Leu|Pro|Leu|Pro|Leu|Glu|Leu|Val|Asp|Ala|Val|Gly|Thr|Val| 260
DB 939 GATGCCAAGATGGAGTTTAACTCCAAACCTCTGAGCTGTGATGCCAGTGGTGGCCAG 998
QY 261 Trp|Ile|Val|Leu|Arg|Val|Asp|Glu|Ile|Asn|Arg|Asp|Val|Ala|Leu|Leu|Val|Tyr|Val|Asn| 280
DB 999 TGGATAGTGTGGAGTGGATGAAATTCAGCTGATGTACCTCTTAACTACGTTGGT 1058
QY 281 Gly|Thr|Cys|Gln|Thr|Thr|Tyr|---Gln|Asn|Ala|Met|Phe|Ser|Gln|Val|Ile|Ile|Ser|Thr| 299
DB 1059 GGGAGCGTCAAGCACTTAATACCAAAATGCGATGTTCTCTCACTTAATATGATCTACT 1118
QY 300 Tyr|Tyr|Asn|Tyr|Met|Ser|Asn|Leu|Gln|Val|Asp|Leu|Phe|Glu|Gly|Phe| 314
DB 1119 TATTAATTAATTAATGATGTTAATCTTGGTATCTTATTTGAAGATTC 1163

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RESULT 4

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US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,694
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REFERENCE/DOCKET NUMBER: OCTRS 3.0-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; TELEX: 139-125
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
;
; US-08-500-694-1
;
; Alignment Scores:
; Pred. No.: 3,25e-139 Length: 1379
; Score: 1235.50 Matches: 239
; Percent Similarity: 86.3% Conservative: 33
; Best Local Similarity: 75.9% Mismatches: 40
; Query Match: 76.4% Indels: 3
; DB: 2 Gaps: 2
;
; US-09-978-274A-2 (1-314) x US-08-500-694-1 (1-1379)
;
; QY 1 Met|Val|Met|Leu|Val|Val|Val|Thr|Leu|Ile|Ala|Trp|Leu|Ile|Ala|Ala|Pro|Thr| 20
; DB 225 ATGAAGTCGATGCTGTGGTGGTGAACAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
;
; QY 21 Ser|Thr|Cys|Ala|Ile|Asn|Thr|Ile|Thr|Phe|Asp|Ala|Gly|Asn|Ala|Thr|Ile|Asn|Val|Tyr| 40
; DB 279 TCAACTGGGCTGTGAAATCAATCAATCAATGTTGGAAGTACCAACCATTAAGCAATAC 338
;
; QY 41 A|A|Thr|Phe|Met|Glu|Ser|Leu|Arg|Asn|Gln|Ala|Leu|Asp|Pro|Leu|Leu|Val|Met|Gly| 60
; DB 339 GGCACCTTTCTGAATGATCTTGGTAAATGAGCGAAGATCCAGATTAAATCTAATGGA 398
;
; QY 61 I|Le|Pro|Met|Leu|Pro|Asp|Thr|Asn|Ser|Thr|Pro|Leu|Gly|Leu|Val|Leu|Gln|Gly| 80
; DB 399 ATAACCAATGCTGCCAATACCAATACCAATGCAAGATCGTTGGTGGTGGATCCCAAGGT 458
;
; QY 81 A|A|Asn|Leu|Leu|Thr|Ile|Thr|Leu|Met|Leu|Arg|Asn|Asn|Leu|Tyr|Val|Met|Gly|Tyr| 100
; DB 459 TCMAATTAATAAAACCATTCACACTAATGCTAGACGAAACCAATTTGATGTGATGGGTTAT 518
;
; QY 101 Ser|Asp|Pro|Phe|Asn|Gln|Val|Asn|Val|Ser|Gly|Thr|Ile|Phe|Asn|Asp|Ile|Thr|Ser|Thr| 120
; DB 519 TCTGATCCCTTTGAAACCAATTAATGCTGTACCATATCTTTAATGATATCTCAGGTAAT 578
;
; QY 121 Glu|Arg|Thr|Asp|Val|Glu|Asn|Thr|Leu|Cys|Ser|Ser|Ser|Ser|Arg|Val|Ala|Met|Ser| 140
; DB 579 GAAAGCCCAAGATGTAGAGACTCTTGGCCCAAAATGCCAAATTCGTGTAGTAAAAAC 638

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QY 141 ILeaenTYraenSerleuTYrProthrmecGluylsValaGluValaasnSerArgasn 160
D 639 ATAAACTTGTATGATCGATATCCAAATGGAATCAAAAGCGAGTAAATCAAGAGT 698
QY 161 GluValaGluLeuGlyIleGlnIleleuSerSerAspIleGlyIleSerGlyValaAsp 180
D 699 CAGGTCCAACTGGGAATTCAAATGACTCGACAGTAAATATTTGGAAGATTTCTGAGATG 758
QY 181 SerpheProValysThrGluAlaPhePheLeuLeuValaIleGlnMetValSerGlu 200
D 759 TCATTACTGAGAAAACGAAAGCCGAATTCCTATTGTAAGCCATCAATGATTCAGAG 818
QY 201 AlaAlaArgPheIleGlyIleGlnValaGlnValysThrAsnPheAsnArgAlaPheTYr 220
D 819 GCACAGCAATTCAGATCAATGAGATCAAGTCAAACTTAATTTTAAACAGCAATTCAC 878
QY 221 ProAspProIysValaIleAsnLeuGluGluIleTYrGlyIleSerGluAlaIleHis 240
D 879 CCTAATCCCAAGTAACTTAATTTGCAAGACATGGGGTAAAGATTTCAACAGCAATTCAT 938
QY 241 AsnAlaIysAsnGlyAlaLeuProIysProIleuGluLeuValaAspAlaIysGlyThrIys 260
D 939 GATGCCAAGATGAGATTTAACCCAACTCTCGAGTGAAGTGCAGTGGTGCAG 998
QY 261 TrpIleValleuArgValaAspGluIleAsnArgAspValaIleuLeuIleTYrValaAsn 280
D 999 TGGATGATGTTGAGAGTGAATGAAATCAAGCTGATGATGACCTTAACTTACAGTGGT 1058
QY 281 GlyThrCysGlnThrThrTYr---GlnAsnAlaMetPheSerGlnValaIleIleSerThr 299
D 1059 GGGAGCTGTCGAGCAACTTATACCAAAATGCAATGTTTCTCACTATATATGCTACT 1118
QY 300 TYrTYrAsnTYrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
D 1119 TATTATATTAATCATGTTAATCTTGATCTATTGGAAGATTC 1163

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RESULT 5
US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nijgun B.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELEPHONE: (314) 537-6039
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-865-169-1

Alignment Scores:
Pred. No.: 3,256-139 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 3 Gaps: 2

US-09-978-274a-2 (1-314) x US-07-865-169-1 (1-1379)
QY 1 MetIysValMetIleuValValaValThrIleuIleAlaTrpLeuIleAlaIleProThr 20
D 225 ATGAAGTCGATGCTTGTTGGTGAACAATATCAATA-----TGGCTATTCTTGACCAACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleTYr 40
D 279 TCAACTGGGCTGTGAATACATCATCTCAATGTTGGAAGTACACCATTAAGCAATAC 338
QY 41 AlaThrPheMetGluSerIleuArgAsnGlnAlaIysAspProIysLeuIysCysTYrGly 60
D 339 GCCACTTTCTGAAATGATCTTCTGTAAGAGCGAAAGATCCAACTTAAATGCTAATGA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProIysTYrLeuLeuValIysLeuGlnGly 80
D 399 ATACCAATGCTGCCCAATACAAATACAAATCCAAAGTACGTTGGTGAAGTCCAAAGT 458
QY 81 AlaAsnLeuIleThrIleThrMetLeuArgAsnAsnLeuTYrValMetGlyTYr 100
D 459 TCAATTAATAAAACCAATCACTAATGCTGAGCAAAACATTTGTATGATGGTAT 518
QY 101 SerAspProPheAsnGlyAsnIysCysArgTYrHisIlePheAsnAspIleThrSerThr 120
D 519 TCTGATCTCTTGAACCAATTAATGTCGTATACATATCTTAAATGATATCTCAGTACT 578
QY 121 GluArgThrAspValGluAsnThrIleuCysSerSerSerSerSerArgValAlaMetSer 140
D 579 GAAGCCCAAGATGAGAGTACTCTTGGCCAAATGCCAATCTCGTTAGTAAATAAC 638
QY 141 ILeaenTYraenSerleuTYrProthrmecGluylsValaGluValaasnSerArgasn 160
D 639 ATAAACTTGTATGATCGATATCCAAATGGAATCAAAAGCGAGTAAATCAAGAGT 698
QY 161 GluValaGluLeuGlyIleGlnIleleuSerSerAspIleGlyIleSerGlyValaAsp 180
D 699 CAGGTCCAACTGGGAATTCAAATGACTCGACAGTAAATATTTGGAAGATTTCTGAGATG 758
QY 181 SerpheProValysThrGluAlaPhePheLeuLeuValaIleGlnMetValSerGlu 200
D 759 TCATTACTGAGAAAACGAAAGCCGAATTCCTATTGTAAGCCATCAATGATTCAGAG 818
QY 201 AlaAlaArgPheIleGlyIleGlnValaGlnValysThrAsnPheAsnArgAlaPheTYr 220
D 819 GCACAGCAATTCAGATCAATGAGATCAAGTCAAACTTAATTTTAAACAGCAATTCAC 878
QY 221 ProAspProIysValaIleAsnLeuGluGluIleTYrGlyIleSerGluAlaIleHis 240
D 879 CCTAATCCCAAGTAACTTAATTTGCAAGACATGGGGTAAAGATTTCAACAGCAATTCAT 938
QY 241 AsnAlaIysAsnGlyAlaLeuProIysProIleuGluLeuValaAspAlaIysGlyThrIys 260
D 939 GATGCCAAGATGAGATTTAACCCAACTCTCGAGTGAAGTGCAGTGGTGCAG 998
QY 261 TrpIleValleuArgValaAspGluIleAsnArgAspValaIleuLeuIleTYrValaAsn 280
D 999 TGGATGATGTTGAGAGTGAATCAACCTGATGATGACCTTAACTATATGCTACT 1058
QY 281 GlyThrCysGlnThrThrTYr---GlnAsnAlaMetPheSerGlnValaIleIleSerThr 299

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Db 1059 GGAGGCTGACGACATTTATTAACCAAAATGCCATGTTCTCAACTATTAATGCTACT 1118
Qy 300 TTTTAAATTTATTAATGCTACTTTGATCTTAATTTGAAGATTC 1163
Db 1119 TATTATTAATTAATGCTACTTTGATCTTAATTTGAAGATTC 1163

RESULT 6
US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilsun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005, 273
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500, 611
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500, 694
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 225..290
; US-09-005-273-1

Alignment Scores:
Pred. No.: 3 25e-139
Score: 1235.50
Percent Similarity: 86.3%
Best Local Similarity: 75.9%
Query Match: 76.4%
DB: 3
US-09-978-274A-2 (1-314) x US-09-005-273-1 (1-1379)

Qy 1 MetIyValMetLeuValValValThrLeuIleAlaThrLeuIleAlaIleProThr 20
Db 225 ATGAATTCATGCTGTGTGGAGCAATATCAAT------TGGCTCATCTTCCAGCCACT 278
Qy 21 SerThrCysAlaIleAenThrIleThrPheAspAlaGlyAsnAlaThrIleAenLeuTy 40
Db 279 TCAACTTGGCTGTGAATCAATCATCTCAATGTTGAAGTACCACCATTTACCAATAC 338
Qy 41 AlaThrPheMetCysLeuArgAsnAlaIleAspProLeuLeuLeuLeuLeuLeuLeu 60
Db 339 GCCACTTCTGTAATGATCTTGTAAATGAAGCGAAAGATCCAGTTAAATGCTATGA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProLeuTyThrLeuValLeuLeuGlnGly 80
Db 399 ATACCAATGCTGCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 458
Qy 81 AlaAsnLeuTyThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
Db 459 TCAATATTAATAAACCATCACTAATGCTGAGACGAAACAAATTTGATGATGGGTAT 518
Qy 101 SerAspProPheAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 519 TGTGATCCCTTGAACCAATTAATGCTGTACATATCTTAATGATATCTCAGGCTACT 578
Qy 121 GluArgThrAspValGluAenThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATTTAGAGCTACTCTTCCCAAAAGCCCAATCTCGTTAGTAAAAAC 638
Qy 141 IleAenTyThrAsnSerLeuTyProThrMetGluValGlyAlaIleAsnSerArgAsn 160
Db 639 ATTAACCTTGATGTGATGATATCCAACTTGATGATCAAAACCGGAGTAAATCAAGAG 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyValIleSerGlyValAsp 180
Db 699 CAGGTCCAACTGGGAATTCATTAATCTCGACAGTAAATGTAAGAAATTTCTGAGTGATG 758
Qy 181 SerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACGTGAGAAACCGAAGCCGAATTCCTATTGGTGACCAATCAATGGATCAGAG 818
Qy 201 AlaAlaArgPheLeuTyThrIleGluAenGlnValIleThrAsnPheAsnArgAlaPheTy 220
Db 819 GCAGCAAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
Qy 221 ProAspProLeuValIleAsnLeuGlnGluTyIleGlyValIleSerGlnAlaIleHis 240
Db 879 CCTAATCCCAAGATCTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACAGCAATTCA 938
Qy 241 AsnAlaIleAsnGlyValaLeuProLeuProLeuGluLeuValaIleAspAlaIleTyThr 260
Db 939 GATGCCAAGATGAGATTTTACCCAAACCTCTGAGCTAGTGATGCCAGTGGTCCAGAG 998
Qy 261 TrpIleValLeuArgValaIlePgluIleAsnArgAspValAlaLeuLeuTyThrVala 280
Db 999 TGGATAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
Qy 281 GlyThrCysGlnThrThrTy---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGAGGCTGTCAGACATTAATCAACCAAAATGCAAGTTCCTCAACTTAATAATGCTACT 1118
Qy 300 TTTTAAATTTATTAATGCTACTTTGATCTTAATTTGAAGATTC 1163
Db 1119 TATTATTAATTAATGCTACTTTGATCTTAATTTGAAGATTC 1163

RESULT 7
PCT-US96-11546-1
; Sequence 1, Application PC/TUS9611546
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilsun E.
; TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein
; NUMBER OF SEQUENCES: 2

;;
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1
Alignment Scores:
Pred. No.: 3.25e-139 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: Gaps: 2
US-09-978-274A-2 (1-314) x PCT-US96-11546-1 (1-1379)
QY 1 MetLeuValMetLeuValValValThrlleuLeaLarThrlleuLeaLarProthr 20
DB 225 ATGAGCGCATGCTTGCGTGAACAATCAATA-----TGGCCATCTTGGACCACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyr 40
DB 279 TCAACTTGGGCTGGATACATCATCATCAATGTGGAGTCCACCATTAAGCATATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGly 60
DB 339 GCCACTTCTGATGATGATCTTCGTAATGAAGCGAAGATCCAGTTTAAATGCTATGA 398
QY 61 ILPEKMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCCCAATACAAATCAAAATCCAAAGTACGGTGGTGAAGCTCAAGGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnLeuTyrValMetGlyTyr 100

DB 459 TCMAATAAAAAACCATCACACTATCTGAGACGAACAATTGTATGTGATGGTTAT 518
QY 101 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTGGAAACCAATTAATGCTGTACCATATCTTATGATATCTCAGTACT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGAGAGACTACTCTTGGCCAAATCCAAATCTCGTGTAGTAAAAAC 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
DB 639 ATAACTTGTATGTGATATTCACACATTGGAAATCAAAACGGAGTAATATCAAGAGT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCCAACTGGGAATTCAAATATCTGCACAGTAATATTTGGAAGAATTTCTGGAGTATG 758
QY 181 SerPheProValLysThrGlnAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
DB 759 TCATTCACCTGAGAAACCGAAGCCGAATTCCTATGTGTACCCAAATGATATTCAGAG 818
QY 201 AlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyr 220
DB 819 GCAGCAAGATTCAGATGATCATAGAGAAATCAGGTGAAAATTAATTAACAGACATTCAC 878
QY 221 ProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAlaIleHis 240
DB 879 CCTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAGATTTCACACGCAATTCAT 938
QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLys 260
DB 939 GATGCCAAGATGAGATTTTACCAACCTCTGAGCTAGTGAATGCAAGTGGCCAG 998
QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn 280
DB 999 TGGATAGTGTGAGAGTGAATGAAATCAACCTGATGATGACATCTTAATCTAGTTGCT 1058
QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTGTGACCACTTATTAACAAAGCCATGTTCTCACTATTAATGATGACTACT 1118
QY 300 TyrTyrAsnTyrMetSerLeuLeuGlyAspLeuPheGluGlyPhe 314
DB 1119 TATTATATTAATCAATGTTAATCTTGGATCTATTTGAAGATTC 1163
RESULT 8
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Tumer, Fatih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Kelti Leberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Alignment Scores:

Pred. No.:	7,49e-139	Length:	1379
Score:	1232.50	Matches:	238
Percent Similarity:	86.3%	Conservative:	34
Best Local Similarity:	75.6%	Mismatches:	40
Query Match:	76.2%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-08-501-253A-1 (1-1379)

QY 1 MetLyValMetLeuValValValThrLeuLeuAlaTrpLeuLeuAlaAlaProThr 20
DB 225 ATGAAATCGATGGTGTGGTGAACAATACATA-----TGGCTCATCTTGGACCAACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
DB 279 TCACTTGGCTCTGATACATCATCATCTTGAAGTACCACTTACCAATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyGly 60
DB 339 GCCACTTTCTGTAATGATCTTCTGAATGAAGCAAGATCCAGTTTAAATGCTATGGA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCCAATACAAATACAAATCCAAAGTACGTTGGTGAAGTCCAAAGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
DB 459 TCBAATTAATAAAACCATCACTAATGCTGAGACGAACAATTGTATGTGATGGTTAT 518
QY 101 SerAspProPheAsnGlnLysAsnLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTGGAAACAATAATATGCTTACCATATCTTTAATGATATCTCAGGTACT 578
QY 121 GlnArgThrAspValGlnAsnThrLeuLysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAAGCCCAAGATCTAAGACTACTCTTGGCCAAAGCCCAATTCGCTGTATGATAAAGAAC 638
QY 141 IleAsnTyAsnSerLeuTyProThrMetGlnLysLeuAlaGlnValAsnSerArgAsn 160
DB 639 ATTAATCTTGATGTGATATTCACACTTGGAAATCGGAACGGGAATTAATAATCAAGAGT 698
QY 161 GlnValGlnLeuGlnLysIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCCAACTGGGAATTCAAATATCTGACAGTAATATGGAAGAATTCCTGGAGTGATG 758
QY 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGln 200
DB 759 TCATTCACGAGAAACCCAGCGCAATTCCTATGCTGAGCCCATACAAATGCTATCAGAG 818
QY 201 AlaAlaArgPheLeuTyTrpIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
DB 819 GCGAGCAAGATTCAGATACATAGAGATCAGGTGAAAACCTAATTTTAAACAGGATTCAC 878

QY 221 ProAspProLysValIleAsnLeuGlnGlyTyTrpGlyLysIleSerGlnAlaIleHis 240
DB 879 CTTAATCCCAAGACTACTTATTTGCAAGAGACATGGGGTAAAGTTTCAACAGCAATTCAT 938
QY 241 AsnAlaLysAsnGlnLysAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
DB 939 GATGCCAAGATGAGATTTTATCCCAAACTCTCGACTGATGATGCCAGTGGTGCAG 998
QY 261 TrpIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
DB 999 TGGATAGCTGTGAGATGATGATCAACCCGATGATGACCTTTAAACTACGTTGGT 1058
QY 281 GlyThrCysGlnThrThrTyTrpGlnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTGCAGCAACTTATACCAAAATGCACTGTTCTCACTTATATATGCTACT 1118
QY 300 TyrTrpAsnTyTrpMetSerAsnLeuGlnLysAspLeuPheGlnGlyPhe 314
DB 1119 TATTATATTAATCAATGGTTAATCTGGTATCTAATTTGAAGATTC 1163

RESULT 9

US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940

GENERAL INFORMATION:

APPLICANT: Turner, Nigun E.

APPLICANT: Lodge, Jennifer K.

APPLICANT: Kaniewski, Wojciech K.

TITLE OR INVENTION: Virus Resistant Potato Plants

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. B84F

ADDRESS: 700 Chesterfield Parkway No. 6015940ch

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/865.169

FILING DATE: 19920407

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Hoerner Jr., Dennis R.

REGISTRATION NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 38-21(10547)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)537-6099

TELEFAX: (314)537-6047

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-865-169-2

Alignment Scores:

Pred. No.:	3.01e-138	Length:	1379
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-07-865-169-2 (1-1379)

QY 1 MetLyValMetLeuValValValThrLeuLeuAlaTrpLeuLeuAlaAlaProThr 20

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Db 225 ATGAAGCAATGCTTGGTGTGACATATCAATA-----TGGCTCATTTCTTGACCAACT 278
Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThr 40
Db 279 TCAACTTGGGCTGGAAATACATCATCATCATGTTGGAAGTACCACTTAAAGCAAAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
Db 339 GCCACTTTTGGGAATGATCTTGGTAATGAACGAAAGATCCAACTTTAAATGCTATGCA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
Db 399 ATACCAATGCTGCCCAATACAAATCAAAATCCAAAGCAGGTGGTGGTGAAGCTCCAAGT 458
Qy 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuValMetGlyThr 100
Db 459 TCAATATTAATAAACAATCACTAATGCTGAGACGAAACAATTTGTATGATGGTAT 518
Qy 101 SerAspProPheAsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTGAAACCAATTAATGCTTACCATATCTTATGATATCTCAGTACT 578
Qy 121 GluArgThrAspValGluAsnThrLeuLysSerSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATGAGAGACTACTCTTGGCCCAATGCCAATCTCGGTGATGAAATAC 638
Qy 141 IleAsnThrAsnSerLeuValProThrMetGlnLysLysAlaGluValAsnSerArgAsn 160
Db 639 ATAACTTTTATGATCATATCAATCAATGGAATGGAACGGAAGGGAATCAAGAAAGT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db 699 CAGGTCCAATCGGAATTCAAATCTCAGACAGTAAATTTGGAAGATTTCTGAGTATG 758
Qy 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACGTAGAAAACCGAAGCCGAATTCCTATTGTTAGCAATACCAATGTATCAGAG 818
Qy 201 AlaAlaArgPheLysThrIleGluAsnGlnValLysThrAsnPheAsnAlaPheThr 220
Db 819 GCGACCAAGATTCAGATCATAGAGAAATCAGGTGAAATCTAATTTTAAACAGGCACTTCAAC 878
Qy 221 ProAspProLysValIleAsnLeuGlnGluLysThrGlyLysIleSerGluAlaIleHis 240
Db 879 CTTAATCCAAAGTACTTAATTTGCAAGACATGCGGTAAATTTCAACAGCAATTCAT 938
Qy 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
Db 939 GATGCCAAGATGAGATTTTAAACCAACTCTCGAGCTAGTGAATGCCAGTGGTGCACAG 998
Qy 261 TrpIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLysThrValAsn 280
Db 999 TGAATAGTGTGAGAGATGAGTAAATCAAGCTGATATCACTTAAACTAGTGTGT 1058
Qy 281 GlyThrCysGlnThrThrTrpLys---GlnAsnAlaMetPheSerGlnValIleSerThr 299
Db 1059 GGAAGCTGTACAGCACTTAATACCAAAATGCCAATGTTTCTCACTTAATATGCTACT 1118
Qy 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
Db 1119 TATTAATATTAACATGTTAATCTTGGTGAATCTAATTTGAAGATTC 1163

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RESULT 10

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US-09-005-273-3
; Sequence 3, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Tumor, Nilgun B.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,273
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,611
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,694
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 225..290
; US-09-005-273-3
; Alignment Scores:
; Pred. No.: 3,01e-138
; Score: 1227.50
; Percent Similarity: 86.0%
; Best Local Similarity: 75.6%
; Query Match: 75.9%
; Gaps: 2
; US-09-978-274a-2 (1-314) x US-09-005-273-3 (1-1379)
Qy 1 MetLysValMetLeuValValValValThrLeuIleAlaTrpLeuIleAlaAlaProThr 20
Db 225 ATGAAGCAATGCTTGGTGTGACATATCAATA-----TGGCTCATTTCTTGACCAACT 278
Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThr 40
Db 279 TCAACTTGGGCTGGAAATACATCATCATCATGTTGGAAGTACCACTTAAAGCAAAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
Db 339 GCCACTTTTGGGAATGATCTTGGTAATGAACGAAAGATCCAACTTTAAATGCTATGCA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
Db 399 ATACCAATGCTGCCCAATACAAATCAAAATCCAAAGCAGGTGGTGGTGAAGCTCCAAGT 458

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QY 81 A1aAenLeuYsThr11eThrLeuMeLeuAArgAaenLeuYrValMeG1Yr 100
: : : : :
Db 459 TCAATATAAAAAACCATCACTAATGCTGAGACGAACATTTGATGATGGGTAT 518
QY 101 SerAaPProPhaenGlyAenYsCyAArgYrH1e1ePhaenAaP1eThrSerThr 120
: : : : :
Db 519 TCTGATCCCTTTAAACCAATTAATGCTGTACCAATCTTTATATGATATCAAGTACT 578
QY 121 GluArgThrAaPValGluAenThrLeuCySerSerSerSerSerAArgValAlaMetSer 140
: : : : :
Db 579 GAACGCCAAGATTAAGACTACTCTTGGCCAAATGCCAATCTGCTGTAGTAAAAAC 638
QY 141 11eAenTYrAaenSerLeuTYrProThrMetGluYsValAgluValAaenSerAArgAa 160
: : : : :
Db 639 ATAACTTTGATGATGATGATCAATTCGAATCAAAAACGGGAGTAAATCAAGAGT 698
QY 161 GluValGluLeuGly11eGlu11eLeuSerSerAaP11eGlyYs11eSerGlyValAaP 180
: : : : :
Db 699 CAGGTCCAACTGGGAATTCAAATCACTGACAGATTAATGGAAGATTCTTGAGTGATG 758
QY 181 SerPhaProValYsThrGluAlaPhaPheLeuValAla11eGluMetValSerGlu 200
: : : : :
Db 759 TCATTCACTGAGAAAACCGAAGCCGAATCTCTATTGTTAGCCATCAAAATGATCAGAG 818
QY 201 A1aA1aArgPheLeuYsThr11eGluAaenGluValYsThrAaPheAaenAArgAlaPheTYr 220
: : : : :
Db 819 GCAGCAAGATTCAAGTACATAGAGATCAAGTCAAACTAATTTTAAACAGACATTCAC 878
QY 221 ProAaPProValYs11eAaenLeuGluGluYsThrGlyYs11eSerGluAla11eH1e 240
: : : : :
Db 879 CCTAATCCCAAACTACTTAATTTGCAAGACACATGGGATTAATTCACACGCAATTCAT 938
QY 241 AaenAlaYsAaenGlyAlaLeuProLYsProLeuGluLeuValAaPAlaYsG1YrThr 260
: : : : :
Db 939 GATGCCAAGATGAGATTATACCAAACTCTGAGCTAGTGCATGCCAGTGGTCCAG 998
QY 261 Trp11eValLeuAArgYsValAaP11eAaenAArgAaPValAlaLeuLeuYsTYrValAa 280
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Db 999 TGGATAGTGTGAGAGTGAATCAAGCCGATGTAGCACTTTAACTACGTTGGT 1058
QY 281 GlyThrCyAgluThrThrTYr---GluAaenAlaMetPheSerGluVal11e11eSerThr 299
: : : : :
Db 1059 GGAAGCTGTCAGCACTTAATTAACAAATGCGATGTTCTCACTTAATTAATGCTACT 1118
QY 300 TYrTYrAaenTYrMetSerAaenLeuGlyAaPLeuPheGluGlyPhe 314
: : : : :
Db 1119 TATTATTAATTAACATGCTTAATCTTGGTGAATCTATTGAGAGATTC 1163
RESULT 11
US-08-138-636-1
/ Sequence 1, Application US/08138636
/ Patent No. 534865
/ GENERAL INFORMATION:
/ APPLICANT: Moon, Young-Ho
/ APPLICANT: Jeon, Hong-Seon
/ APPLICANT: Choi, Kyu-Whan
/ APPLICANT: Lee, Kwan Ho
/ APPLICANT: Kim, Man Keun
/ TITLE OF INVENTION: No. 534865el Genome Coding PhytoIaccA Antiviral
/ TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DARBY & DARBY
/ STREET: 805 THIRD AVE.
/ CITY: NEW YORK
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/138,636
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ludwig, S. Peter
/ REGISTRATION NUMBER: 25,351
/ REFERENCE/DOCKET NUMBER: 0136/08818
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 527-7700
/ TELEFAX: (212) 753-6237
/ TELEX: 236687
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 918 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: PhytoIaccA insularis
/ IMMEDIATE SOURCE:
/ CLONE: antiviral protein (PIP)
US-08-138-636-1
Alignment Scores:
Pred. No.: 9,1e-115 length: 918
Score: 1031.00 Matches: 210
Percent Similarity: 80.3% Conservative: 39
Best Local Similarity: 67.7% Mismatches: 56
Query Match: 63.8% Indels: 7
DB: 2 Gaps: 4
US-09-978-274a-2 (1-314) x US-08-138-636-1 (1-918)
QY 1 MeLySValMeLeuValVal1ThrLeu1eAlaTrpLeu11eAlaAProThr 20
: : : : :
Db 1 ATGAAGTATGCTT-----GTGGGACAAATATCACTATGCTCTTTCGACCAACA 54
QY 21 SerThrCyAAla11eAenThr11eThrPheAaPAlaGlyAaenAlaThr11eAenYsTYr 40
: : : : :
Db 55 TCTACTTGGCCGCGTGAATCCATCATCTACATGTTGGAAGTACCACTTGAACCTAT 114
QY 41 AlaThrPheMeGluSerLeuAArgAaenGluAlaYsAaPProLYsLeuYsTYrGly 60
: : : : :
Db 115 GCAACTTTTG---ATACTTGTCTGACGAAGCGAAGATCCA--GTATGTGCTATGGA 168
QY 61 11eProMeLeuProAaPThrAaenSerThrProLYsTYrLeuLeuValYsLeuGluGly 80
: : : : :
Db 169 ATACCAATCTGCTCCCAATATTTGATCAAAATCCAAATATCATTTGTTAGCTCCAAAGT 228
QY 81 A1aAenLeuYsThr11eThrLeuMeLeuAArgAaenLeuTYrValMeG1Yr 100
: : : : :
Db 229 TCAAAATGAAGAGGCGCTCACTAATGTCAAGACGAACAAATTTATATGTGATGCTAT 288
QY 101 SerAaPProPhaenGlyAaenYsCyAArgYrH1e1ePhaenAaP11eThrSerThr 120
: : : : :
Db 289 TCTGATCCCTTACAC---AATAGGTGCTGTTTCACTCTTTAAGGCTATCTCAGGTA 345
QY 121 GluArgThrAaPValGluAenThrLeuCySerSerSerSerAArgValAlaMetSer 140
: : : : :
Db 346 GAACGCCAAGATTAAGACTACTCTTGGCCAAATGCCAATCTGCTGTAGTAAAAAC 405
QY 141 11eAenTYrAaenSerLeuTYrProThrMetGluYsValAgluValAaenSerAArgAa 160
: : : : :
Db 406 ATAACTTAATGATGATGATCAATTCGAATCAAAAACGGGAGTAAATCAAGAGT 465
QY 161 GluValGluLeuGly11eGlu11eLeuSerSerAaP11eGlyYs11eSerGlyValAaP 180
: : : : :
Db 466 CAGGTCCAACTGGGAATTCGAATCACTGACAGTGGCATTTGGAAGATTCTGAGTGAGC 525

QY 181 SerPheProValIystrHguAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
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Db 526 TCATTCTAGAGAACCGAAGTGAATTCCTACTGGTAGCCATACCAATGATTCAGAG 585
QY 201 AlAlaIarGPhelysTyrIleGluAengInValIystrAenPheAenAglAlaPheTyr 220
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Db 586 GCAGCAAGATTCAAGTACATAGAGATCAAGTCAAACTAATTTTAAACAGCCATTCAC 645
QY 221 ProAspProIyValIleAenLeuGluGluIystrGlyIystrIleSerGluAlaIleHis 240
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|||
Db 646 CCAATCCCAAGACTTATATTCAGAGACATGGGGTGAATTTCTTCAGCAATTCAT 705
QY 241 AsnAlaIySaengIyAlaLeuProIySProLeuGluLeuValAlaAspAlaIySglYthrIlys 260
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Db 706 GGTCCAGAGATGAGTTTATCCCAATCCTCTACAGCTAGTGCATGGCAATGGTCAAT 765
QY 261 TTPlleValIeuaIyValaAspGluIleAenAryaValAlaLeuLeuIystrValaAsn 280
|||
|||
Db 766 TGGATGATGTTGAGAGAGATGAATCAAGCTGATGTGCACTTAACTACGTATT 825
QY 281 GlyThrCysGlnThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
|||
|||
Db 826 GGAAGCTCCAGAGAACTTATACCAAAATGCCATGTTTCTCACTTAATATGTCTACT 885
QY 300 TyrTyrAsnTyrMetSerAenLeuGlyAsp 309
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Db 886 TATTATATTAATCAATGGCTAATCTTGGTGAT 915

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A

Patent No. 5656466
GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,622A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/0A445

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7700

TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: Leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Alignment Scores:

Pred. No.:	9.1e-115	Length:	918
Score:	1031.00	Matches:	210
Percent Similarity:	80.3%	Conservative:	39
Best Local Similarity:	67.7%	Mismatches:	56
Query Match:	63.8%	Indels:	7
DB:	2	Gaps:	4

US-09-978-274A-2 (1-314) x US-08-319-622A-1 (1-918)

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Db 55 TCTACTTGGCGCGGTGAATACCATCATCTACATGTTGAAGTACCACTTAGAACTAT 114
QY 41 AlaThrPheMetGluSerLeuArgAengIAlaIyAspProIySLeuIySgYthrGly 60
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Db 115 GCAACTTTTGG---ATACTCTGACTGAAGGCGAAGATCCA--GTTATGTCTATGA 168
QY 61 IleProMetLeuProAspThrAenSerThrProIySLeuValIySLeuGlnIy 80
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Db 169 ATACCAATGCTGCCAATATGATGATCAATCCAAATACATTTGTTGATGCTCAAGT 228
QY 81 AlaAenLeuIystrIleThrLeuMetLeuArgAenAenLeuTyrValMetGlyTyr 100
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QY 121 GluArgThrAspValIleAenThrLeuCysSerSerSerSerArgValAlaMetSer 140
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Db 346 GAACGCAAGATGATGAGACTACTCTTGGCCAAATGCCATTTCTGTTGGTAAAC 405
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Db 406 ATAACTATGATGATGATGATTCACATTCGAATCAAAAGCAGAGTAAATTCAGAGAT 465
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Db 586 GCAGCAAGATTCAAGTACATAGAGATCAAGTCAAACTAATTTTAAACAGACATTCAC 645
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QY 261 TTPlleValIeuaIyValaAspGluIleAenAryaValAlaLeuLeuIystrValaAsn 280
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Db 766 TGGATGATGTTGAGAGTGAATCAAGCTGATGTGCACTTAACTACGTATT 825

APPLICANT: Lappi, Douglas A.
APPLICANT: Barthelemy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: SAPORIN-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,161
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,161
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5916772tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.404US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-69 in Example 1.B.2."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-356-161-7
Alignment Scores:
Pred. No.: 6,51e-34 Length: 804
Score: 361.50 Matches: 100
Percent Similarity: 56.1% Conservative: 56
Best Local Similarity: 36.0% Mismatches: 97
Query Match: 22.4% Indels: 25
DB: 2 Gaps: 11
US-09-978-274a-2 (1-314) x US-08-356-161-7 (1-804)
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DB 1 GCATGATCCTGCTTCATTTTCAGTCGACAACTGATGCGGCATCATCATCACA 60
QY 30 PheAspAlaGlyAsnAlaThrIleAsnLysThrAlaThrPheMetGluSerLeuArgAsn 49
DB 61 TTAGATTAAGTAAATCCGACCGCGGTCATATCACTCTTTTGGATTAATCCGAAC 120
QY 50 GlnAlaLysAspProLysLeuLysCysGlyGlyIlePheMet--LeuProAspThrAsn 68

DB 121 AACGTAAAGATCCAAACCTGAAATACCGGTGATACCGACATAGCCGATAGGCCCACT 180
QY 69 SerThrProLysThrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeu 88
DB 181 TCTTAAGAAAAATTCCTTAGAATTAATTTCCAAAGTCCCGA---GGAAAGGTCTCACTT 237
QY 89 MetLeuArgArgAsnLeuLysThrValMetGlyThr-----SerAspProPheAsnGly 106
DB 238 GGCCTAAACGCAATTAATCTGTATGTGTCGCTGATCTTGCAATGATTAACAGCAATGTT 297
QY 107 AsnLysCysArgThrIlePheAsnAspIleThrSerThrGlnArgThrAspValGlu 126
DB 298 AATCGGCA---TATTACTTCAGATCAGAAATTACTTCCCGCAGTTAAC----- 345
QY 127 AsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnThrAsnSerLeu 146
DB 346 ---GCCCTTTTCCAGAGCCACAACTGCAATCAGAAACCTTAGAATACACAGAAAT 402
QY 147 TyrProThrMetGluLysValAlaGluVal-----AsnSerArgAsnGlnVal 162
DB 403 TATCAGTCGATTAAGAAATGCGCAGATTAACACAGAGATCAAGTAAAGTAAAGAACTC 462
QY 163 GlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
DB 463 GGGTTGGGAGTATGACTTACTTCAAGTCATGGAAGCAATGAAC---AAGAAGCAAGT 519
QY 183 ProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 202
DB 520 GTGGTTTAAACAGCAAGCTAATTCCTTATGCTATTCAGATGACGGCTGAGGACGG 579
QY 203 ArgPheLysThrIleGlnGlnGlnValLysThrAsnPheAsnArgAlaPheThrProAsp 222
DB 580 CGATTAGGTACATCAAACTGTTATCATCAAGAACTTCCCAACAGTTCAACTCGGAA 639
QY 223 ProLysValIleAsnLeuGlnGluLysThrGlyLysIleSerGluAlaIleHis---Asn 241
DB 640 AACAAAGTATTCAGTTGAGTTAGCTTAAGTAAAGAAATTTCTACGGCAATATACGGGAT 699
QY 242 AlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysThr 261
DB 700 GCCAAAAACGGCGTGTATTAATAAGATTAGATTTCGCGTTTGAAAA----- 747
QY 262 IleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysThrVal 279
DB 748 ---GTAGGCAAGGTGAAGACTTG-----CAATGGGACTCTTATGATTTTG 792
RESULT 15
US-08-718-904-23
Sequence 23, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424

GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: April 9, 2006, 00:06:24 ; Search time 4658.27 Seconds
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Title: US-09-978-274A-3

Perfect score: 792
Sequence: 1 atgataataacagatcacctc.....gaacctgtcagacaacttaa 792

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_in:*
3: gb_env:*
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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	786.4	99.3	945	6	AX427702 Sequence
3	783.2	98.9	1249	15	PAPAPSRIP
4	768.4	97.0	786	15	AB071855
5	766	96.7	1092	6	AX427720 Sequence
6	582.8	73.6	783	15	AB071854
7	539	68.1	1114	15	AF533515
8	535	67.6	882	6	A67183
9	534.2	67.4	942	15	AY572976
10	534.2	67.4	1164	15	AY049785
11	534.2	67.4	1164	15	PAPAP
12	534.2	67.4	1195	6	A42103
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14	534.2	67.4	1195	6	I55866
15	532.6	67.2	942	15	AY547315
16	532.6	67.2	1379	6	AR009535
17	532.6	67.2	1379	6	AR136704
18	532.6	67.2	1379	6	AX427731

19	531	67.0	1195	6	A36639	A36639 Sequence 1
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21	530.2	66.9	2472	6	E05033	E05033 DNA encodin
22	530.2	66.9	2472	15	PTCAPAP	D106500 P. american
23	529.4	66.8	1378	6	AX427732	AX427732 Sequence
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25	527.8	66.6	939	15	AY327475	AY327475
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27	493	62.2	951	6	A67185	A67185 Sequence 3
28	493	62.2	2369	15	AF141331	AF141331
29	487.6	61.6	714	15	AY603354	AY603354
30	477.4	60.3	714	15	AY603353	AY603353
31	476.4	60.2	714	15	AF338910	AF338910
32	476.4	60.2	714	15	AY603352	AY603352
33	462	58.2	465	6	AX427706	AX427706
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36	460.6	58.2	918	6	A48150	A48150
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ALIGNMENTS

RESULT 1
AX427704
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITL
JOURNAL
FEATURES
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/organism="Phytolacca americana"
/mol_type="unassigned DNA"
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463. .492
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612
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681. .686
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complement(765. .792)
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790. .792
/note="Stop codon added via PCR primer"

Query Match 100.0%; Score 792; DB 6; Length 792;

Best Local Similarity 100.0%; Pred. No. 4,5e-177; Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTAATACGATCACTTTGATGCTGGAAATGCCACCTTAACAATATGACCTTT 60
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Db 1 ATGATTAATACGATCACTTTGATGCTGGAAATGCCACCTTT 60

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QY 361 AATAGCTATATCCGACCATGAGAAAGAAAGAGAGTAATCAAGAAATCAAGTCAA 420
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481 GTAAAAACCTGAGGCTTTTCTTCTACGTGAGCCATCAAAATGTTTCAAGGAGGCA 540
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QY 541 TTCAAGTATATGAGAAACCAAGTCAAGATTAATTTAATAGACATTCCTGATCC 600
541 TTCAAGTATATGAGAAACCAAGTCAAGATTAATTTAATAGACATTCCTGATCC 600
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QY 781 CAGACAACTTAA 792
781 CAGACAACTTAA 792
Db 781 CAGACAACTTAA 792

RESULT 2
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS AX427702
DEFINITION Sequence 1 from Patent WO023107.
ACCESSION AX427702
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
1

AUTHORS Neelam A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 023107-A 1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source Location/Qualifiers
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misc_feature /note="Binding site for primer PPS1BF"
complement(735..776)
/note="Binding site for primer PSXDR"
736..777
misc_feature /note="Binding site for primer PSXDF"
750..759
variation /note="Sequence replacing removed XbaI site"
complement(922..945)
misc_feature /note="Binding site for primer PPS2SR"

ORIGIN
Query Match 99.3%; Score 786.4; DB 6; Length 945;
Best Local Similarity 99.9%; Pred. No. 9,2e-176;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATAAATACGATCACTTTGATGCTGAAATGACACCATTAACAATATGCACTTTATG 63
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133 GAATCTCTTGTATCAAGGAAATCCAAAATAAATGCTATGAGCAATGCTTA 192
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253 ACCATTAACCTAATGCTGAGCAAAATTAATTAAGTATGAGGCTATTCGATCC 312
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QY 244 AATGGCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAAT 303
313 AATGGCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAAT 372
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373 GTGGAATTAATCTTTGCTCAAGTCTAGTCTGCTGTTGCAATGCTAATACAT 432
Db 373 GTGGAATTAATCTTTGCTCAAGTCTAGTCTGCTGTTGCAATGCTAATACAT 432

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433 AGCTATATCCGACCATGAGAAAGAAAGAGAGTAATCAAGAAATCAAGTCAA 492
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493 GGAATTAATTAATCTCAAGGATCAATTTGAAATATCTGAGATTGATTCCTGTA 552
Db 493 GGAATTAATTAATCTCAAGGATCAATTTGAAATATCTGAGATTGATTCCTGTA 552

QY 484 AAAAAGGCTTTTCTTCTAATGAGGATCAAAATGTTTCAAGGAGGAGGCAATC 543
553 AAAAAGGCTTTTCTTCTAATGAGGATCAAAATGTTTCAAGGAGGAGGCAATC 612
Db 553 AAAAAGGCTTTTCTTCTAATGAGGATCAAAATGTTTCAAGGAGGAGGCAATC 612

QY 544 AAGTACATGAGAAACCAAGTCAAGATTAATTTAATAGACATTCCTGATCCAAA 603
613 AAGTACATGAGAAACCAAGTCAAGATTAATTTAATAGACATTCCTGATCCAAA 672
Db 613 AAGTACATGAGAAACCAAGTCAAGATTAATTTAATAGACATTCCTGATCCAAA 672

QY 604 GTAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCA 663
673 GTAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCA 732
Db 673 GTAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCA 732

QY 664 GGGGCTTATCCAAACCTGAGTATGAGTCAAGGCAAGGTATGAGTATGATTTCT 723
733 GGGGCTTATCCAAACCTGAGTATGAGTCAAGGCAAGGTATGAGTATGATTTCT 792
Db 733 GGGGCTTATCCAAACCTGAGTATGAGTCAAGGCAAGGTATGAGTATGATTTCT 792

Qy	724	AGAGGAGTAAATCAATACGAGATGTGACATCTTAACTAGTACCTTAATGAACCTGTCAG	783
Db	793	AGAGTGATGAATCAATACGATGTGACATCTTAACTAGTACCTTAATGAACCTGTCAG	852
Qy	784	ACAACTTA	791
Db	853	ACAACTTA	860
RESULT 3			
PAPASRIP		1249 bp	linear
LOCUS			PLAN 18-APR-2005
DEFINITION	P. americana mRNA for pokeweed antiviral protein.		
ACCESSION	X98079		
VERSION	X98079.1		
KEYWORDS	GI:1707648		
SOURCE	PAP-S gene; pokeweed antiviral protein (PAP) ; ribosome-inactivating protein.		
ORGANISM	Phytolacca americana (American pokeweed)		
	Phytolacca americana		
	Bakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.		
REFERENCE	1		
AUTHORS	Poyet, J.L. and Hoeveler, A.		
TITLE	cDNA cloning and expression of pokeweed antiviral protein from seeds in Escherichia coli and its inhibition of protein synthesis in vitro		
JOURNAL	FEBS Lett. 406 (1-2), 97-100 (1997)		
PUBMED	9109394		
REFERENCE	2 (bases 1 to 1249)		
AUTHORS	Poyet, J.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Moleculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE		
REMARK	Revised by author 20-SRP-1996		
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	106..1050		
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	/db_xref="GOA:P93444"		
	/db_xref="InterPro:IPR001574"		
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	1212..1217		
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ORIGIN			
Query Match	98.9%	Score 783.2; DB 15; Length 1249;	
Best Local Similarity	99.6%	Pred. No. 5e-175;	

Matches	785;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0
QY	4	ATAAATACGATCACCTTGGATGCTGGAAATGCCACATTAACAATATGCCACTTTATG	63						
Db	178	ATAAATACGATCACCTTGGATGCTGGAAATGCCACATTAACAATATGCCACTTTATG	237						
QY	64	GAATCTCTTGCTAATCAGCGGAAAGATCCAAATCTAATATGCTATGCAATGCTA	123						
Db	238	GAATCTCTTGCTAATCAGCGGAAAGATCCAAATCTAATATGCTATGCAATGCTA	297						
QY	124	CTGTATCTAATTTGACACCCCTTAAGTACTTATTTGGTATAGCTCAAGGCGCAACCTTAAA	183						
Db	298	CTGTATCTAATTTGACACCCCTTAAGTACTTATTTGGTATAGCTCAAGGCGCAACCTTAAA	357						
QY	184	ACCATTAACATAATGCTGAGACGAAATTAATTAACGATAGGGCTATCTGATCCCTTC	243						
Db	358	ACCATTAACATAATGCTGAGACGAAATTAATTAACGATAGGGCTATCTGATCCCTTC	417						
QY	244	AATGGCAATTAAGTGTCTGTTACCATATATTTATATGATATTAACAAGACCGAAAGCACTGAT	303						
Db	418	AATGGCAATTAAGTGTCTGTTACCATATATTTATATGATATTAACAAGACCGAAAGCACTGAT	477						
QY	304	GTGGAGAAATACCTTTTGCTCAAGTTCTAAGTCTGTGTGTGAAGATGCCATTAACTACAAT	363						
Db	478	GTGGAGAAATACCTTTTGCTCAAGTTCTAAGTCTGTGTGTGAAGATGCCATTAACTACAAT	537						
QY	364	AGCTTATATCCGACCATGGAAGAAAGAAAGACAGAGTAAACTCAAGAAATCAAGTCCCAATG	423						
Db	538	AGCTTATATCCGACCATGGAAGAAAGAAAGACAGAGTAAACTCAAGAAATCAAGTCCCAATG	597						
QY	424	GGAATTCAAATATCTCAGCAGTGAATGGAAGAAATCTCTGAGATTGATTCATTCCTGTGA	483						
Db	598	GGAATTCAAATATCTCAGCAGTGAATGGAAGAAATCTCTGAGATTGATTCATTCCTGTGA	657						
QY	484	AAAATGAGGCTTTTTTTCTAATCTGTAGCCATCCAAATGTTTGTAGAGCGAGCCGCGATTC	543						
Db	658	AAAATGAGGCTTTTTTTCTAATCTGTAGCCATCCAAATGTTTGTAGAGCGAGCCGCGATTC	717						
QY	544	AAGTACATATAGGAACCAAGTCMAAGACTAATTTTATATAGACATCTACCTCGATCCCAA	603						
Db	718	AAGTACATATAGGAACCAAGTCMAAGACTAATTTTATATAGACATCTACCTCGATCCCAA	777						
QY	604	GTAATTAATCTTGAAGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCAAATGCCAAGAT	663						
Db	778	GTAATTAATCTTGAAGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCAAATGCCAAGAT	837						
QY	664	GGGGCTTATCCCAACCAACCTTGAGCTATGCTATGTCGCAAGGTACCAAGTGGATGTTCTT	723						
Db	838	GGGGCTTATCCCAACCAACCTTGAGCTATGCTATGTCGCAAGGTACCAAGTGGATGTTCTT	897						
QY	724	AGAGTGAATGAATCAATCGTATGTATGGCACTCTTAAGTACGTTAATGGAACCGTGAG	783						
Db	898	AGAGTGAATGAATCAATCGTATGTATGGCACTCTTAAGTACGTTAATGGAACCGTGAG	957						
QY	784	ACAACCTTA 791							
Db	958	ACAACCTTA 965							

RESULT 4

AB071855

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1

Honjo,B. and Watanabe,K.

786 bp DNA linear

Pln 19-MAR-2002

Phytolacca americana paps2 gene for PAP-S2, partial cds.

GI:19570839

Phytolacca americana (American pokeweed)

Phytolacca americana

Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 786)

AUTHORS Watanabe,K. and Honjo,E.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail:watakei@saga-u.ac.jp, Tel:01-952-28-8774, Fax:01-952-28-8774)

FEATURES

source location/Qualifiers

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/organism="Phytolacca americana"

/mol_type="genomic DNA"

/db_xref="taxon:3527"

1..786

/gene="pap82"

<1..>786

/gene="pap82"

/note="mature pokeweed antiviral protein-S2"

/codon_start=1

/product="PAP-S2"

/protein_id="BAB86350.1"

/db_xref="GI:19570840"

/translation="INTFTFDAGNSTINKYATFMESLRNQADPKLKYGIENLPDPTN STPKYLIVKIQGANLKITITLMRRNMLYVGYDPRGNCRVHIFNDITSTRTVE NTLSSSSSVAMNSINYSPLTEKKAEVNSRQVLOGIQLISDGIQVDSDFV KTEAPFLVAVIOMVSEAPRKYEINQKTNPNAPFDPPIVNLSEKMGKISAHINA KNGALPKPLEIVAKGKTWIVLAVDEINRVALTKYNGCQAT"

ORIGIN

Query Match 97.0%; Score 768.4; DB 15; Length 786;

Best Local Similarity 98.6%; Pred. No.1.8e-171;

Matches 775; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 ATATAATACATCCCTTTGCTGCGAATGCCACCTTAACAATATGCCACCTTATG 63

1 ATCAATACTTCACTTTGATGCTGGAATTCACCACTTAACAATATGCCACCTTATG 60

64 GAATCTCTTGATCAAGGAAAGATCCAAATCTAATAATGCTATGACATACCAATGCTA 123

61 GAATCTCTTGATCAAGGAAAGATCCAAATCTAATAATGCTATGACATACCAATGCTA 120

124 CCGATATCAATTCGACCCCTTAAGTACTTATGCTTCCAGAGTGCAACCTTAAA 183

121 CCGATATCAATTCGACCCCTTAAGTACTTATGCTTCCAGAGTGCAACCTTAAA 180

184 ACCATTACACTATGCTGAGACGAATTAATTAAGTATGCTTCCAGAGTGCAACCTT 243

181 ACCATTACACTATGCTGAGACGAATTAATTAAGTATGCTTCCAGAGTGCAACCTT 240

244 AATGCAATAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTA 303

241 AATGCAATAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTA 300

304 GTGAGAAATACCTTTGCTCAAGTCTAAGTCTCGTGTGCAATGTCATTAACTAAT 363

301 GTGAGAAATACCTTTGCTCAAGTCTAAGTCTCGTGTGCAATGTCATTAACTAAT 360

364 AGCTTATATCCGCAATGAGAAAGCAAGAACTCAAGAAATCAAGTCAATG 423

361 AGCTTATATCCGCAATGAGAAAGCAAGAACTCAAGAAATCAAGTCAATG 420

424 GGAATTCATAATACGAGTACATTTGAAATATCTGAGAGTGAATCATTCCTGTA 483

421 GGAATTCATAATACGAGTACATTTGAAATATCTGAGAGTGAATCATTCCTGTA 480

484 AAAAAGAGGCTTTTCTTACTGTAGCCATCAATGCTTCAAGGCGAGCGATTC 543

481 AAAAAGAGGCTTTTCTTACTGTAGCCATCAATGCTTCAAGGCGAGCGATTC 540

544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGACATTTTACCTGATCCCAA 603

Db 541 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGACATTTTACCTGATCCCAA 600

Qy 604 GTAATTAATCTTGAGAGAAAGTGGGCAAAATCTCGAGCAATTCACATGCGCAAT 663

Db 601 GTAATTAATCTTGAGAGAAAGTGGGCAAAATCTCGAGCAATTCACATGCGCAAT 660

Qy 664 GGGGCTTATCCCAACCACTTGAGTATGATGCCAAGAGTACCAAGTGAATGTTCTT 723

Db 661 GGGGCTTATCCCAACCACTTGAGTATGATGCCAAGAGTACCAAGTGAATGTTCTT 720

Qy 724 AGAGTGATGAATCAATGCTGATGTGGCACTCTTAAGTACCTTAATGGAACCTGTG 783

Db 721 AGAGTGATGAATCAATGCTGATGTGGCACTCTTAAGTACCTTAATGGAACCTGTG 780

Qy 784 ACAACT 789

Db 781 GCCACT 786

RESULT 5

AX427720 1092 bp DNA linear PAT 20-JUN-2002

LOCUS AX427720

DEFINITION Sequence 19 from Patent WO0233107.

ACCESSION AX427720

VERSION AX427720.1 GI:21537829

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Neelam,A.; Atkinson,H.J.; Mcpherson,M.J. and Thomas,C.J.R.

TITLE Plant cell death system

JOURNAL Patent: WO 0233107-A 19 25-APR-2002;

CAMBRIDGE ADVANCED TECH (GB)

FEATURES

source location/Qualifiers

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="PAP-8/Cystatin fusion"

1..29

/note="Binding site for primer PS1BP"

681..686

/note="Modified XbaI site"

/note="complement(742..786)"

/note="Binding site for primer PCS-PAPSR"

766..806

/note="Binding site for primer PCS-Delta86F"

766..786

/note="REV NIA protease cleavage site"

complement(1066..1092)

/note="Binding site for primer SYNPODelta86SR"

ORIGIN

Query Match 96.7%; Score 766; DB 6; Length 1092;

Best Local Similarity 100.0%; Pred. No.6.1e-171;

Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGATTAATACGATCACCTTTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60

1 ATGATTAATACGATCACCTTTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60

61 ATGGAATCTCTTGATATCAAGGAAAGATCCAAATCTAATAATGCTATGCAATCAAG 120

61 ATGGAATCTCTTGATATCAAGGAAAGATCCAAATCTAATAATGCTATGCAATCAAG 120

121 CTACCTGATATCAATTCGACCCCTTAAGTACTTATGCTTCAAGGCGAGCGATTC 180

121 CTACCTGATATCAATTCGACCCCTTAAGTACTTATGCTTCAAGGCGAGCGATTC 180

181 AAAACATTAACATTAATGCTGAGACGAATTAATTAATGATGAGGCTATTTGATCCC 240

Db 181 AAAACATTACCTAATGCTGAGCAAGAAATACTTATGATGAGGCTATTCTGATCC 240
Qy 241 TTCAATGSCAATTAAGTGTGTTACCATTAATTATTAATTAACAGCAACGAGCACT 300
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Qy 361 AATAGCTTATATCCAGCAATGAGAAAGAGCAAGTAATCTCAAGAAATCAAGTCCA 420
Db 361 AATAGCTTATATCCAGCAATGAGAAAGAGCAAGTAATCTCAAGAAATCAAGTCCA 420
Qy 421 TTGGGAATTCAAATCTAGCAGAGTGAATGGAATAATCTGAGAGTGAATTCATTCCT 480
Db 421 TTGGGAATTCAAATCTAGCAGAGTGAATGGAATAATCTGAGAGTGAATTCATTCCT 480
Qy 481 GTAAAACTGAGGCTTTTCTTCTAGTGGTACCATCAATGTTTCAAGGCAAGCGCA 540
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Qy 601 AATGTAATTAATCTGAGAGAGAGTGGGCAAAATCTGAGGCAATTCAGAAAGCCAG 660
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Qy 661 AATGGGCTTTTACCCAAACCACTTGAAGTGAATGCAAGTCAAGTGAATGTT 720
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Qy 721 CTTAGAGTGAATGAATCAATGCTGATGTCGATCTCTTAAGTACG 766
Db 721 CTTAGAGTGAATGAATCAATGCTGATGTCGATCTCTTAAGTACG 766

RESULT 6
LOCUS AB071854 783 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paps1 gene for PAP-S1, partial cds.
ACCESSION AB071854
VERSION AB071854.1 GI:19570837
KEYWORDS
SOURCE phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
1 Unpublished
2 (bases 1 to 783)
JOURNAL Watanabe, K. and Honjo, E.
AUTHORS Direct Submission
TITLE Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
JOURNAL Department of Applied Biological Sciences; Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watakei@saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)

FEATURES
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Query Match 73.6%; Score 582.8; DB 15; Length 783;
Best Local Similarity 84.7%; Pred. No. 1.7e-127;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

Qy 4 ATAAATAGATACCTTTGATGCTGGAATGCAACATTAACAATATGCACTTTATG 63
Db 1 ATCAATAGATAGTTCGACGTGAAATGCAACATTAACAATATGCTTATG 60
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Db 61 GAATCTCTGCTATCAAGCAAGATCCAAACTTAATATCTATGCTATACCAATGCTA 120
Qy 124 CCTGATCTAATTCGACCCCTTATGCTATGTTAAGTCAAGGTCACCACTTAA 183
Db 121 CCTGATCTAATTCGACCATTAATGCTATGTTAAGTCAAGGTCACCACTTAA 180
Qy 184 ACCATTAACATATGCTGAGACGAATTAATCTTATAGCTATGAGGCTATTCCTCTTC 243
Db 181 ACCATTAACATATGCTGAGACGAATTAATCTTATAGCTATGAGGCTATTCCTCTTC 238
Qy 244 AATGCAATAGTGTGCTTACCATTAATTTATATATTTACAGACCGAAGCACTGAT 303
Db 239 -ACGACATATAGTGTGCTTACCATTAATTTATATATTTAAGGCACTGATATAGTAT 297
Qy 304 GTGAGAAATCTCTTGTCTCAAGTTCGATTCGTGTCGATGCAATGTCATTAATCAAT 363
Db 298 GTGAGAAATCTCTTGTCTCAAGTTCGATTCGTGTCGATGCAATGTCATTAATCAAT 357
Qy 364 AGCTTATATCCAGCATGAGAAAGAGCAAGTAACTCAAGAAATCAAGTCCAAATG 423
Db 358 GGCTTATATCCAGCATGAGAAAGAGCAAGTAACTCAAGAAATCAAGTCCAAATG 417
Qy 424 GAATTTCAATATCTCAGCAGTGAATGGAATAATCTCTGAGTGTATTCATTCCTCTGA 483
Db 418 GAATTTCAATATCTCAGCAGTGAATGGAATAATCTCTGAGTGTATTCATTCCTCTGA 477
Qy 484 AATAGTGAAGCTTTTCTTCTAGTGGTACCATCAATGTTTCAAGGCAAGCGCATTC 543
Db 478 AATAGTGAAGCTTTTCTTCTAGTGGTACCATCAATGTTTCAAGGCAAGCGCATTC 537
Qy 544 AATGATATAGAGAACCAAGTCAAGATTAATTTATAGACATTCACCTGATCCCAA 603
Db 538 AATGATATAGAGAACCAAGTCAAGATTAATTTATAGACATTCACCTGATCCCAA 597
Qy 604 GTATTTAATCTTGAAGGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 663
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Qy 664 GGGGCTTTACCAACCACTGAGCTGATGAGCCAAAGTTCACAGTGAATGATGTTCTT 723
Db 658 GGGGCTTTACCAACCACTGAGCTGATGAGCCAAAGTTCACAGTGAATGATGTTCTT 717
Qy 724 AGAGTGAATGAATCAATGCTGATGTCGACCTCTTAAGTACGTTAATGAGACCTGTACAG 783
Db 718 AGAGTGAATGAATCAATGCTGATGTCGACCTCTTAAGTACGTTAATGAGACCTGTACAG 777
Qy 784 ACAACT 789
Db 778 GCCACT 783

RESULT 7
AF533515 1114 bp mRNA linear PLN 01-AUG-2005
LOCUS Phytolacca octandra anti-viral protein (pap) mRNA, partial cds.
DEFINITION AF533515
ACCESSION AF533515
VERSION AF533515.1 GI:33329822
KEYWORDS
SOURCE Phytolacca octandra
ORGANISM Phytolacca octandra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Lin, J.S. and McNally, K.P.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Reproductive Technologies, AgResearch
Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand
FEATURES
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ORIGIN
Query Match 68.1%; Score 539; DB 15; Length 1114;
Best Local Similarity 80.3%; Pred. No. 3,9e-117;
Matches 63; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 5 TAAATACGATCACCTTGATGCTGGAATGCCACCATTAACAATATGCCACTTTATG 64
DB 46 TGAATACATCATCTCAATAGTGGAGTACCAACATTAACAATATGCCACTTTATG 105
QY 65 AATCTCTGCTATCAAGCGAAGATCCAAATGCTATGCTATGCCATGCTTAC 124
DB 106 ATGATCTTCGTAAATGAGCGAAGATCAAAATTAATGCTATGGAATCAATGCTGC 165
QY 125 CTGATTAATAATGACCCCTAAGTACTTATGTTAGTCCAAAGTGAACCTTAAAA 184
DB 166 CCAATCAATCCAGATCCAAAGTACGTGTGTTAGCTCCAAAGTCCAAATAAAAA 225
QY 185 CCAATCACTAATGCTGAGCGAATTAATTAATGATGAGTGGCTATTCCTCTCA 244
DB 226 CCAATCACTAATGCTGAGCGAATTAATTAATGATGAGTGGCTATTCCTCTTG 285
QY 245 ATGGCAATAGTGCCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 286 ATACCAATAGTGCCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 345
QY 305 TGGAGATACTCTTGTCAAGTTCATGTTCTCGTGTGCAATGTCATTAACATTA 364
DB 346 TAGAGACTACTTGTGCCAAATCCCAATTCGTGTATTAATAAATTAATTAATTA 405
QY 365 GCTTAATCCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 424
DB 406 GTGATATCCCAATGAGATCAAAAGCGGAGTAATCAAGAGTCAAGTCAACTGG 465
QY 425 GAATTAATAATCAGAGTGAATGAGAAATCTGTGAGTTGATTCCTCTTAA 484

Db 466 GAATTCAAATACCTTGACAGTGAATTCGAGAGTGAATTCGAGAGTGAATTCGAGAG 525
QY 485 AATCGAGCTTTTCTTCTAGTGTGATCCATCCAAATGTTTGAAGGACGAGGATTTCA 544
Db 526 AATCCGAGGCGAATTCCTTCTAGTGTGATCCATCCAAATGTTTGAAGGACGAGGATTTCA 585
QY 545 AGTACATGAGAAACCAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 604
Db 586 AATACATGAGAAATCAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 645
QY 605 TAATTAATCTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGATG 664
Db 646 TACTTAATTTTGAGAGAGACATGGGGTAAAGATTTCTACAGCAATTCATGATGCCAAGATG 705
QY 665 GGGCTTTACCCCAACCACTGAGCTAGTGAATGCCAAGTGAATTCAGTGAATGTTCTTA 724
Db 706 GAGTTTACCCCAACCACTGAGCTAGTGAATGCCAAGTGAATTCAGTGAATGTTCTTA 765
QY 725 GAGTGAATGAATCAATCGTGAATGAGCACTCTCTTAAGTAACTGAACCTGTCAGA 784
Db 766 GAGTGAATGAATCAATCGTGAATGAGCACTCTCTTAAGTAACTGAACCTGTCAGA 825
QY 785 CAACCTTA 791
Db 826 CAACCTTA 832
RESULT 8
A67183 882 bp DNA linear PAT 05-MAY-1999
LOCUS A67183
DEFINITION Sequence 1 from Patent EP0808902.
ACCESSION A67183
VERSION A67183.1 GI:4756167
KEYWORDS
SOURCE .
ORGANISM Phytolacca insularis
Phytolacca insularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Moon, Y., Choi, J., Yun, Y., Jin, J., Hong, E., Lee, J., Choi, K., Lee, J.,
Song, S., Choi, Y., Kim, C. and Kim, W.
TITLE Novel genes encoding antiviral proteins of Phytolacca insularis
COMMENT Nakai and recombinant microorganisms expressing the same proteins
JOURNAL Patent: EP 0808902-A 1 26-NOV-1997;
JINRO LTD (KR)
Other publication JP 9308489 19971202
Other publication CA 2186303 19971123
Other publication AU 6570696 19971127.
Other publication
FEATURES
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/clone_lib="GENOMIC LIBRARY FROM PHYTOLOACCA"
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Query Match 67.6%; Score 535; DB 6; Length 882;
Best Local Similarity 79.8%; Pred. No. 3.6e-116;
Matches 63; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 1 ATGATTAATACGATCACTTGTAGTGTGGAATGCGACATTAACAATATGCGACCTTT 60
Db 1 ATGATTAATACGATCACTTGTAGTGTGGAATGCGACATTAACAATATGCGACCTTT 60
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Db 121 TTGCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 180

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 AY572976 942 bp mRNA linear PLN 05-APR-2004
 LOCUS Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
 DEFINITION AY572976
 ACCESSION AY572976
 VERSION AY572976.1 GI:45826466
 KEYWORDS
 SOURCE
 ORGANISM
 Phytolacca americana (American pokeweed)
 Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.
 1 (bases 1 to 942)
 Xtao,Z.A. and Jiang,Y.
 A gene encoding the pokeweed antiviral protein in the leaf of
 Phytolacca americana
 Unpublished
 2 (bases 1 to 942)
 Xtao,Z.A.
 Direct Submission
 Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
 University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
 100875, China
 location/Qualifiers
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Query Match 67.4%; Score 534.2; DB 15; Length 942;
 Best Local Similarity 79.9%; Pred. No. 5.5e-116;
 Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 5 TAATACGATCACCCTTGATGCTGGAATGCCCAATTAACAATATGCACTTTATGG 64
 Db 68 TGAATACAAATCATCTCAATGTTGGAAGTACCAATAGCAATATAGCCACTTTCTGA 127
 QY 65 AATCTCTGTAATCAAGCAAGATCCAAATCTAATGCTATGCAATCAATGCTAC 124
 Db 128 ATGATCTTGTAATGAAAGCAAGATCCAAATGCTAATGCAATGCAATGCTGC 187
 QY 125 CTGATACTAATTCGACCCCTAAGTACTTATGTTAAGTCCAAAGTGCACCACTTAAAA 184
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 QY 545 AGTACATAGAGAAAGCAAGTCAAGATTAATTTAATAGACATTTCTACCTGATCCCAAG 604
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 QY 605 TAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCATTAATGCAATGCAAGAT 664
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 Db 728 GAGTTTACCCAAACCTCTCGAGCTAGTGAATGCAAGATTCATTAATGCAAGATGCTTA 787
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 Db 788 GAGTGAATGAATCAAGCTGATGATGAGCACTCTTAATAGATTAATGCAAGATGCTTA 847
 QY 785 CAACCTTA 791

DB	848 CACTTA 854	
RESULT 10		
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LOCUS		PLN 23-OCT-2001
DEFINITION	Phyolacca actinosa anti-viral protein PAP (PAP)	mRNA, complete cds.
ACCESSION	AY049785	
VERSION	AY049785.1 GI:16356654	
KEYWORDS		
SOURCE		
ORGANISM	Phyolacca actinosa (food pokeweed)	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;	
	Caryophyllales; Phyloclaccaceae; Phyolacca.	
	1 (bases 1 to 1164)	
	Peng,X., Yuan,J. and Qiang,B.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (27-JUL-2001) Department of Biochemistry, Institute of	
TITLE	Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong	
JOURNAL	Dan San Tiao, Beijing 100005, P.R. China	
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ORIGIN		
Query Match	67.4%; Score 534.2; DB 15; Length 1164;	
Best Local Similarity	79.9%; Pred. No. 5.2e-116;	
Matches	629; Conservative 0; Mismatches 159; Indels 0; Gaps 0;	
OY	5 TAAATAGCATCACTTGATGTGGAAATGCACCATTAAACAATATGCGACCTTTATGG	64
DB	69 TGAATACATCATCTTCAATGTTGGAAATCACCATTAAGCAATAATCCCACTTTTCGG	128
OY	65 AATCTTTCGTATCAAGCAGAATGCCAAACTAAAATGCTATGCGATACCAATGCTAC	124
DB	129 ATAACTCTCGTATGAGCGAAATGCAAGTTCAGATTAAATGCTATGGAATACCAATGTTGC	188
OY	125 CTGATACCTAATTCGACCCCCTTAAGTACTTATTTGGTTAAGCTCGAAGGTGCAACTAAAAA	184
DB	189 CCAATACAAATCCAATCAATCAAAGTAGCGTTGGTTGAGCTCCAAAGGTTCAATTAATAAAA	248
OY	185 CCATTACACTATGCTGAGACGAATAACTATACGTATGGGCTATTCGATCCCTTCA	244
DB	249 CCAATGACCTATGCTGAGACGAACAAATTTGATGATGATGGGCTATTCGATCCCTTGG	308
OY	245 ATGGCAATAGTGTGCTTACCAATATATTAAATGATATTACAAGACCGAACGCACTGATG	304
DB	309 ATACCAATAGATGTGCTTACCAATATCTTTAAGTATCTCAGGTATCTGAACGCAAGATG	368
OY	305 TGGAATATACCTTTGCTCAAGTCTAGTCTCGTGGTGAATGTCATTCATTAATCAATATA	364
DB	369 TAGAGACTACTCTTGGCCCAATCCCAATTCCTCGGTATGATTAATAACATTAATGATTA	428
OY	365 GCTTATATCCAGCATGGAAGAAAGCAAGTAGTAATCTCAAGAAATCCAAATGCAATTTGG	424

Db		429	GTCGATATCCAAACATTGGAAATCAAAAAGCGGAGTMAAATCAAAGAATCAGTTCAACTGG	488
Oy		425	GAATTCGAAATCTCAGCAGTGACATGTGGAAAAATCTCTGGAGTTGATTCAATTCCTGTAA	484
Db		489	GAATTCAAATTA CTGCACAGTAATATGTGAAAGATTTCTGGAGTGACGTCATTCACTGAGA	548
Oy		485	AAACTGAGGCTTTTTTCTACTGTTACCATCCAAATGCTTTCAGAGGACGCCGATTTCA	544
Db		549	AAACCGAAGCGAAATTCCTACTGTGTAGCCATAAATGTATTCAGAGGCAGCAAGATTCA	608
Oy		545	AGTACATAGAGAACCAAGTCACAAGCTAATTTAATAGACATTCCTACCTGATCCCAAG	604
Db		609	AGTCAATRGGGAATCAGGTGAAACTAATTTTACAGAGCATTTAACTCTAATCCCAAG	668
Oy		605	TAAATTAAC TTGGAGAGAAAGTGGGCGAAATCTCTGAGGCCAATTCACAAATCCCAAGATG	664
Db		669	TACTTAATTTTGGAGAAGACATGGGGGTAAAGATTTCTACAGCAATTCATGATGCCAAGATG	728
Oy		665	GGGCTTAAACCCAACCACTTGAGCTAGTATGATGCGAAAGTACCAAGTGATTAATTCTTA	724
Db		729	GAGTTTAAACCAAACTCTCGAGCTAATGTGATGCCAATGTGGCCAAATGTGATTAATGTGTA	788
Oy		725	GAGTGAGTGAATCAATCGTAGATGTGGCACTCCTTAAGTACGTAAATGGAACCTGTGAGA	784
Db		789	GAGTGAGTGAATTCAGACCTGATATGACATCTTAACTACGTTGTGGAGCTGCCAA	848
Oy		785	CAACTTA 791	
Db		849	CACCTTA 855	
RESULT	11			
PAPAP				
LOCUS			1164 bp mRNA linear	PLN 18-NOV-1991
DEFINITION			P.americana PAP gene for anti-viral protein.	
ACCESSION			X55383	
VERSION			X55383.1 GI:20421	
KEYWORDS			antiviral protein; cell wall protein; PAP gene; ribosome inactivating protein. Phytolacca americana (American pokeweed)	
SOURCE			Phytolacca americana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.	
REFERENCE			1 (bases 1 to 1164) Lan, Q., Chen, Z.C., Antoniw, J.F. and White, R.P.	
AUTHORS			anti-viral protein from Phytolacca americana	
TITLE			Plant Mol. Biol. 17 (4), 609-614 (1991)	
JOURNAL			1912488	
PubMed			2 (bases 1 to 1164)	
REFERENCE			Antoniw, J.F.	
TITLE			Direct Submission	
AUTHORS			Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops	
JOURNAL			Research, Dept. of Plant Pathology, Rothamsted Experimental	
			Station, Harpenden, Hert, AL5 2UQ, UK	
FEATURES			location/Qualifiers	
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CDS				

ORIGIN

Query Match	67.4%	Score 534.2	DB 15	length 1164
Best Local Similarity	79.9%	Pred. No. 5.2e-116		
Matches 629; Conservative	0	Mismatches 158;	Indels 0	Gaps 0

	QY	5	TAAATACGATCACTTGGATCTGGAAATGCACACTTAACAATAATGCACCTTTATGG	64
Db	69	TGAATPACAAATCATCTACAAATTGTGGAAATACCACTTAGAGAAATAGCCACTTTTCGA	128	
QY	65	AATCTCTTGTAATCAGCGAAGAATCCAAACTAANAATGCTATGGCATCOAATGTAC	124	
Db	129	ATGATCTTCGTAAAGAACGAAAGATCCAACTTTAAATGCTAATGAATPACCAATGTGC	188	
QY	125	CTGATATCTAATTCGACCCCTAAGTACTAATGTGGTTAAAGCTCCAAAGTGCAAACCTAATAA	184	
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QY	185	CCATTACACTATGCTGAGACGAAATAACTTAATACGTATAGGGCTATCTGATCCCTTCA	244	
Db	249	CCATCACACTATGCTGAGACGAAACAAATTTGTATGTATAGGTTATTTCTATCCCTTTG	308	
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Db	309	AAACCAATPAATATGCTGTACCATATCTTAATGATATCTCAGGTATGAAAGCCAAAGATG	368	
QY	305	TGGAGATATCTTTGCTCAAGTTCTAAGTTCTCGTGTGCAATGTCCTTAACCTAATA	364	
Db	369	TAGAGACTATCTTTGCCCAATGECATATCTCGGTATGTAATAACATAAATCTTGATTA	428	
QY	365	GCTTATATCCGACATGGAAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCCAAATGG	424	
Db	429	GTCAATATCCAACTTGGATTCAAAGCCGAGATBAATCAAGAAATCAAGTCCAACTGG	488	
QY	425	GAATTCAAATATCTCAGCAGTACATTTGAAAAATCTCTGAGTTGATTCATTCCTGTAA	484	
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QY	485	AAACTGAGGCTTTTTTTCTACTGTGAGCCATCCAAATGTTTCAAGSGACGCGATTC	544	
Db	549	AAACCGAAGCCGAATCTTATTTGGTAGCATRACAAATGTAATCAGAGGCACAAAGATTC	608	
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QY	605	TAAATTAATCTTGAGAGAGATGGGGCAAAATCTCTGAGGCAATTCACATGSCAAGATG	664	
Db	669	TACTTAATTTTGCAGAGACATGGGGTAAATTTCAACAGCAATTCATGATGCCAAGATG	728	
QY	665	GGGCTTTTACCCAACCACTTGAAGCTAGTGAATGCCAAAGGTACCAAGTGAATGTTCTTA	724	
Db	729	GAGTTTATCCCAAACTCTCGAGCTAGAGATGCCAAGTGGTCCAAAGTGAATGTTGTA	788	
QY	725	GAGTGGATGAATCAATGTGATGTGGGCACTCTCTTAAGTACGTTAATGAAACCTGTGAGA	784	
Db	789	GAGTGGATGAATCAAGCTGATGTAGCACTTTAACTACGTTGGTGGAGCTGTGAGA	848	
QY	785	CAACTTA 791		
Db	849	CAACTTA 855		
RESULT 12				
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LOCUS		DNA	linear PAT 05-MAR-1997	
DEFINITION	Sequence 1 from Patent Ep0637591.			

ACCESSION	A42103
VERSION	A42103.1
KEYWORDS	GI:2297595
SOURCE	
ORGANISM	Phytolacca americana (American pokeweed)
REFERENCE	Phytolacca americana
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
TITLE	1 (bases 1 to 1195)
JOURNAL	Woon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.
COMMENT	A novel expression vector for phytolacca antiviral protein
	Patent: EP 0637591-A 1 08-FEB-1995;
	JINRO LIMITED (KR)
	Other publication AU 662844 950914
	Other publication JP 7067660 950314
	Other publication CA 2102859 950103
	Other publication AU 5064293 950119.
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Source	Location/Qualifiers
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Query Match	67.4%	Score 534.2	DB 6	Length 1195
Best Local Similarity	79.9%	Pred. No. 5.2e-116		
Matches 629	Conservative 0	Mismatches 158	Indels 0	Gaps 0
QY	5	TAATACGATCACCTTGATGCTGGAATGCGCACATTAAACAATATAGCCACTTTATG	64	
Db	100	TGAATTAACATCATTTAAATGTTGGAAGTACACCACTTACCAATATAGGCCACTTTTCGA	159	
QY	65	AATCTCTCGTAATCAAGCGAAATATCAAACTTAATGCTATGAGATCCAAATGCTAC	124	
Db	160	ATGATCTTCGTAAGGAAGCGAAATATCAAGTTTAAATGCTATGAGATATCCAAATGCTC	219	
QY	125	CTGATTAATAATTCGACCCCTAAGACTTAATGTTAGTTCGAAGTCAAACTTAATAA	184	
Db	220	CCATTAACAATTAACAATTCGAAGTACGTGTTGTTGAGCTCCAAAGTTCAAATTAATAA	279	
QY	185	CCATTACAATAATGCTGAGAGAAATACCTTAATCGTATGAGGCTATTCGATCCCTCA	244	
Db	280	CCATCACACTAATGCTGAGAGAAACAATTGATGATGAGGTTATTCGATCCCTTGG	339	
QY	245	ATGCGAATAAGTGTGTTACCATATATTTAATGATATTACAGACCGAAGCGACTGATG	304	
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QY	305	TGAGGAATACCTTTGCTCAAGTCTGAGTCTGCTGTGGAATGCAATCAATTAATCAATA	364	
Db	400	TAGGACTACTCTTTGCGCCAAATGCGCAATTCGTGTAGTAAACCAATAATCTTGATA	459	
QY	365	GCTATATTCGACCATGGAAGAAAGACAAAGTAATCTCAAGAAATCAAGTCCAAATGG	424	
Db	460	GTCATATTCCAACTTGGAAATCAAAACGGGAGTAATCAAGAAATCAAGTCCAAATGG	519	
QY	425	GAATTCAAATCTCAGAGTGAACATTTGAAAAATCTCGAGTTGATTCATCCCTGTA	484	
Db	520	GAATTCAAATCTCAGAGTGAATTTGAAAAATTTCTGAGTGAATCTCAATCACTGAGA	579	
QY	485	AAATCGAGGCTTTTCTACTGTATGACCATCCAAATGTTTCAGAGCGAGCGGATTC	544	
Db	580	AAACCGAAGCGAATTCCTATTTGTATGCCAATACAAATGATATCAGAGCGACAAGATTC	639	
QY	545	AGTACATAGGAACCAAGTCAAGCTAATTTTAATAGAGATTCACCGATGCCAAG	604	
Db	640	AGTACATAGGAATCAAGTGAATACTAATTTTAACAGAGATTCACCGATGCCAAG	699	
QY	605	TAATTTAATCTGAGAGAAATGGGGCAAAATCTCTGAGCAATTCAAATGCCAAGATG	664	
Db	700	TACTTAATTTGCAAGAGACATGGGGTAAGTTTCAACAGCAATTCATGATGCCAAGATG	759	
QY	665	GAGGCTTAACCAACCACTTGAGCTAGTGAATGCCAAAGGTACCAAGTGAATGTTCTTA	724	

Db 760 GAGTTTACCAACCACTCTGAGTGTGATGCGACGTGGCCCAAGTGAATGTGTGA 819
Qy 725 GAGTGAATGAATCAATCGTGAATGGCACTCCTTAAGTACCTTAATGAACCTGTGAGA 784
Db 820 GAGTGAATGAATCAACCTGATGTAGCACTTAACTACGTGTGGAGCTGTGAGA 879
Qy 785 CAACCTTA 791
Db 880 CAACCTTA 886

RESULT 13
143835 1195 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1 from patent US 5633155.
DEFINITION 143835
ACCESSION 143835
VERSION 143835.1 GI:2468933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Kim,M.-K., Lee,K.-H., Na,B.-K., Jeong,H.-S., Choi,K.-W., Moon,Y.-H.
and Jeon,H.-S.
TITLE Expression vector for phytoalexin antiviral protein and process for
preparing transgenic plant transformed therewith
JOURNAL Patent: US 5633155-A 1 27-MAY-1997;
FEATURES
source location/Qualifiers
1..1195
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ORIGIN
Query Match 67.4%; Score 534.2; DB 6; Length 1195;
Best Local Similarity 79.9%; Pred. No. 5.2e-116;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 5 TAAATACGATCACCTTGTGATGCTGGAATGCCACATTAACAATAATGCCACCTTATGG 64
Db 100 TGAATACATCATCTCAATGTTGGAAGTACCAACATTAACAATAATGCCACCTTATGG 159
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Qy 185 CCAATTAATCAATGCTGAGACGAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
Db 280 CCAATCAATTAATGCTGAGACGAATTAATTAATGATGAGGCTATTCGATCCCTTCA 339
Qy 245 ATGCGATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Db 340 AAACCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399
Qy 305 TGGAGATTAATCTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 364
Db 400 TAGAGACTACTCTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 459
Qy 365 GCTTAATTCGACCATGGAAGAAAGCAAGATTAATTAATTAATTAATTAATTAATTA 424
Db 460 GTCGATATCCAACTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 519
Qy 425 GAATTAATTAATCTGACGATGATGGAATTAATTAATTAATTAATTAATTAATTAATTA 484
Db 520 GAATTAATTAATCTGACGATGATGGAATTAATTAATTAATTAATTAATTAATTAATTA 579
Qy 485 AAACCTGAGGCTTTTCTACTGCTGATGCAATTAATTAATTAATTAATTAATTAATTA 544
Db 580 AAACCTGAGGCTTTTCTACTGCTGATGCAATTAATTAATTAATTAATTAATTAATTA 639

Qy 545 AGTACATAGAGAACCAAGTCAAGACTAATTTAATAGACATTCACCTGATCCCAAG 604
Db 640 AGTACATAGAGAACCAAGTCAAGACTAATTTAATAGACATTCACCTGATCCCAAG 699
Qy 605 TAAATTAATTTGAGGAGAAATGAGGCAAAATCTCTGAGCAATTCACATGCCAAGATG 664
Db 700 TAAATTAATTTGAGGAGAAATGAGGCAAAATCTCTGAGCAATTCACATGCCAAGATG 759
Qy 665 GGGCTTACCCAAACCACTTGAAGTGTGATGATGATGATGATGATGATGATGATGATG 724
Db 760 GAGTTTACCAACCACTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 819
Qy 725 GAGTGAATGAATCAATCGTGAATGGCACTCCTTAAGTACCTTAATGAACCTGTGAGA 784
Db 820 GAGTGAATGAATCAACCTGATGTAGCACTTAACTACGTGTGGAGCTGTGAGA 879
Qy 785 CAACCTTA 791
Db 880 CAACCTTA 886

RESULT 14
155866 1195 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1 from patent US 5648234.
DEFINITION 155866
ACCESSION 155866
VERSION 155866.1 GI:2476660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Moon,Y.-H., Jeon,H.-S., Choi,K.-W., Lee,K.-H. and Kim,M.-K.
TITLE Expression vector for phytoalexin antiviral protein
JOURNAL Patent: US 5648234-A 1 15-JUL-1997;
FEATURES
source location/Qualifiers
1..1195
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.4%; Score 534.2; DB 6; Length 1195;
Best Local Similarity 79.9%; Pred. No. 5.2e-116;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 5 TAAATACGATCACCTTGTGATGCTGGAATGCCACATTAACAATATGCCACCTTATGG 64
Db 100 TGAATACATCATCTCAATGTTGGAAGTACCAACATTAACAATAATGCCACCTTATGG 159
Qy 65 AATCTCTTGTATCAAGCAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
Db 160 ATGATCTTGTATGAAGCAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 219
Qy 125 CTGATCTATTTGACCCCTTAAGTACTTATGTTAGTCCCAAGGTGCAAACTTAAAA 184
Db 220 CCAATCAATTAATCAATTCCAAAGTACGTGTGAGTCCCAAGGTGCAAACTTAAAA 279
Qy 185 CCAATTAATCAATGCTGAGACGAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
Db 280 CCAATCAATTAATGCTGAGACGAATTAATTAATGATGAGGCTATTCGATCCCTTCA 339
Qy 245 ATGCGATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Db 340 AAACCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399
Qy 305 TGGAGATTAATCTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 364
Db 400 TAGAGACTACTCTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 459
Qy 425 GAATTAATTAATCTGACGATGATGGAATTAATTAATTAATTAATTAATTAATTAATTA 484
Db 520 GAATTAATTAATCTGACGATGATGGAATTAATTAATTAATTAATTAATTAATTAATTA 579
Qy 485 AAACCTGAGGCTTTTCTACTGCTGATGCAATTAATTAATTAATTAATTAATTAATTA 544
Db 460 GTCGATATCCAACTTTGCTCAAGTTCTAGTCTGCTGTGCAATGTCATTAATTAACATA 639

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 23:57:17 ; Search time 477.387 Seconds
(without alignments)
11056.934 Million cell updates/sec

Title: US-09-978-274A-3

Perfect score: 792
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001s: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	792	6 AAD42716	Aad42716 Pokeweed
2	786.4	99.3	945	6 AAD42715	Aad42715 Pokeweed
3	766	96.7	1092	6 AAD42729	Aad42729 Pokeweed
4	535	67.6	882	2 AAT99556	Aat99556 Pokeweed
5	532.6	67.2	1164	11 ADM74751	Adm74751 HIV-1 inh
6	532.6	67.2	1164	11 ADM74765	Adm74765 HIV-1 inh
7	532.6	67.2	1378	12 ADG76061	Adg76061 American
8	532.6	67.2	1379	3 AAZ45197	Aaz45197 Wild-type
9	532.6	67.2	1379	3 AAZ59220	Aaz59220 Pokeweed
10	532.6	67.2	1379	6 AAD42738	Aad42738 Pokeweed
11	532.6	67.2	1379	10 ADI05787	Adi05787 DNA encod
12	531	67.0	1195	2 AAQ56672	Aaq56672 Sequence
13	531	67.0	1379	4 AAC87929	Aac87929 P. ameriec
14	530.2	66.9	2472	2 AAQ43967	Aaq43967 Pokeweed
15	529.4	66.8	1195	2 AAQ81457	Aaq81457 Phytolacc
16	529.4	66.8	1378	6 AAD42739	Aad42739 Pokeweed
17	529.4	66.8	1379	3 AAZ59221	Aaz59221 Variant p
18	493	62.2	2369	2 AAT99557	Aat99557 Phytolacc
19	493	62.2	2369	2 ABA96543	Aba96543 Phytolacc

20	462	58.3	465	6 AAD42717	Aad42717 Pokeweed
21	460.6	58.2	918	2 AAQ64893	Aaq64893 Antiviral
22	460.6	58.2	918	2 AAT04782	Aat04782 DNA pMVC2
23	328.4	41.5	333	6 AAD42718	Aad42718 Pokeweed
24	101	12.8	934	3 AAZ45198	Aaz45198 Wild-type
25	101	12.8	934	6 AAD42740	Aad42740 Pokeweed
26	97.8	12.3	600	2 ABA96716	Aba96716 Cloning v
27	97.8	12.3	603	2 ABA96547	Aba96547 Cloning v
28	88.2	11.1	774	2 AAQ22981	Aaq22981 Gelonin t
29	86.4	10.9	765	3 AAZ61131	Aaz61131 DNA encod
30	86.4	10.9	984	3 AAZ61125	Aaz61125 DNA encod
31	86.4	10.9	993	3 AAZ61128	Aaz61128 DNA encod
32	86.4	10.9	999	3 AAZ61122	Aaz61122 DNA encod
33	86.4	10.9	999	3 AAZ61119	Aaz61119 DNA encod
34	84.2	10.6	864	1 AAN91504	Aan91504 DNA of r1
35	82	10.4	1233	2 AAT43997	Aat43997 E. coli c
36	82	10.4	1233	3 AA12896	Aa12896 Bacterioph
37	82	10.4	1233	9 ACD27613	Acd27613 Bacterioph
38	82	10.4	1233	10 ADC34646	Adc34646 B. coli c
39	82	10.4	1233	10 ADH92070	Adh92070 Fibroblas
40	81	10.2	804	2 AAQ53895	Aaq53895 Saporin c
41	81	10.2	804	2 AAQ53896	Aaq53896 Saporin c
42	81	10.2	804	2 AAQ85385	Aaq85385 Saporin c
43	81	10.2	804	2 AAQ85384	Aaq85384 Saporin c
44	81	10.2	804	2 AAQ99041	Aaq99041 M13mpl8-G
45	81	10.2	804	2 AAQ99042	Aaq99042 M13mpl8-G

ALIGNMENTS

RESULT 1
AAD42716
ID AAD42716 standard; DNA; 792 BP.
AC AAD42716;
XX
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed mature PAP-S protein encoding DNA.
DE
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW gene; ds.
XX
OS Phytolacca americana.
XX
XX
XX Key Location/Qualifiers
FH 1.792
FT CDS
FT /*tag= a
FT /product= "Mature PAP-S protein"
FT 1.29
FT /*tag= b
FT /bound_moiety= "Primer PS1BP"
FT complement (436.462)
FT /*tag= c
FT /bound_moiety= "Primer PS1SR"
FT 463.492
FT /*tag= d
FT /bound_moiety= "Primer PS2BP"
FT 681.686
FT /*tag= e
FT /note= "Sequence replacing removed XbaI site"
FT complement (765.792)
FT /*tag= f
FT /bound_moiety= "Primer PS2SR"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
PD
XX 15-OCT-2001; 2001WO-GB004593.
PF
XX 14-OCT-2000; 2000GB-00025217.
PR

PAP', PAPi and PAP-S, where the gene(s) comprises a promoter which acts in response to the application of a specific stimulus to the plant so as to facilitate expression of the pokeweed antiviral protein in specific cells of the plant. The method is useful for inducing a necrotic effect in specific cells of a plant. The present sequence is pokeweed pro-PAP-S protein encoding DNA

Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

Query Match 99.3%; Score 786.4; DB 6; Length 945;

Best Local Similarity 99.9%; Pred. No. 2e-215;

Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 4 ATAAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCACTTATG 63
DB 73 ATAAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCACTTATG 132
QY 64 GAATCTCTTGTATCAAGCGAAAGATCCAAAATAAATGCTATGCGATACCAATGCTA 123
DB 133 GAATCTCTTGTATCAAGCGAAAGATCCAAAATAAATGCTATGCGATACCAATGCTA 192
QY 124 CCGATATCAATATCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCAGAACTTAAA 183
DB 193 CCGATATCAATATCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCAGAACTTAAA 252
QY 184 ACCATTACACTAATGCTGAGACGAAATACCTTATAGCTGATGGGCTATTCGATCCCTTC 243
DB 253 ACCATTACACTAATGCTGAGACGAAATACCTTATAGCTGATGGGCTATTCGATCCCTTC 312
QY 244 AATGCGAATAGTGTGCTTACCATATATTAATGATATTAACAGACCGAAGCACTGAT 303
DB 313 AATGCGAATAGTGTGCTTACCATATATTAATGATATTAACAGACCGAAGCACTGAT 372
QY 304 GTGGAATATCTCTTGTCTGAAGTTCGATGTCGTGCTGCTGCTGCTGCTGCTGCTGCT 363
DB 373 GTGGAATATCTCTTGTCTGAAGTTCGATGTCGTGCTGCTGCTGCTGCTGCTGCTGCT 432
QY 364 AGCTTATATCCGACCATGAGAAAGAAAGAGAGTAACTCAAGAAATCAAGTCCAAATG 423
DB 433 AGCTTATATCCGACCATGAGAAAGAAAGAGAGTAACTCAAGAAATCAAGTCCAAATG 492
QY 424 GGAATTCAAATTAATCTGACAGTGAATTTGAAATATCTTGAAGTTGATTCCTCTGTA 483
DB 493 GGAATTCAAATTAATCTGACAGTGAATTTGAAATATCTTGAAGTTGATTCCTCTGTA 552
QY 484 AAAAAGAGGCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
DB 553 AAAAAGAGGCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
QY 544 AAGTACATAGAGAACCAAGTCAAGACTATTTTAAATGAGCACTTACCCGATCCCAA 603
DB 613 AAGTACATAGAGAACCAAGTCAAGACTATTTTAAATGAGCACTTACCCGATCCCAA 672
QY 604 GTAATTAATTTGAGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACAAATGCAAGAT 663
DB 673 GTAATTAATTTGAGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACAAATGCAAGAT 732
QY 664 GGGGCTTTTACCCCAACCACTTGAGCTAGTGAATGCCAAAGTACCAAGTATGTTCTT 723
DB 733 GGGGCTTTTACCCCAACCACTTGAGCTAGTGAATGCCAAAGTACCAAGTATGTTCTT 792
QY 724 AAGTGGATGAATTCATGCTGATGTTGGCACTGCTTAAGTACGTTATATGAGACCTGTCAG 783
DB 793 AAGTGGATGAATTCATGCTGATGTTGGCACTGCTTAAGTACGTTATATGAGACCTGTCAG 852
QY 784 ACAACTTA 791
DB 853 ACAACTTA 860

```

RESULT 3
AAD42729 standard; DNA; 1092 BP.

```

XX AAD42729;
AC 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX chimeric; rice; cystatin delta D86; N1A protease cleavage site; PCS; ds.
OS Phytophthora americana.
OS Oryza sativa.
OS Tobacco; Etch virus.
OS Chimeric.
XX
FH Key
FT primer_bind
FT 1..29
FT /tag= a
FT /bound_moiety= "Primer PS1BP"
FT
FT misc_feature
FT 581..686
FT /tag= b
FT /note= "Modified XbaI site"
FT /complement (742..786)
FT
FT primer_bind
FT /tag= c
FT /bound_moiety= "Primer PCS-PAPSR"
FT 766..806
FT /tag= d
FT /bound_moiety= "Primer PCS-Delta86F"
FT
FT misc_feature
FT 766..786
FT /tag= e
FT /note= "TEV N1A protease cleavage site"
FT /complement (1066..1092)
FT
FT primer_bind
FT /tag= f
FT /bound_moiety= "Primer SYNPODELta86R"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADT8-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson WJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Disclosure; Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPi and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is a fusion DNA. This
XX sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
XX and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
XX on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

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Query Match 96.7%; Score 766; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.5e-209;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGATTAATACGATCACCCTTTGATGCTGGAATATGCCACCAATTAAACAATAATGCCACCTTT 60
DB 1 ATGATTAATACGATCACCCTTTGATGCTGGAATATGCCACCAATTAAACAATAATGCCACCTTT 60
QY 61 ATGGAATCTCTTGATATCAAGGGAAGATCCAAATCTAAATAGCTATGCGCATACCAATG 120
DB 61 ATGGAATCTCTTGATATCAAGGGAAGATCCAAATCTAAATAGCTATGCGCATACCAATG 120
QY 121 CTACCTGATATTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAAACTTA 180
DB 121 CTACCTGATATTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAAACTTA 180
QY 181 AAAACCATTAACATAATGCTGAGACGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 AAAACCATTAACATAATGCTGAGACGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTCAATGGCAATAGTGTGCTTACCAATATTTAAAGATTTTCAAGACCCGAAACGCACT 300
DB 241 TTCAATGGCAATAGTGTGCTTACCAATATTTAAAGATTTTCAAGACCCGAAACGCACT 300
QY 301 GATGTGAGAAATATCTTTGCTCAAGTTCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GATGTGAGAAATATCTTTGCTCAAGTTCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 AATAGCTTATATTCGACCATGGAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 420
DB 361 AATAGCTTATATTCGACCATGGAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 420
QY 421 TTGGGAATTCAAATATCTGACGACGATGACATGGAAGAAATCTGGAAGTGAATTCATTCCTC 480
DB 421 TTGGGAATTCAAATATCTGACGACGATGACATGGAAGAAATCTGGAAGTGAATTCATTCCTC 480
QY 481 GTAAAAATCGAGGCTTTTCTTCTACTGTAAGCCATCCAAATGTTTCAAGAGCGAGCGCA 540
DB 481 GTAAAAATCGAGGCTTTTCTTCTACTGTAAGCCATCCAAATGTTTCAAGAGCGAGCGCA 540
QY 541 TTCAAGTACATAGAAACCAAGTCAGAGATTAATTTAAATAGAGATTTCACTGATGCC 600
DB 541 TTCAAGTACATAGAAACCAAGTCAGAGATTAATTTAAATAGAGATTTCACTGATGCC 600
QY 601 AAAGTAAATTAATCTGAGAGGAAGTGGGGCAAAATCTGAGGCAATTCACAAATGCGCAG 660
DB 601 AAAGTAAATTAATCTGAGAGGAAGTGGGGCAAAATCTGAGGCAATTCACAAATGCGCAG 660
QY 661 AATGGGGCTTTTACCCCAACCACTTGAAGTATGAGTATGCAAAAGTATCAAGTATGAT 720
DB 661 AATGGGGCTTTTACCCCAACCACTTGAAGTATGAGTATGCAAAAGTATCAAGTATGAT 720
QY 721 CTTAAGTATGATGAATCAATGCTGATGCTGAGCACTCTTAAATGACG 766
DB 721 CTTAAGTATGATGAATCAATGCTGATGCTGAGCACTCTTAAATGACG 766

RESULT 4
AAT99556
ID AAT99556 standard; DNA; 882 BP.
AC AAT99556;
XX 17-OCT-2003 (revised)
DT 08-JUN-1998 (first entry)
XX
DE Phytoleuca insularis antiviral protein gp12 gene.
XX
KW Antiviral protein; gp12 gene; virolicide; transgenic plant;
XX virus resistance; immunocongulate; AIDS; cancer; therapy; ss.
XX
OS Phytoleuca insularis; Nakai.
XX
FH Key Location/Qualifiers
FT CDS 1..882
FT /*tag= a

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FT XX /tranel_except= (pos:715..717, aa:11e)
PN XX EP808902-A2.
XX XX
PD 26-NOV-1997.
XX XX
PF 30-SEP-1996; 96EP-00307159.
XX XX
PR 22-MAY-1996; 96KR-00017404.
XX XX
PA (JINR-) JIN RO LTD.
XX XX
PI Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J;
PI Song S, Choi Y, Kim C, Kim M;
XX XX
DR WPI; 1998-001788/01.
XX XX
PT Antiviral proteins of Phytoleuca insularis Nakai and their genes - useful
PT in plant antiviral agents and immunocongulates for the treatment of
PT and cancer.
XX XX
PS Claim 2; Page 10-12; 26pp; English.
XX XX
CC This polynucleotide comprises the coding region of the Phytoleuca
CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
CC designated gp12 (see AAM26773). The gp12 gene was isolated from leaf
CC genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
CC AAT99557), encoding a 35.7 kDa protein (see AAM26774) designated gp150,
CC has also been isolated from P. insularis Nakai. Also claimed are vectors
CC encoding these antiviral proteins and host cells transformed or
CC transfected with these vectors. E. coli XL1-Blue MRF' (KCM-10080)
CC host cells are claimed, as is a process for preparing antiviral protein
CC by culturing these cells and purifying the protein from inclusion
CC bodies. The antiviral proteins and recombinant proteins inhibit protein
CC synthesis. They can be used as active ingredients of antiviral agents of
CC plant viruses, and employed in the manufacture of immunocongulates for
CC the treatment of AIDS and cancer. The isolated genes can be used in the
CC breeding of transgenic plants having viral resistance. (Updated on 17-OCT
CC -2003 to standardise OS field)
XX XX
SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;

Query Match 67.6%; Score 535; DB 2; Length 882;
Best Local Similarity 79.8%; Pred. No. 3.5e-143;
Matches 631; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 1 ATGATTAATACGATCACCCTTTGATGCTGGAATATGCCACCAATTAAACAATAATGCCACCTTT 60
DB 1 ATGATTAATACGATCACCCTTTGATGCTGGAATATGCCACCAATTAAACAATAATGCCACCTTT 60
QY 61 ATGGAATCTCTTGATATCAAGGGAAGATCCAAATCTAAATAGCTATGCGCATACCAATG 120
DB 61 ATGGAATCTCTTGATATCAAGGGAAGATCCAAATCTAAATAGCTATGCGCATACCAATG 120
QY 121 CTACCTGATATTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAAACTTA 180
DB 121 CTACCTGATATTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAAACTTA 180
QY 181 AAAACCATTAACATAATGCTGAGACGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 AAAACCATTAACATAATGCTGAGACGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTCAATGGCAATAGTGTGCTTACCAATATTTAAAGATTTTCAAGACCCGAAACGCACT 300
DB 241 TTCAATGGCAATAGTGTGCTTACCAATATTTAAAGATTTTCAAGACCCGAAACGCACT 300
QY 301 GATGTGAGAAATATCTTTGCTCAAGTTCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GATGTGAGAAATATCTTTGCTCAAGTTCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 AATAGCTTATATTCGACCATGGAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 420
DB 361 AATAGCTTATATTCGACCATGGAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 420

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```

ADM74765
ID ADM74765 standard; cDNA; 1164 BP.
XX
XX ADM74765;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX HIV-1 inhibition activity related Tat cDNA.
DE
XX
XX human immunodeficiency virus; HIV-1; tumour; plant;
KM Chinese phylolacca leaf; trans-acting activation factor; Tat; mutant;
KM gene; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX Key Location/Qualifiers
FH 2..943
FT CDS /*tag= a
FT /product= "Tat HIV-1 protein"
PT
XX
XX CN1400220-A.
XX
XX 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX Peng X, Bai L, Yin B;
XX
XX WPI; 2003-469263/45.
XX
XX P-PSDB; ADM74766.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT its expression, separation and purification method in protokaryon.
XX
XX Example 9; Page 11-12; 17pp; Chinese.
XX
XX
XX The present invention relates to two kinds of cDNA which can inhibit
CC human immunodeficiency virus (HIV-1) activity, including separation clone
CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC and application of the cDNA in preparation of preparation for curing the
CC virus and tumours. One of the described cDNAs is obtained by separation
CC and cloned from a plant Chinese phylolacca leaf, and one from the trans-
CC acting activation factor (Tat) mutant coded by human immunodeficiency
CC virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
CC used in the HIV-1 inhibition activity of the invention.
XX
XX
XX Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;
SQ
XX
XX Query Match 67.2%; Score 532.6; DB 11; Length 1164;
XX Best Local Similarity 79.8%; Pred. No. 1.9e-142;
XX Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
XX
XX
XX 5 TAAATGATGACCTTGTGATGCTGAAATGSCACATTAACAATATGCACTTATG 64
XX |||||
XX 69 TGAATGACATGATCTACATGTTGGAAGTACACATGACCAATAGCAGCTTTCTG 128
XX |||||
XX 65 AATCTCTGATGATCAAGGAAAGATCCAAACTAAATGCTATGCGATACCATGCTAC 124
XX |||||
XX 129 ATATATCTTGATGAAAGGAAAGATCCAAAGTTTAAATGCTATGGAATCCATGTTGC 188
XX |||||
XX 125 CTGATCTAATGACCCCTTAAGTACTTATGTTAGTTCGCAAGGTGCAAAATTAATAAAA 184
XX |||||
XX 189 CCAATGCAATCCAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAAAATTAATAAAA 248
XX |||||
XX 185 CCATTACACTAATGCTGAGAGCAAAATTAATTAACGATGAGGCTATTGATCCCTTCA 244
XX |||||
XX 249 CCATGCACTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTGATCCCTTGG 308
XX |||||
XX 245 ATGGCAATAGTGTGCTTACCATATATTTAATGATATTAACAGACCGAAGCACTGATG 304
XX |||||

```

```

Db 309 ATACCAATAGTGTGCTTACCATATCTTTTGTGATATCTCAGGATACGAAGCCAAATG 368
|||
Qy 305 TGGAGAACTACTCTTTGTGCTCAAGTTCTAGTCTGTGTGCAATGTCATTACTACATA 364
|||
Db 369 TAGAGACTACTCTTTGCCCCAAATCCCAATTCGTGTGTAGTAAACATTAACATATGATA 428
|||
Qy 365 GCTTATATCCGACATGAGAAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCAAATGG 424
|||
Db 429 GTGATATTCACATTTGGAATTCAAAGCGAGATTAATCAAGAAATCAAGTCCAAATGG 488
|||
Qy 425 GAAATCAATATCTCAGAGTGAATGAAATTTCTGTGAGTTGATTCATTCCTGTAA 484
|||
Db 489 GAAATCAATATCTCAGAGTGAATGAAATTTCTGTGAGTTGATTCATTCCTGTAA 548
|||
Qy 485 AATCTGAGGCTTTTCTCTGTGATGATCCATTCCAATGTTTCAAGGACGCGCATTC 544
|||
Db 549 AAACCGAAGCCGAATTCCTGCTGAGCCATTAACAAATGATATCAGGCGCAAGATTTCA 608
|||
Qy 545 AGTACATGAGAACCAAGTCAAGACTAATTTTATGAGCACTTCCCTGATCCCAAG 604
|||
Db 609 AGTACATGAGAACCAAGTCAAGACTAATTTTATGAGCACTTCCCTGATCCCAAG 668
|||
Qy 605 TAAATTAATTGAGAGAAAGTGGGCAAAATCTGTAGGCAATTCACATGCCAAGATG 664
|||
Db 669 TACTTAATTTGAAAGAGACATGGGGTAAAGTTTCTACAGCAATTCATGATGCCAAGATG 728
|||
Qy 665 GGGCTTTACCCAAACCACTTGAAGTATGATGATGATGATGATGATGATGATGATGATG 724
|||
Db 729 GAGTTTAACTCCAAACCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATG 788
|||
Qy 725 GAGTGAATGAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784
|||
Db 789 GAGTGAATGATATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 848
|||
Qy 785 CAATCTTA 791
|||
Db 849 CAATCTTA 855
|||
RESULT 7
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
XX
XX ADG76061;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX American pokeweed antiviral protein (PAP) DNA Segid 1.
DE
XX
XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KM american pokeweed; retroviral.
XX
XX OS
XX Phylolacca americana.
XX
XX WO2003106479-A2.
XX
XX PD 24-DEC-2003.
XX
XX PF 17-JUN-2003; 2003WO-US019141.
XX
XX PR 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating

```


CC transgenic plants have a normal and fertile phenotype
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 2e-142;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
QY 5 TAAATACGATCACCTTGTGATGCTGAATATGCGACCATTAACAATATATGCCACTTTATGG 64
DB 292 TGAATACATCATCTACATGTTGAGATGACCAATAGCAATAGCCACTTTCTG 351
QY 65 AATCTCTTGTATCAAGCAAGATCAAAAATAAATGCTATGCAATCAATGCTAC 124
DB 352 ATGATCTTGTATGAAGCAAGATCAATTAATGCTATGAAATCAATGCTGC 411
QY 125 CTGATCTATATGAGCCCTAAGTACTTATGTTAGTCTCAAGGTGCAAACTATAAA 184
DB 412 CCAATACAAATACAAATCAAGTACGTTGTTGCTTCAAGTTCAAAATAAAAA 471
QY 185 CCATTACACTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTTGATCCCTCA 244
DB 472 CCATCACACTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTTGATCCCTTG 531
QY 245 ATGCAATTAAGTCTGTTACCATATATTAATGATTAATTAAGCAAGCAAGCACTGATG 304
DB 532 AAACCAATTAATGCTGTTACCATATATTAATGATTAATTAAGCAAGCAAGCAAGT 591
QY 305 TGGAGATATCTTTGCTCAAGTTCTGATGCTGCTGTTGCAATGCTCAATTAATCAATA 364
DB 592 TAGAGCTACTCTTTGCTCAAGTTCTGATGCTGCTGTTGCAATGCTCAATTAATCAATA 651
QY 365 GCTTATATCCGACCATGAGCAAGCAAGTAACTCAAGCAATCAATCAATTTG 424
DB 652 GTGATATATCAATGATGATGATCAAGGAGGAGTAAATCAAGAGTCAATGCTG 711
QY 425 GAATTCAAATATCTGAGATGATCAATGGAATTAATCTGAGATGATCAATGCTG 484
DB 712 GAATTCAAATATCTGAGATGATGATCAAGGAGTAAATCAAGAGTCAATGCTG 771
QY 485 AAATGAGGCTTTTCTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 544
DB 772 AAACCGAAGCGAATTCCTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 831
QY 545 AGTACATAGAGCAAGCAAGTCAATTAATTAATGATGATGATGATGATGATGATG 604
DB 832 AGTACATAGAGCAAGTCAATTAATTAATGATGATGATGATGATGATGATGATG 891
QY 605 TAATTAATCTTGAAGAGAGTGGGCAAAATCTCTGAGCAATTCATGATGCAAGATG 664
DB 892 TACTTAATTTGCAAGAGATGAGGCTGATGATGATGATGATGATGATGATGATG 951
QY 665 GGGCTTAAACCAACCACTGAGCTGATGATGATGATGATGATGATGATGATGATG 724
DB 952 GAGTTTAAACCAACCACTGAGCTGATGATGATGATGATGATGATGATGATGATG 1011
QY 725 GAGTGAATGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATG 784
DB 1012 GAGTGAATGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATG 1071
QY 785 CAACTTA 791
DB 1072 CAACTTA 1078
RESULT 9
ID AA259220 standard; cDNA; 1379 BP.
XX
AC AA259220;
XX
DT 20-APR-2000 (first entry)
XX

DE pokeweed antiviral protein coding sequence spring leaf form.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KM resistance; potato virus X; potato virus Y; potato leaf roll virus;
KW tuber; ss.
XX
XX Phytojalca americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
PD
PF 07-APR-1992; 92US-00865169.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS) MONSANTO CO.
PA
XX
XX Kanlewski WK, Turner NE, Lodge JK;
PI
XX
XX WPI; 2000-126326/11.
DR
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
PT antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 6; Fig 4; 30pp; English.
PS
XX
CC This is the coding sequence for the spring leaf form of the pokeweed
CC antiviral protein (PAP) which is used to generate transgenic potato
CC plants. PAP is able to confer resistance to infection by potato virus X
CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC potato plant or tuber expressing PAP
CC
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 2e-142;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
QY 5 TAAATACGATCACCTTGTGATGCTGAATATGCGACCATTAACAATATATGCCACTTTATGG 64
DB 292 TGAATACATCATCTACATGTTGAGATGACCAATAGCAATAGCCACTTTCTG 351
QY 65 AATCTCTTGTATCAAGCAAGATCAAAAATAAATGCTATGCAATCAATGCTAC 124
DB 352 ATGATCTTGTATGAAGCAAGATCAATTAATGCTATGAAATCAATGCTGC 411
QY 125 CTGATCTAATTTGACCCCTAAGTACTTATGTTAGTCTCAAGGTCAAACTATAAA 184
DB 412 CCAATACAAATACAAATCAAGTACGTTGTTGCTTCAAGTTCAAAATAAAAA 471
QY 185 CCATTACACTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTTGATCCCTTCA 244
DB 472 CCATCACACTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTTGATCCCTTG 531
QY 245 ATGCAATTAAGTCTGTTACCATATATTAATGATTAATTAAGCAAGCAAGCACTGATG 304
DB 532 AAACCAATTAATGCTGTTACCATATATTAATGATTAATTAAGCAAGCAAGCAAGT 591
QY 305 TGGAGATATCTTTGCTCAAGTTCTGATGCTGCTGTTGCAATGCTCAATTAATCAATA 364
DB 592 TAGAGCTACTCTTTGCTCAAGTTCTGATGCTGCTGTTGCAATGCTCAATTAATCAATA 651
QY 365 GCTTATATCCGACCATGAGCAAGCAAGTAACTCAAGCAATCAATCAATTTG 424
DB 652 GTGATATATCAATGATGATGATCAAGGAGGAGTAAATCAAGAGTCAATGCTG 711
QY 425 GAATTCAAATATCTGAGATGATCAATGGAATTAATCTGAGATGATCAATGCTG 484
DB 712 GAATTCAAATATCTGAGATGATGATCAAGGAGTAAATCTGAGATGATCAATGCTG 771
QY 485 AAATGAGGCTTTTCTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 544


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Db      772 AAACCGAAGCCGAATTCCTATTGTGAGCCATACAAATGTATTCAGAGGCGAGCAAGATTCA 831
Qy      545 AGTACATGAGAGAACCAAGTCAAGACTAATTTTAATAGAGCAATTCACCTGATCCCAAG 604
      |||
Db      832 AGTACATGAGAGAACCAAGTCAAGACTAATTTTAATAGAGCAATTCACCTGATCCCAAG 891
Qy      605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTGTAGGCAATTCACAAATGCCAAGATG 664
      |||
Db      892 TACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAGACGCAATTCATGATGCCAAGATG 951
Qy      665 GGGCTTTACCCAAACCACTTGAAGCTAGTGAATGCCAAAGGTAACCAATGATAGTTCTTA 724
      |||
Db      952 GAGTTTAACTCCAAACCTCTCGAGTGAATGCCAGTGGCCAAAGTGAATAGTGTGA 1011
Qy      725 GAGTGAATGAATCAATGATGATGCACTCTTAAGTAACTTAATGAAACCTGTGCA 784
      |||
Db      1012 GAGTGAATGAATCAAGCTTAATGATGATGCACTTAATCACTAGGTGGAGCTGTGCA 1071
Qy      785 CAACTTA 791
      |||
Db      1072 CAACTTA 1078

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RESULT 10

AAD42738
ID AAD42738 standard; DNA; 1379 BP.

XX AAD42738;

DT 15-NOV-2002 (first entry)

DE Pokeweed PAP' DNA #1.

KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.

OS Phytolacca americana.

XX Key Location/Qualifiers

FT m18c_feature 290..1076

FT /note= "Mature PAP' sequence"

XX WO200233107-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-GB004593.

XX 14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;

XX WPI; 2002-489891/52.

PT Inducing necrotic effect in specific cells of plant by transforming plant

PT with a chimeric gene encoding pokeweed antiviral protein and a promoter

PS which acts in response to application of specific stimulus to plant.

XX Claim 5; Page 86; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in

XX specific cells of a plant. The method involves transforming the plant

XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely

XX PAP', PAVI and PAP-S, where the gene(s) comprises a promoter which acts

XX in response to the application of a specific stimulus to the plant so as

XX to facilitate expression of the pokeweed antiviral protein in specific

XX cells of the plant. The method is useful for inducing a necrotic effect

XX in specific cells of a plant. The present sequence is pokeweed PAP' DNA

XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 67.2%; Score 532.6; DB 6; Length 1379;
Best Local Similarity 79.8%; Pred. No. 2e-142;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

```

Qy      5 TAAATGATGACCTTGTGATGCTGAAATGCGACCATTAACAAATATGCACTTTATG 64
      |||
Db      292 TGAATACAAATCATCTACAAATGTTGAGTACCAATTAAGCAAAATAGCCACTTTTCTGA 351
Qy      65 AATCTCTCCGAATCAAGCCGAAATATCCAAACTTAAATGATATGCAATGCAATGCTAC 124
      |||
Db      352 ATGATCTTGGTAAAGAGCCGAAATATCAAGTTTAAATGCTAATGAAATACCAATGCTGC 411
Qy      125 CTGATTAATTAATGACCCCTTAATGATTAATGTTAGTTCAGAGTCCAAACCTTAAAA 184
      |||
Db      412 CCAATTAATTAATGACCAATTCAAAGTACGTTGTTGAGTTCAGAGTTCAAATTAATTA 471
Qy      185 CCATTACATTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTAATTCGATCCCTTCA 244
      |||
Db      472 CCATCACTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTAATTCGATCCCTTTC 531
Qy      245 ATGCAATTAATGCTGATCAATTAATTAATGATTAATTAATGATTAATGATTAATGAT 304
      |||
Db      532 AATCAATTAATGCTGATCAATTAATTAATGATTAATGATTAATGATTAATGATTAATG 591
Qy      305 TGAGAAATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 364
      |||
Db      592 TAGAATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 651
Qy      365 GCTTAATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 424
      |||
Db      652 GTGATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 711
Qy      425 GAATTAATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 484
      |||
Db      712 GAATTAATTAATGCTGATCAATTAATGATTAATGATTAATGATTAATGATTAATGATTA 771
Qy      485 AATCTGAGGCTTTTCTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 544
      |||
Db      772 AAACCGAAGCCGAATTCCTATTGTGAGCCATACAAATGATTAATGAGGCGAGCAATTTCA 831
Qy      545 AGTACATGAGAGAACCAAGTCAAGACTAATTTTAATAGAGCAATTCACCTGATCCCAAG 604
      |||
Db      832 AGTACATGAGAGAACCAAGTCAAGACTAATTTTAATAGAGCAATTCACCTGATCCCAAG 891
Qy      605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTGTAGGCAATTCACAAATGCCAAGATG 664
      |||
Db      892 TACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAGACGCAATTCATGATGCCAAGATG 951
Qy      665 GGGCTTTACCCAAACCACTTGAAGCTAGTGAATGCCAAAGGTAACCAATGATAGTTCTTA 724
      |||
Db      952 GAGTTTAACTCCAAACCTCTCGAGTGAATGCCAGTGGCCAAAGTGAATAGTGTGA 1011
Qy      725 GAGTGAATGAATCAATGATGATGCACTCTTAAGTAACTTAATGAAACCTGTGCA 784
      |||
Db      1012 GAGTGAATGAATCAAGCTTAATGATGATGCACTTAATCACTAGGTGGAGCTGTGCA 1071
Qy      785 CAACTTA 791
      |||
Db      1072 CAACTTA 1078

```

RESULT 11

ID ADI05787 standard; DNA; 1379 BP.

XX ADI05787;

DT 15-APR-2004 (first entry)

DE DNA encoding the wild-type pokeweed antiviral protein.

XX ribosome depurination; antifungal; antiviral; viroinide; anti-HIV;

XX cytosolic; immunosuppressive; agricultural biotechnology; pharmaceuticals;

KM medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
 KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
 XX db.
 OS Phytolacca americana.
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "wild-type pokeweed antiviral protein"
 PN W0200262952-A2.
 XX 15-AUG-2002.
 XX 01-FEB-2002; 2002MO-US002792.
 XX PF 01-FEB-2001; 2001US-0266396P.
 XX PR 02-FEB-2001; 2001US-0266396P.
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX PA Tumer NB, Hudak KA, Parikh B;
 XX PI WPI; 2003-156656/15.
 XX DR P-PSDB; ADI05788.
 XX DR
 XX PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 PT or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 1; 51bp; English.
 XX
 CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer. AIDS, viral infection or autoimmune
 CC diseases associated with proliferation of unwanted T-cells or B-cells.
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.
 XX
 XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 SO
 Query Match 67.2%; Score 532.6; DB 10; Length 1379;
 Best Local Similarity 79.8%; Pred. No. 2e-142;
 Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 305 TGGAGATACCTCTTGGCTCAAGTTCAGTTCGCTGTTGGCAATGTCATTACTACATATA 364
 DB 592 TAGAGACTACTCTTGGCCAAATGCGCAATTCTGCTGTATTAATAAACAATTGATA 651
 QY 365 GCTTATATCCGACCATGGAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCATTGG 424
 DB 652 GTCGATATCCAACTTGGAATCAAAAGCGGAGATTAATAAGAAAGTCAGTCCACTGG 711
 QY 425 GAATCAATATCTCAGCAGTGCATTTGGAAGAAATCTCTGGAGTTGATTCCTCTGTA 484
 DB 712 GAATTCAAATATCTGACAGTAAATTTGGAAGAAATTTCTGGAGTGTCTTCACTAGA 771
 QY 485 AAACCTGAGGCTTTTCTTCTGTAAGTCCATCCAAATGTTTCAAGGACGCGGATTA 544
 DB 772 AAACCGAAGCCGAATTCCTATGTTGAGCCATTAACAAATGATACAGGCGCAAGATTCA 831
 QY 545 AGTACATAGGAACCAAGTCAAGCTAATTTTATAGAGATTTCTGATCCCAAG 604
 DB 832 AGTACATAGGAATCAAGTGAATAATTTTAAACAGAGATTCACCTTAATCCCAAG 891
 QY 605 TAAATTAATCTGAGGAGGAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGATG 664
 DB 892 TACTTAATTTGCAAGAGACATGGGGTAAATTTCAACAGCAATTCATGATGCCAAGATG 951
 QY 665 GAGCTTTACCCAAACCACTTGAAGCTAGTGAATCCAAAGGTACCAAGTGAATGTTCTTA 724
 DB 952 GAGTTTACCCAAACCTTCTGAGCTAGTGAATCCAGTGGTGCAGAGTGAATGTTGTA 1011
 QY 725 GAGTGAATGAATCAATCGTATGATGCACTCTTAAATGCTTAATGAACTGTGCA 784
 DB 1012 GAGTGAATGAATCAACCTGATGTAGCACTTAAACTAGTGGAGGAGCTGTGCA 1071
 QY 785 CAACCTTA 791
 DB 1072 CAACCTTA 1078

RESULT 12
 AA056672
 ID AA056672 standard; cDNA; 1195 BP.
 XX
 AC AA056672;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 04-SEP-1994 (first entry)
 XX
 XX Sequence of Phytolacca antiviral protein (PAP) cDNA.
 XX
 KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
 XX
 OS Phytolacca americana; L.
 FH Key Location/Qualifiers
 FT CDS 33..974
 FT /*tag= a
 PN BP585554-A1.
 XX
 PD 09-MAR-1994.
 XX
 PF 30-JUN-1993; 93EP-00110445.
 XX
 PR 16-AUG-1992; 92KR-00014895.
 XX
 PA (JINR-) JIN RO LTD.
 XX
 PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
 XX WPI; 1994-076002/10.
 XX DR P-PSDB; AAR48548.
 XX
 PT Expression vector for phytolacca antiviral protein - used for producing

transgenic virus-resistant plants and for producing the antiviral agent.
 Disclosure; Fig 1, 15pp; English.

To isolate PAP gene, total cellular mRNA was purified from leaves of
Phytolacca americana L. obtd. in Korea. A cDNA library was constructed.
 The PAP gene was selected by immunoscreening employing anti-PAP antibody.
 A deletion mutant was prepd. from the isolated PAP gene, and the DNA
 sequence of the PAP genomes was determined. (Updated on 25-MAR-2003 to
 correct PW field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match 67.0%; Score 531; DB 2; Length 1195;
 Best Local Similarity 79.7%; Pred. No. 5,6e-142;
 Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY 5 TAAATACGATCACCTTGATGCTGGAATGCGCAACCATTAACAAATATGCCACTTTATG 64
DB 100 TGAATACATCATCATCAATGTTGGAGTAGACACCATTAAGCAATATAGCCACTTTCTGA 159
QY 65 AATCTCTGCTATCAAGCGAAAGATCCAAACTAAATGCTATGCGCATACCATGCTAC 124
DB 160 ATGATCTTGTGAATGAAGCGAAGATCCAGTTTAAATGCTATGGAATACCAATGCTGC 219
QY 125 CTGATTAATTAATGACCCCTTAAGTACTTATGTTAGCTCGAAGGTGCAAACTTAATA 184
DB 220 CCATTAACAAATACAAATCAAGTACGTTGTTGAGTTCAGAGTTCAAAATATATATA 279
QY 185 CCATTAACCTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 244
DB 280 CCATCAACCTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 339
QY 245 ATGCAATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 304
DB 340 AAACCACTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 399
QY 305 TGGAGATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 364
DB 400 TAGAGATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 459
QY 365 GCTTAATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 424
DB 460 GTGATTAATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 519
QY 425 GAATTAATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 484
DB 520 GAATTAATTAATGCTGAGAGCAAAATTAATAGTATGAGTGGCTATTCGATCCCTTCA 579
QY 485 AAATGAGGCTTTTCTAATGAGGCAATCAAAATGTTTCAAGGCGAGGATTC 544
DB 580 AAACCGAAGCGAATTTCTAATGAGGCAATCAAAATGTTTCAAGGCGAGGATTC 639
QY 545 AGTACATAGAGCAAGTCAAGTCAATATTTAAATAGAGATTTACCTGATCCCAAG 604
DB 640 AGTACATAGAGCAAGTCAAGTCAATATTTAAATAGAGATTTACCTGATCCCAAG 699
QY 605 TAATTAATGAGAGCAAGTCAAGTCAATATTTAAATAGAGATTTACCTGATCCCAAG 664
DB 700 TACTTAATGAGAGCAAGTCAAGTCAATATTTAAATAGAGATTTACCTGATCCCAAG 759
QY 665 GGGCTTAACCAACCTTGAGGATGAGTCAAGGCAAGGATGAGTCAAGTCAAG 724
DB 760 GAGTTTAAACCAACCTTGAGGATGAGTCAAGGCAAGGATGAGTCAAGTCAAG 819
QY 725 GAGTGAATGAATCAATGATGATGAGTCAAGTCAAGTCAAGTCAAGTCAAG 784
DB 820 GAGTGAATGAATCAATGATGATGAGTCAAGTCAAGTCAAGTCAAGTCAAG 879
QY 785 CAACCTTA 791
DB 880 CAACCTTA 886

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RESULT 13

AAC87929
 ID AAC87929 standard; DNA; 1379 BP.

AC AAC87929;

DT 06-MAR-2001 (first entry)

DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.

XX Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;

KW biotherapeutic; fusion protein; immunocytotoxic; mutant; cytotoxic;

KW anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;

XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; B8.

OS Phytolacca americana.

FT Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "pokeweed antiviral protein (PAP)"

XX US6146628-A.

XX 14-NOV-2000.

PP 11-JUL-1995; 95US-00501253.

XX 11-JUL-1995; 95US-00501253.

XX (MINU) UNIV MINNESOTA & RUTGERS.

PA (UTNE-) UNIV STATE NEW JERSEY.

PI Uckun FM, Turner NE;

XX WPI: 2001-040422/05.

DR P-PSDB; AAB36500.

PT Immunocytotoxic useful for treating cancer and acquired immunodeficiency

PT syndrome, comprises mutant pokeweed anti-viral protein and a targeting

PT molecule that binds a cell surface receptor.

XX Disclosure; Col 47-50; 32pp; English.

XX The present invention describes a fusion protein or an immunocytotoxic
 CC (I), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
 CC acid substitution at residue 75, 97 or 176 of native PAP and a targeting
 CC moiety that binds a cell surface receptor. (I) can have cytosolic and
 CC anti-HIV activities, and is an inhibitor of cellular RNA or protein
 CC synthesis. (I) is useful for treating AIDS and cancers including
 CC leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
 CC tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
 CC colon cancer. Immunocytotoxins prepared using PAP mutants exhibit an
 CC improved therapeutic index over immunocytotoxins containing either wild-
 CC type PAP or variant PAP. The present sequence encodes the wild-type PAP,
 CC which is given in the exemplification of the present invention

XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 67.0%; Score 531; DB 4; Length 1379;
 Best Local Similarity 79.7%; Pred. No. 5,9e-142;
 Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY 5 TAAATACGATCACCTTGATGCTGGAATGCGCAACCATTAACAAATATGCCACTTTATG 64
DB 292 TGAATACATCATCATCAATGTTGGAGTAGACACCATTAAGCAATATAGCCACTTTCTGA 351
QY 65 AATCTCTGCTATCAAGCGAAAGATCCAAACTAAATGCTATGCGCATACCATGCTAC 124
DB 352 ATGATCTTGTGAATGAAGCGAAGATCCAGTTTAAATGCTATGGAATACCAATGCTGC 411
QY 125 CTGATTAATTAATGACCCCTTAAGTACTTATGTTAGTCAAGGTCAGAACTTAATA 184

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Db      412  CCAATACAAATACAAATCCAAAGTACGTTGGTGTGAGTCCAAAGTTCAAATAAAAA 471
Qy      185  CCAATACAAATACGTTGAGAGAAATTAATTAATGAGAGGCTATTCAGTCCCTCA 244
Db      472  CCAATACAAATACGTTGAGAGAAATTAATTAATGAGAGGCTATTCAGTCCCTCA 531
Qy      245  ATGCAATTAAGTGTCTTACCATATATTAATTAATTAATTAATTAATTAATTAATTA 304
Db      532  AAACCAATTAATGTCGTTACCAATCTTATTAATTAATTAATTAATTAATTAATTA 591
Qy      305  TGAAGAACTACTCTTCTGCTCAAGTTCTAGTCTGCTGTTGCAATCTCAATTAACA 364
Db      592  TAAGAGTACTCTTCTGCTCAAGTTCTAGTCTGCTGTTGCAATCTCAATTAACA 651
Qy      365  GCTTAATCCGACATGCAAGAAAGAAAGCAAGTAACTCAAGAAATCAATGCAATGG 424
Db      652  GTGATATTCCAATCTTGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCACTGG 711
Qy      425  GAAATCAATATCTCAGAGTGAATGAAAAATCTGAGAGTTGATTCATTCCTGTAA 484
Db      712  GAAATCAATATCTCAGAGTGAATGAAAAATCTGAGAGTGAATTCATTCCTGTAA 771
Qy      485  AAATGAGGCTTTTCTTCTACTGTTACCATCCAAATGCTTTCAGAGGCGCGGATTC 544
Db      772  AAACCCAAAGCGGAATCTTATGTTGACCAATCAAAATGATTCAGAGGCGAGATTC 831
Qy      545  AGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGAGATTCCTGATCCGATCA 604
Db      832  AGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGAGATTCCTGATCCGATCA 891
Qy      605  TAAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCATGCGCAAGAT 664
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Qy      665  GGGCTTTACCAAAACCACTTGAAGTATGATGCGCAAGGATCCAGTGAATGTTTGA 724
Db      952  GAGTTTAAACCAAAACCTCTGAGCTATGATGCGCAAGTGAATGTTTGA 1011
Qy      725  GAGTGAATGAATCAATCGTATGATGCGCAATCTCTTAAATGAATGAACCTGTGAG 784
Db      1012  GAGTGAATGAATCAATCGTATGATGCGCAATCTCTTAAATGAATGAACCTGTGAG 1071
Qy      785  CAACTTA 791
Db      1072  CAACTTA 1078

RESULT 14
AAQ43967 standard; DNA; 2472 BP.
XX      AAQ43967;
AC      09-NOV-1993 (first entry)
XX      DE      Pokeweed antiviral protein.
XX      KW      Pokeweed; ricin; protein synthesis inhibitor; cancer;
XX      KM      polymerase chain reaction; PCR; 88.
XX      OS      Phytolacca americana.
XX      FH      Key      Location/Qualifiers
XX      FT      CAAT_signal 549..552
XX      FT      CAAT_signal 627..630
XX      FT      TATA_signal 845..850
XX      FT      sig_peptide 1014..1085
XX      FT      mat_peptide 1086..1868

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XX      01-JUN-1993.
PD      20-NOV-1991.
PE      20-NOV-1991; 91JP-00329672.
PR      20-NOV-1991; 91JP-00329672.
PR      (NIBS ) JAPAN TOBACCO INC.
PA      WPI; 1993-211306/26.
DR      P-PSDB; AAR37345.
XX      DR      P-PSDB; AAR37345.
XX      PS      Claim 2; Page 11-13; 14pp; Japanese.
XX      CC      PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The
XX      CC      protein may be obtained all year round by recombinant DNA techniques. PAP
XX      CC      can be used partic. against cancer and as an agricultural chemical. Total
XX      CC      mRNA, is extracted from the seeds, leaves and roots of pokeweed and used
XX      CC      to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA
XX      CC      fractions, which are introduced into a cloning vector EMB3 and then into
XX      CC      host E.coli PLK-17 (P2) to produce PAP
XX      SQ      Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;

Query Match      66.9%; Score 530.2; DB 2; Length 2472;
Best Local Similarity 82.0%; Pred. No. 1,2e-141;
Matches 649; Conservative 0; Mismatches 133; Indels 9; Gaps 3;

Qy      4      ATAAATACGATCACTTTGATGCTGGAATGCAACCATTAACAATATGCACTTATG 63
Db      1086  ATAAATACGATCACTTTGATGCTGGAATGCAACCATTAACAATATGCACTTATG 1145
Qy      64      GAATCTCTTGTATCAAGCGAAAGATCCAAAATTAATATGCTATGCAATGCAATGCTA 123
Db      1146  GAATCTCTTGTATCAAGCGAAAGATCCAAAATTAATATGCTATGCAATGCAATGCTA 1205
Qy      124  CCTGATACCTAATCGAACCCTAATGCTATGCTTAACTGATGCAAGTGAACCTTAA 183
Db      1206  CCTGATACCTAATCGAACCCTAATGCTATGCTTAACTGATGCAAGTGAACCTTAA 1265
Qy      184  ACCATTAACCTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCCTTC 243
Db      1266  ACCATTAACCTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCCTTC 1325
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Db      1326  AATGCAATTAAGTGTCTTACCATATATTAATTAATTAATTAATTAATTAATTA 1382
Qy      301  GATGGAAGAAATCTTTGCTCAAGTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGT 360
Db      1383  GATGGAAGAAATCTTTGCTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 1442
Qy      361  AATAGCTTATTCGACGACATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCCA 420
Db      1443  AATAGCTTATTCGACGACATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCCA 1499
Qy      421  TTGGGAATTCAAATCTCAGAGTGAATGAAAAATCTCTGGAATTAATTCATTCCT 480
Db      1500  TTGGGAATTCAAATCTCAGAGTGAATGAAAAATCTCTGGAATTAATTCATTCCT 1559
Qy      481  GTTAAATCAAGGCTTTTCTTCTGCTCAAGTTCTAGTCTGCTGTTGCAATCTCA 540
Db      1560  GTTAAATCAAGGCTTTTCTTCTGCTCAAGTTCTAGTCTGCTGTTGCAATCTCA 1619

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 3751.92 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-3

Perfect score: 792

Sequence: 1 atgataataatcgatcacctt.....gaacctgtcgacacttaa 792

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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3: gb_ests3.*
4: gb_hnc.*
5: gb_ests4.*
6: gb_ests5.*
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SUMMARIES

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C 1	88.6	11.2	993	2	BR035039 MM02A03 M
C 2	82.2	10.4	816	2	BR035038 MM02A01 M
C 3	64	8.1	1033	2	BR036541 MP01B07 M
4	62.2	7.9	498	5	BQ588134
5	61.6	7.8	829	7	CN7882289 ESN00385
6	57.4	7.2	649	6	CA838757 MCT020B02
7	57.4	7.2	649	6	CA838757 MCT020B02
8	57.4	7.2	661	6	CA838757 MCT020B02
9	57.4	7.2	671	6	CA838757 MCT020B02
10	57.4	7.2	689	6	CA838757 MCT020B02
11	57.4	7.2	689	6	CA838757 MCT020B02
12	55.8	7.0	639	6	CA838757 MCT020B02
13	53.8	6.8	1038	2	BR03546
14	52.4	6.6	405	8	T24255
15	51.6	6.5	639	2	BR037217
16	46.6	5.9	489	2	BR130330
17	45.6	5.8	837	1	AM053634
18	45.4	5.7	267	1	AA856221
19	45.2	5.7	919	10	CN80296A
C 20	44	5.6	701	9	B2031330
21	43	5.4	1021	2	BR036639
22	42.6	5.4	414	10	CG637661

C 23	42.4	5.4	561	9	AQ156306
C 24	41.8	5.3	658	10	CZ857242
C 25	40.8	5.2	788	10	CG690741
26	40.8	5.2	1001	10	CNS0078E
27	40.4	5.1	228	10	CG503780
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29	40.4	5.1	431	10	CG517501
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31	40.4	5.1	526	10	CL256443
32	40.4	5.1	557	1	AM230870
33	40.4	5.1	563	9	AQ670952
34	40.4	5.1	575	5	BUT43805
35	40.4	5.1	579	3	BJ365833
36	40.4	5.1	616	5	BY729128
C 37	40.4	5.1	630	7	CO102355
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41	40.4	5.1	810	6	CA751457
42	40.4	5.1	812	7	CV557169
43	40.4	5.1	813	5	BU961361
44	40.4	5.1	831	5	BU961701
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ALIGNMENTS

RESULT 1
BR035039 993 bp mRNA linear EST 07-JUN-2000
DEFINITION MM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
anti-viral protein, mRNA sequence.

ACCESSION BR035039
VERSION BR035039.1 GI:8330048
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.,
Functional Genomics of Plant Stress Tolerance
(2000)

TITLE JOURNAL
COMMENT Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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Location/Qualifiers

FEATURES
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XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

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Best Local Similarity 60.5%; Pred. No. 4 6e-13;

Matches 164; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

QY 386 AGAAGCAGAGTAACTCAAGAAATCAAGTCAATGGGAATCAATCAAGCAGG 445
DB 681 AGAAGCTGCCGCTCAAGCAGAAACAGTATGATTGGGCTTCAACTAGAGTTTG 622

QY 446 ACAATGGAAAAATCTCGAGTTGATTCATTCCTCGTAAAAAAGTAGAGCTTTTCTTAC 505
 DB 621 CCATCGATGATTTATGTGTAABAAAAGATCGATGGAATCTGAGGCCAAATTTCTAC 562
 QY 506 TGTGATCCATCCAAATGGTTTCAGAGCGCGCATTCATCAATGATAGAACCAAGT-- 563
 DB 561 TGATTCGATCCATCGATGGTTTCAGAGCGCGCATTCATCAATGATAGAACCAAGT 502
 QY 564 -CAAGACTAATTTTAAATAGACATTCCTACCTGATCCCAAGTAAATTAATCTGGAGAGA 622
 DB 501 CCGAAATGGGTGCATCGTTTCGTTCAAAACCCGATCCGAAGTGAATTAATCTGGAGACA 442
 QY 623 AGTGGGCGAAATCTCTGAGCGCAATTCACA 653
 DB 441 ACTGGGGAAGATTTCCGATGAGATTCATTA 411

RESULT 2
 BE035038/c 816 bp mRNA linear EST 07-JUN-2000
 LOCUS NM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION antiviral protein, mRNA sequence.
 ACCESSION BE035038
 VERSION BE035038.1 GI:8330047
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 1 (bases 1 to 816)
 Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbmw@u.arizona.edu.
 Location/Qualifiers
 source 1..816
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ORIGIN
 Query Match 10.4%; Score 82.2; DB 2; Length 816;
 Best Local Similarity 59.0%; Pred. No. 2.5e-11;
 Matches 160; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

QY 386 AGAAGACGAAGTAACTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAGTG 445
 DB 680 AGAAACCTGCCGTCAAGCAGAAACAGTATTCGTTGGGGCTTGCTAAATAGAGTTTG 621
 QY 446 ACAATGGAAAAATCTCGAGTTGATTCATTCCTCGTAAAAAAGTAGAGCTTTTCTTAC 505
 DB 620 CCATCGATGATTTATGTGTAABAAAAGATCGATGGAATCTGAGGCCAAATTTCTAC 561
 QY 506 TGTGATCCATCCAAATGGTTTCAGAGCGCGCATTCATCAATGATAGAACCAAGT-- 563
 DB 560 TGATTCGATCCATCGATGGTTTCAGAGCGCGCATTCATCAATGATAGAACCAAGT 501
 QY 564 -CAAGACTAATTTTAAATAGACATTCCTACCTGATCCCAAGTAAATTAATCTGGAGAGA 622

DB 500 CCGAAATGGGTGCATCGTTTCGTTCAAAACCCGATCCGAAGTGAATTAATCTGGAGACA 441
 QY 623 AGTGGGCGAAATCTCTGAGCGCAATTCACA 653
 DB 440 ACTGGGGAAGATTTCCGATGAGATTCATTA 410

RESULT 3
 BE036541 1033 bp mRNA linear EST 07-JUN-2000
 LOCUS MF01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION antiviral protein, mRNA sequence.
 ACCESSION BE036541
 VERSION BE036541.1 GI:8331550
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 1 (bases 1 to 1033)
 Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbmw@u.arizona.edu
 An open reading frame exists.
 Location/Qualifiers
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 Matches 149; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 384 AAGAAAGCAGAAGTAACTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAG 443
 DB 193 AGAAGAGGTGCAAGCAAGCGCGGAATGCAATGATGAGGGTGAAATTAATAGAGTT 252
 QY 444 TGACATTTGAAAAATCTCTGAGATTGATTCATTCCTCTGTAATAACTGAGGCTTTTCT 503
 DB 253 TGGATTCGAGTCGGTTTGTGTAAGAACCGATTAATGAGGAGTTGAGGCCAAATTCCT 312
 QY 504 ACTGTAGCCATCCAAATGGTTTCAGAGCGCGCATTCATCAATGATAGAACCAAGT 563
 DB 313 GCTGATTCGATACATCGTTTCTGAGAGCAGCGTTTAAATTAATGAAATAGAGT 372
 QY 564 CA---AGACTAATTTTAAATAGACATTCCTACCTGATCCCAAGTAAATTAATCTGGAG 620
 DB 373 GACCCAAAGTGGTTTCAATGCGTCGTTCAATACCCGACCCGAAGTCTGAGTTTGAGAA 432
 QY 621 GAAGTGGGCGAAATCTCTGAGCGCAATTCACA 652
 DB 433 CAATGGGGGGAAGATTTCCAGAGATTCATA 464

RESULT 4
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 LOCUS BQ588134
 DEFINITION B012337-024-009-G14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

024-009-G14 5-PRIME, mRNA sequence.
 ACCESSION BO588134
 VERSION BO588134.1 GI:26117717
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 498)
 REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,W., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radejof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by RWS Kleinwanzlebener Saatgut AG Bindeck, Germany, contact: b.schulz@rws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 7.9%; Score 62.2; DB 5; Length 498;
 Best Local Similarity 56.7%; Pred. No. 7.3e-06;
 Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;
 QY 14 TCACCTTGTGATGCGAAATGCCACATTAACAATATGCACTTATGGAATCTCTC 73
 DB 169 TAACCTTTGACCTTGAACAGCTTCAAGCAAAATATGACATTTCTTAAGCATATAC 228
 QY 74 GTATCAAGGAAAGATCCAAACTAAATAGTATGCGATACCAATGCTACTATCTA 133
 DB 229 GCAACATATGTAAGATTCAAAGCTATATACGAAGAAATCCATGCTCCCTGCACAT 288
 QY 134 ATTGACCCCTAAGTATTTATGTTAGTCCCAAGTGCAGAA-----CCTAAAA 184
 DB 289 CAAACAGCAAAATACCTTTAGCCGAGCTAAAGCTAAAGGCGGTAATGACATTA 348
 QY 185 CCATTACATTAATGCTGAGAGCAATATCTATAGTATGCTATTTGATCCCTTCA 244
 DB 349 CCATCAACTTGTCTGTAGCAAAATATGCTATATGATGCTTTTACGATCAAGTAG 408
 QY 245 ATGGCAA 251
 DB 409 CAGGTAA 415

RESULT 5
 CN782289
 LOCUS
 DEFINITION CN782289 829 bp mRNA linear EST 21-MAY-2004
 EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to antiviral ribosome-inactivating protein CAP308 [Chenopodium album], mRNA sequence.
 ACCESSION CN782289
 VERSION CN782289.1 GI:47561753
 KEYWORDS EST.
 SOURCE Chenopodium quinoa (quinoa)
 ORGANISM Chenopodium quinoa
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Chenopodium.
 1 (bases 1 to 829)
 REFERENCE Coles,N.D., Coleman,C.E., Christensen,S.A., Jellen,B.N., Stevens,M.R., Bonifacio,A., Rojas-Baltran,J.A., Fairbanks,D.J. and Maughan,P.J.
 Development and use of an expressed sequenced tag library in quinoa (Chenopodium quinoa Willd.) for the discovery of single nucleotide polymorphisms
 Plant Sci. 168 (2), 439-447 (2005)
 CONTACT: Coleman, Craig B.
 Department of Plant and Animal Sciences
 Brigham Young University
 275 WIDB, Brigham Young University, Provo, UT 84602, USA
 Tel: (801) 422-5145
 Fax: (801) 422-0008
 Email: craig.coleman@byu.edu
 Plate: 02 row: J column: 22
 Seq primer: M13 Forward
 High quality sequence stop: 829.
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ORIGIN

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 QY 90 TCCAAACTTAATATGCTATGCAATACCAATGCTGATCTAATTTGACCCCTAAGTA 149
 DB 175 TCCAAAGTTAGTATGTAAGAAATCCCAATGATCCGACCAACCAACCAATACATA 234
 QY 150 CTTATTTGTTAGTCCCAAGTGAACCTAAAC-----CATTACACTAATGCT 200
 DB 235 TCTTTTGTGACCTTGAACTTAAAGATTAAGATGAGATTTCACTTACCTTGCTTT 294
 QY 201 GAGACGAATTAATTAATGCTATGATGCTATTTGATCCCTTCAATGCAATAGTGTG 260
 DB 295 AAGTAAAGACACTGTATGATGATGCTTGTGCTGATTAATTTGAGGCAAGTGGCG 354
 QY 261 TTACATATATTTAATGATTTTCAAGCACCGAAGCACTGATGTGAGATATCTTTG 320
 DB 355 CCAATTTCTTTTCAATCTTAACATGACCATTTGATGAGCAAGAA-----AGTTTTTC 410
 QY 321 CTCAGTTTCTAGTCTGTGTCGAATGTCATTAATCAATAGCTTATATCCGACCAT 380

Db 411 CAGAGTTCAGGTTTC-----ATTAATATTAAGGAGGAAAGTACAGTCAAT 462
 Qy 381 GGAAGAGAGAGAGAGTAAGTCAAGAAATCAAGATCGCAATTGGGAAATTCAAATACAG 440
 Db 463 CGAAGAGAGAGAGTGTGTAAGAGCAATTAAGT---TTTCGGTGGGGTTGATACCTTAA 519
 Qy 441 CAGTGAATTGAGAAAATCTCTGAGAGTGAATTCATTCCTGTA-----AAACTGA 491
 Db 520 AACTACATGAGAAAGGCTATGGATGATGATACTAAGGCAAGATTAATAGCAAACTGA 579
 Qy 492 GGGTTTTTTCTACTGTAGCCATCCAAATGGTTTCAGAGCGAGCGGATTCAGATCAT 551
 Db 580 AGCTCGGTTCTCTACTCGCAATCAAAAGGTTGACAGAGCGCGACGTTTCAAGTCAAT 639
 Qy 552 AGAAGACCAAGTCAAGACTAATTTAAT 579
 Db 640 CCAAGGAGAGCTATCTACTACAAAT 667

RESULT 6
 CA838757 649 bp mRNA linear EST 12-DEC-2002
 LOCUS MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5
 DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
 (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02.5,
 mRNA sequence.

ACCESSION CA838757.1 GI:26566522
 VERSION CA838757
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 649)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 020 row: B column: 02
 Seq primer: T3 20mer
 High quality sequence stop: 649.
 Location/Qualifiers

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 /db_xref="taxon:3544"
 /clone="MCT020B02"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression
 library, 5 days 0.5 M NaCl treatment, Crassulacean acid
 metabolism, phase IV (5:30 PM)."
 /note="Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 7.2%; Score 57.4; DB 6; Length 649;
 Best Local Similarity 53.5%; Pred. No. 0.00016;
 Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy 384 AAAGAAAGCAGAGTAAGTCAAGAAATCAAGTCCATTGGGAATTCAAATCTCAGCAG 443
 Db 87 AGAGATGCTGCAAAACCAACGACGAGAGCAATAGAGTTAGGGGTGATTAATCAGAGT 146
 Qy 444 TGACATTGAAAAATCTCTGAGATTGATTCATTCCTGTAAATACTGAGGCTTTTTCCT 503
 Db 147 TGGATCGAGTCCGTTTATAGTAAACATCGACAAGTCAAGAGAAATGAGGCCAAATTCCT 206
 Qy 504 ACTGTAGCATCAATAGGTTTCAAGAGAGCGCATTCATCAATAGAGAACCAAGT 563
 Db 207 GCTGATTCCTATCAAGATGGTTTCTAAGAGGAGAGTTCAAGTATATGAGATAGT 266
 Qy 564 CAAGCTAATTT-----TAATAGCATTCTACCTGATCCCAAGTAATTAATCTGGA 617
 Db 267 GAACCAAGTGGCTTGAATTAATGATCGTTCTTACCGACGACCAAAATGCTGTTTGA 326
 Qy 618 GGAAGAGTGGGCAAAATCTCTGAGCAATTC 650
 Db 327 GACCAATGGGGAGAGATTCGACGAGATTCA 359

RESULT 7
 CA839330 649 bp mRNA linear EST 12-DEC-2002
 LOCUS MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5
 DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
 (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11.5,
 mRNA sequence.

ACCESSION CA839330
 VERSION CA839330.1 GI:26567095
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 649)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 026 row: C column: 11
 Seq primer: T3 20mer
 High quality sequence stop: 649.
 Location/Qualifiers

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 /clone="MCT026C11"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression
 library, 5 days 0.5 M NaCl treatment, Crassulacean acid
 metabolism, phase IV (5:30 PM)."
 /note="Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 7.2%; Score 57.4; DB 6; Length 649;

Best Local Similarity 53.5%; Pred. No. 0.00016;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAAGAAGCGAAGTAATCTCAAGAAATCAAGTCCAAATGGGAATTCAAATCTCAGAG 443
DB 87 AGAAGATGCTGCAACCAAGACGAGAAAGCATAGATTAGGGGTGATTAAGAGTT 146
QY 444 TGACATTGGAATAATCTCTGAGATTGATTCAATCCCTGTAATAAATGAGGCTTTTCT 503
DB 147 TGGCATGAGTGGGTTTATGTTATGTTAGACATCGACAAAGTACAGAAATGAGGCAATTTCT 206
QY 504 ACTGTAGCCATCCAAATGTTTTCAGAGCAGCGGATTCAGATACATAGAAACCAAGT 563
DB 207 GCTGATTGCCATACAGATGTTTCTGAAAGCAGCAAGGTTCAAGTATATGAGATAGGT 266
QY 564 CAAGACTAATTT-----TATAGAGCATTTCACTCCGTATCCCAAGTAATTAATTGGA 617
DB 267 GAACCAAGTGGCGTTAGATTATGAAATGTTTACCCGACCCGAAATGCTGCTTTTGA 326
QY 618 GGAGAAGTGGGGCAAAATCTCTGAGGCAATTCA 650
DB 327 GACCAATTGGGGGAGATTTCGACGAGATTCA 359

RESULT 8
CA835532 661 bp mRNA linear EST 12-DEC-2002
LOCUS MCS038A11.160572 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS038A11.5, mRNA
sequence.
CA835532
VERSION
KEYWORDS
SOURCE
ORGANISM

EST. CA835532.1 GI:26563297
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alstroceae; Mesembryanthemum.
1 (bases 1 to 661)
Cushman, J.C.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
Location/Qualifiers
1. .661
/organism="Mesembryanthemum crystallinum"
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/clone="MCS038A11"
/rissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 7.2%; Score 57.4; DB 6; Length 661;
Best Local Similarity 53.5%; Pred. No. 0.00016;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAAGAAGCGAAGTAATCTCAAGAAATCAAGTCCAAATGGGAATTCAAATCTCAGAG 443
DB 98 AGAAGATGCTGCAACCAAGACGAGAAAGCATAGATTAGGGGTGATTAAGAGTT 157
QY 444 TGACATTGGAATAATCTCTGAGATTGATTCAATCCCTGTAATAAATGAGGCTTTTCT 503
DB 158 TGGCATGAGTGGGTTTATGTTATGTTAGACATCGACAAAGTACAGAAATGAGGCAATTTCT 217
QY 504 ACTGTAGCCATCCAAATGTTTTCAGAGCAGCGGATTCAGATACATAGAAACCAAGT 563
DB 218 GCTGATTGCCATACAGATGTTTCTGAAAGCAGCAAGGTTCAAGTATATGAGATAGGT 277
QY 564 CAAGACTAATTT-----TATAGAGCATTTCACTCCGTATCCCAAGTAATTAATTGGA 617
DB 278 GAACCAAGTGGCGTTAGATTATGAAATGTTTACCCGACCCGAAATGCTGCTTTTGA 337
QY 618 GGAGAAGTGGGGCAAAATCTCTGAGGCAATTCA 650
DB 338 GACCAATTGGGGGAGATTTCGACGAGATTCA 370

RESULT 9
CA839511 671 bp mRNA linear EST 12-DEC-2002
LOCUS MCT028D04.172117 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04.5,
mRNA sequence.
CA839511
VERSION
KEYWORDS
SOURCE
ORGANISM

EST. CA839511.1 GI:26567276
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alstroceae; Mesembryanthemum.
1 (bases 1 to 671)
Cushman, J.C.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.
Location/Qualifiers
1. .671
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/rissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the

ORIGIN Lambda UniZapXR vector and cDNA synthesis kit."

Query Match 7.2%; Score 57.4; DB 6; Length 671;
Best Local Similarity 53.5%; Pred. No. 0.00017;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAGAAAGCAGAACTAATCAAGAAATCAAGTCCAAATGGAAATTCATACTACAGC 443
DB 87 AGGAATGCTGCACCAACGACGACGAGCATGAGTGGGTGATTAAGTAACTAGAGT 146
QY 444 TGACATTTGAAAAATCTCTGAGATGATTCATTCCTCGTAAATCTAGAGCTTTTCT 503
DB 147 TGGATGAGTCCGTTTATGTTAGTAAACATGACATGACAAATGAGAAATGAGCCAAATCTT 206
QY 504 ACTGTAGCCATCCAAATGGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 563
DB 207 GCTGATGGCATACAGATGGTTTCTGAGGACGACAGTTCAAGTATTTAGAGTAAAGT 266
QY 564 CAAGACTAATTT-----TAATAGAGCATTCACCTGATCCCAAGTAAATTAATTGA 617
DB 267 GAACCAAGTGCCTTATGATTCATGATGTTCTTACCCGACCGAAATGCTGCTTTGGA 326
QY 618 GGAGAGTGGGGCAAAATCTCTGAGCAATTCA 650
DB 327 GACCAATGGGGGAAGTTTCGACGAGATTCA 359

RESULT 10 689 bp mRNA linear EST 12-DEC-2002
LOCUS CA833333
DEFINITION MCS021A09_151944 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.

ACCESSION CA833333
VERSION CA833333.1 GI:26561098
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 689)
Cushman, J.C.

REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)
JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 021 row: A column: 09
Seq primer: T3 20mer
High quality sequence stop: 689.
Location/Qualifiers
1..689
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library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:"

ORIGIN EcoRI, Site 2: XhoI, library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

Query Match 7.2%; Score 57.4; DB 6; Length 689;
Best Local Similarity 53.5%; Pred. No. 0.00017;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAGAAAGCAGAACTAATCAAGAAATCAAGTCCAAATGGGAATTCATACTACAGC 443
DB 98 AGGAATGCTGCACCAACGACGACGAGCATGAGTGGGTGATTAAGTAACTAGAGT 157
QY 444 TGACATTTGAAAAATCTCTGAGATGATTCATTCCTCGTAAATCTAGAGCTTTTCT 503
DB 158 TGGATGAGTCCGTTTATGTTAGTAAACATGACATGACAAATGAGAAATGAGCCAAATCTT 217
QY 504 ACTGTAGCCATCCAAATGGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 563
DB 218 GCTGATGGCATACAGATGGTTTCTGAGGACGACAGTTCAAGTATTTAGAGTAAAGT 277
QY 564 CAAGACTAATTT-----TAATAGAGCATTCACCTGATCCCAAGTAAATTAATTGA 617
DB 278 GAACCAAGTGCCTTATGATTCATGATGTTCTTACCCGACCGAAATGCTGCTTTGGA 337
QY 618 GGAGAGTGGGGCAAAATCTCTGAGCAATTCA 650
DB 338 GACCAATGGGGGAAGTTTCGACGAGATTCA 370

RESULT 11 689 bp mRNA linear EST 12-DEC-2002
LOCUS CA833383
DEFINITION MCS021F04_152044 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA sequence.

ACCESSION CA833383
VERSION CA833383.1 GI:26561148
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 689)
Cushman, J.C.

REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)
JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 021 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 689.
Location/Qualifiers
1..689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021F04"
/cruise_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid

Db 537 GCCT 540

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Job time : 3754.92 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 274.935 Seconds
(without alignments)
5120.590 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RG_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534.2	67.4	1195	2 US-08-373-858-1	Sequence 1, Appl
2	534.2	67.4	1195	2 US-08-342-7868-1	Sequence 1, Appl
3	532.6	67.2	1379	2 US-08-500-611-1	Sequence 1, Appl
4	532.6	67.2	1379	2 US-08-500-694-1	Sequence 1, Appl
5	532.6	67.2	1379	3 US-07-865-169-1	Sequence 1, Appl
6	532.6	67.2	1379	3 US-09-005-273-1	Sequence 1, Appl
7	532.6	67.2	1379	6 PCT-US96-11546-1	Sequence 1, Appl
8	531	67.0	1379	3 US-08-501-253A-1	Sequence 1, Appl
9	529.4	66.8	1379	3 US-07-865-169-2	Sequence 2, Appl
10	529.4	66.8	1379	3 US-09-005-273-3	Sequence 3, Appl
11	460.6	58.2	918	2 US-08-138-636-1	Sequence 1, Appl
12	460.6	58.2	918	2 US-08-319-622A-1	Sequence 1, Appl
13	460.6	58.2	918	2 US-08-471-564-1	Sequence 1, Appl
14	88.2	11.1	774	6 PCT-US91-05766-1	Sequence 1, Appl
15	82	10.4	1233	3 US-08-718-904-80	Sequence 80, Appl
16	82	10.4	1233	3 US-09-449-249-80	Sequence 80, Appl
17	81	10.2	804	2 US-08-356-161-6	Sequence 6, Appl
18	81	10.2	804	2 US-08-356-161-7	Sequence 7, Appl
19	81	10.2	804	3 US-08-718-904-22	Sequence 22, Appl
20	81	10.2	804	3 US-08-718-904-23	Sequence 23, Appl
21	81	10.2	804	3 US-09-449-249-22	Sequence 22, Appl
22	81	10.2	804	3 US-09-449-249-23	Sequence 23, Appl
23	81	10.2	804	6 PCT-US93-05702-6	Sequence 6, Appl
24	81	10.2	804	6 PCT-US93-05702-7	Sequence 7, Appl

25	81	10.2	804	6 PCT-US95-10973A-6	Sequence 6, Appl
26	81	10.2	804	6 PCT-US95-10973A-7	Sequence 7, Appl
27	75	9.5	1167	6 PCT-US95-10973A-57	Sequence 57, Appl
28	75	9.5	1230	2 US-08-356-161-12	Sequence 12, Appl
29	75	9.5	1230	2 US-08-356-161-13	Sequence 13, Appl
30	75	9.5	1230	3 US-08-718-904-53	Sequence 53, Appl
31	75	9.5	1230	3 US-09-449-249-53	Sequence 53, Appl
32	75	9.5	1230	6 PCT-US93-05702-12	Sequence 12, Appl
33	75	9.5	1230	6 PCT-US93-05702-13	Sequence 13, Appl
34	75	9.5	1230	6 PCT-US95-10973A-12	Sequence 12, Appl
35	75	9.5	1230	6 PCT-US95-10973A-13	Sequence 13, Appl
36	75	9.5	1251	3 US-08-718-904-74	Sequence 74, Appl
37	75	9.5	1251	3 US-09-449-249-74	Sequence 74, Appl
38	75	9.5	1260	3 US-08-718-904-72	Sequence 72, Appl
39	75	9.5	1260	3 US-09-449-249-72	Sequence 72, Appl
40	75	9.5	1266	3 US-08-718-904-75	Sequence 75, Appl
41	75	9.5	1266	3 US-09-449-249-75	Sequence 75, Appl
42	75	9.5	1269	3 US-08-718-904-78	Sequence 78, Appl
43	75	9.5	1269	3 US-09-449-249-78	Sequence 78, Appl
44	75	9.5	1275	3 US-08-718-904-73	Sequence 73, Appl
45	75	9.5	1275	3 US-09-449-249-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytolecta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: cDNA to mRNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 67.4%; Score 534.2; DB 2; Length 1195;
Best Local Similarity 79.9%; Pred. No. 1.9e-150;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

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QY 5 TAAATACGATCACTTTGATGCTGGAATGCCACCATTAACAAATATGCGACCTTTATGG 64
DB 100 TGAATACATCACTCAATCAATGTTGAGATCCACCATTAACAAATATGCGACCTTTATGG 159
QY 65 AATCTCTTGTAAATCAAGCAAGATCCAAATCTAAATGCTAATGCGATCCAAATGCTAC 124
DB 160 ATGATCTTCTTAATGAGAGCAAGATCCAAATGCTAATGCTAATGCGATCCAAATGCTAC 219
QY 125 CTGATTAATTAATGACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTA 184
DB 220 CCAATACAAATATCAAAATCCAAAGTATGTTGTTGAGCTCCAAAGTTCAATTAATAAAA 279
QY 185 CCATTACATTAATGCTGAGAGCAAAATTAATTAATGCTAATGCTAATGCTAATGCTAATG 244
DB 280 CCATCACTAATGCTGAGAGCAAAATTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 339
QY 245 ATGCAATTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 340 AAACCAATTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399
QY 305 TGGAGATTAATCTTTGCTCAAGTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 400 TAGAGCTACTCTTTGCTCAAGTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
QY 365 GCTTAATCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
DB 460 GTCGATTAATCAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 519
QY 425 GAATTAATTAATCAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 484
DB 520 GAATTAATTAATCAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 579
QY 485 AAATCTGAGGCTTTTCTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTA 544
DB 580 AAATCTGAGGCTTTTCTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTA 639
QY 545 AGTACATTAATGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 604
DB 640 AGTACATTAATGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 699
QY 605 TAAATACGATCACTTTGATGCTGGAATGCCACCATTAACAAATATGCGACCTTTATGG 664
DB 700 TGAATACATCACTCAATCAATGTTGAGATCCACCATTAACAAATATGCGACCTTTATGG 759
QY 665 GAGGCTTTTCTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 724
DB 760 GAGGCTTTTCTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 819
QY 725 GAGTGAATGAATCAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 784
DB 820 GAGTGAATGAATCAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 879
QY 785 CAACCTTA 791
DB 880 CAACCTTA 886
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RESULT 2
US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234
GENERAL INFORMATION:

```
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for Phytolacca
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana L.
IMMEDIATE SOURCE:
CLONE: PAP
US-08-342-786B-1
```

Query Match 67.4%; Score 534.2; DB 2; Length 1195;
Best Local Similarity 79.9%; Pred. No. 1.9e-150;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

```
QY 5 TAAATACGATCACTTTGATGCTGGAATGCCACCATTAACAAATATGCGACCTTTATGG 64
DB 100 TGAATACATCACTCAATCAATGTTGAGATCCACCATTAACAAATATGCGACCTTTATGG 159
QY 65 AATCTCTTGTAAATCAAGCAAGATCCAAATCTAAATGCTAATGCTAATGCTAATGCTAATG 124
DB 160 ATGATCTTCTTAATGAGAGCAAGATCCAAATGCTAATGCTAATGCTAATGCTAATGCTA 219
QY 125 CTGATTAATTAATGACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 184
DB 220 CCAATACAAATATCAAAATCCAAAGTATGTTGTTGAGCTCCAAAGTTCAATTAATAAAA 279
QY 185 CCATTACATTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 244
DB 280 CCATCACTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 339
QY 245 ATGCAATTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 340 AAACCAATTAATGCTGAGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399
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?
? REFERENCE/DOCKET NUMBER: 38-21(10547)A
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (314)537-6099
?
? TELEFAX: (314)537-6047
?
? INFORMATION FOR SEQ ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 1379 base pairs
?
? TYPE: NUCLEIC ACID
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: cDNA
?
US-07-865-169-1

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Query Match	67.2%;	Score 532.6;	DB3;	Length 1379;
Best Local Similarity	79.8%;	Pred. No. 6e-150;		
Matches 628;	Conservative	0;	Mismatches 159;	Indels 0;
				Gaps 0;

QY	5	TTAAATACGATCACCTTGGATGCTGGAAATGCGACCACTTAACTAAATATCCACCTTATG	64
Dp	292	TGAATACGATCATCTACAAATGTTGGAAATACCAACCTTAGCAAAATAGCCACTTTTCTGA	351
QY	65	AATCTCTTCGTAATCGAGCGAAAGATCCAAAATAAAATGCTATGGCATACCAATGCTAC	124
Dp	352	ATGATCTTCGTAAAGAAAGCGAAAGTCCAGCTTTAAATGATAGAAATTAACCAATGCTGC	411
QY	125	CTGATCTCAATTCGACCCCTAAGTACTATATGGTTAACTGACTCAAGTGCAAATCTTAAAA	184
Dp	412	CCAAATCAAAATCAAAATCCAAAGTAGCGTGGTGGAGCTCCAGGTCCAATATAAAAAA	471
QY	185	CCATTACACTAATGCTGAGCGAAATATCTTATACGTATGGGCTATCTGATCCCTTCA	244
Dp	472	CCATCACACTAATGCTGAGCGAAACAAATTTGTATGTATGGGTTATTTCTATCCCTTGG	531
QY	245	ATGGCAATAAATGTCGTTACCATATATTTAATGATATTAACAAGCAGCAAGCACTGATG	304
Dp	532	AAACCAATAAATGTCGTTACCATATCTTAAATGATATCTGAGTACTGAAGCCAAAGATG	591
QY	305	TGAGAAATPACTCTTTCGCTCAAGTTCTAGTTCGTCGTTGCAATGTCATTTAACTACATA	364
Dp	592	TAGGACTACTCTTTGCCCCAATGCAATTCCTCGTGTATGTAATAACATAAATTGATTA	651
QY	365	GCTTATATCCGACCATGGAAGAAAGCAAGTAATAACTCAAGAAATCAAGTCCAATG	424
Dp	652	GTGCATATCCAACTTGGAAATCAAAAGGGAGTAAATCAAGAAAGTCAAGTCCAACTGG	711
QY	425	GAATTCAAATCTCAAGCACTGACACTTGGAAAAATCTCTGAGTGTATCATTTCCCTGTA	484
Dp	712	GAATTCAAATPACTGACAGTAAATTTGGAAAGATTTCTGAGTGCATCTTCACTGAGA	771
QY	485	AAACTGAGGCTTTTTTCTACTGATAGCAATCCAAATGCTTCAAGGCAACCGGATCA	544
Dp	772	AAACCGAAGCCGAATTCCTATTGTTGACATACAAATGTATTCAGAGGCACCAAGATTCA	831
QY	545	AGTACATAGAAACCAAGTCAAGACTAATTTTAAATAGACATTTCAACCTGATCCCAAG	604
Dp	832	AGTACATAGAAATCAAGTGAATACTAATTTTAAACAAGCAATTCACCTTAATCCCAAG	891
QY	605	TAAATTACTTGAGAGAAATGTTGGGCAAAATCTCTGAGGCAATTCACATGCCCAAGATG	664
Dp	892	TACTTAATTTTGCAGAGACATGTTGGGTAAATTTCAACAGCAATTCATGATCCCAAGATG	951
QY	665	GGGCTTATACCAACCACTTGAGGCTAGTGAATGCAAGGTAACCAAGTGAATGTTCTTA	724
Dp	952	GAGTTTATCCCAACTCTCTGAGCTAGTGAATGCAAGGTTGCAAGTGAATGTTGTTGA	1011
QY	725	GAGTGAATGAATCAATCTGATGATGGCACTCTTAAGTACGTTAATGGAACCTGTGAGA	784
Dp	1012	GAGTGAATGAATCAAGCTGATGTAGACCTTAACTAGCTGTGGAGCTGTGAGA	1071
QY	785	CAACTTA	791
Dp	1072	CAACTTA	1078

RESULT 6

US-09-005-273-1
! Sequence 1, Application US/09005273

GENERAL INFORMATION:

TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
AND/OR ANTI-ENZYMAL ACTIVITY IN PLANTS

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 4

ADDRESS: MENTILIK
; ADDRESS: DAVID, KRUMHOLTZ &

CITY: Westfield

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:

```

FILED DATE: 09-JAN-1998

PRIOR APPLICATION DATA:

FILING DATE: 11-JUL-1995

APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-TH-1995

APPLICATIION NUMBER: PCT/US96/111546

FILED DATE: 11-02-1998
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,

TELECOMMUNICATION INFORMATION:

TELEFAX: 908-654-7866

```

; SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs

```

STRANDEDNESS: single

MOLECULE TYPE: CDNA

NAME/KEY:	CDS
-----------	-----

FEATURE:

LOCATION: 225..290
; MS-09-005-273-1

Query Match 67.

US-09-005-273-1

Query Match	67.2%	Score 532.6;	DB 3;	Length 1379;
Best Local Similarity	79.8%;	Pred. No.66-150;		
Matches 628;	Conservative	0;	Mismatches 159;	Indels 0;
				Gaps 0;

QY 5 TAAATACATCACTTTATGCTGGAATGCAACATTAACAAATATGCCACTTTATG 64
Db 292 TGAATACATCATCAATGTTGGAATACACACATTAGCAATATACGCCACTTTCTGA 351
QY 65 AATCTCTGTATCAAGCAAGATCCAAAATGTAATGTAATGCAATGTCAC 124
Db 352 ATGATCTTGTATAGCAAGATCCAACTTTAAATGTAATGCAATGCAATGCTGC 411
QY 125 CTGATCTAATTCGACCCCTAGTACTATTGGTTAAAGCTCGAAGTGCAACTTAAAA 184
Db 412 CCAATACAAATCAATCCAAAGTACGTTGGTTGAGCTCCAAAGGTTCAAAATAAAAA 471

Db 892 TACTTAATTTGCAAGACATGGGGTAAATTTCAACAGCAATTCATGATGCCAAGAATG 951
QY 665 GGGCTTACCCAAACCACTTGAGTAGTGAGTGCAGAAAGTAAACCAAGTGAATATTCTTA 724
Db 952 GAGTTTACCCAAACCTCTGAGCTAGTGAGTGCAGTGGCCAAAGTGAATGTTGA 1011
QY 725 GAGTGATGAATCAATCGTATGTGGCACTCTTAAGTAAATGATGAAGTGA 784
Db 1012 GAGTGATGAATCAACCTGATGTAGCACTTAACTAGCTGGTGGAGCTGTGAGA 1071
QY 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 8
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Ukun, Fatih
APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 67.0%; Score 531; DB 3; Length 1379;
Best Local Similarity 79.7%; Pred. No. 1.8e-149;
Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCTTGTGATGCTGAAATGCCACCATTAACAATATGCCACTTATG 64
Db 292 TGAATACATCATCTTAATGTTGAAATGACCAACATTAAGCAATAGCCACTTTCGA 351
QY 65 AATCTCTGTAATCAAGCAAGAAAGATCCAAACCTAAATGCTATGATGCAATGTAC 124
Db 352 ATGATCTTCTGTAAGCAAGCAAGAAATCCAGTTTAAATGCTATGAAATGCCAATGCTGC 411
QY 125 CTGATACATAATCGACCCCTTAAGTACTTATGTGTTAAGCTCCAGTGCAAACTTAAAA 184

Db 412 CCAATGAATATACAAATCCAAAGTACTGTGGTGAAGCTCCAAAGTTCATAATAAAAA 471
QY 185 CCATTACATTAATGCTGAGACGAATATACCTTAATGCTGATGGGCTATTGATCCCTCA 244
Db 472 CCATCACACTAATGCTGAGACGAACAAATTTGATGATGAGGTTATTCGATCCCTTG 531
QY 245 ATGCAATTAAGTGTGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Db 532 AAACCAATTAATGCTGTACCATATCTTAATATATCTGAGTACTGAACGCAAGATG 591
QY 305 TGGAGATACCTCTTGTCTCAAGTTCAGTTCGCTGTTGCAATGCTCAATTAACATACA 364
Db 592 TAGAGTACTCTTGTGCCAAATGCAATTCGTGTGATGTAATTAATTAATTAATTAAT 651
QY 365 GCTTATATCCAGCAGTGAAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 424
Db 652 GTGATATCCAAATGGAATCAAAAGCGGAGTAAATCAAGAAATGCAAGTCCAACTGG 711
QY 425 GAATTCAAATACCTCAGCAGTGAATGGAATTAATCTGAGTGAATTCATTCCTGTAA 484
Db 712 GAATTCAAATACCTCAGCAGTGAATGGAATTAATCTGAGTGAATTCATTCCTGTAA 771
QY 485 AAATGAGGCTTTTCTTCTACTGTAGCCATCCAAATGTTTGAAGAGCGGCAATTC 544
Db 772 AAACCAAGCGCAATTCCTATTTGTAGCCATTAAGATGATGAGGCAAGATTC 831
QY 545 AGTACATAGAAACCAAGTCAAGATTAATTTAATAGAGATTCATCTGATCCCAAG 604
Db 832 AGTACATAGAAATCAGGTGAATTAATTTTAAACAGACATTCACCTTAATCCCAAG 891
QY 605 TAAATTACTTGGAGGAGAAATGGGGCAAAATCTCTGAGCAATTCACATGCCAAGATG 664
Db 892 TACTTAATTTGCAAGACATGGGGTGAATTTCAACAGCAATTCAGATGCCAAGATG 951
QY 665 GGGCTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTCAAGTGAATGTTCTTA 724
Db 952 GAGTTTACCCAAACCTCTGAGCTAGTGATGCCAGTGGTGCAGATGATGTTGA 1011
QY 725 GAGTGATGAATCAATCGTATGTGGCACTCTTAAGTAAATGAACTGTGAGA 784
Db 1012 GAGTGATGAATCAACCTGATGTAGCACTTAACTAGCTGGTGGAGCTGTGAGA 1071
QY 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 9
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21 (10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match 66.8%; Score 529.4; DB 3; Length 1379;
Best Local Similarity 79.5%; Pred. No. 5.5e-149;
Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

5 TAAATACGATCACCCTTGTGATGCTGGAATGCGACCATTAACAATATGCCACCTTTATG 64
292 TGAATCAATCACTACATCTTGAAGTACCACTTACCAATACGCCACTTTTCGGA 351
65 AATCTCTTGTATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
352 ATGATCTTGTATGAAGCAAGATCCAGTTTAAATGCTATGGAATCAATGCTGC 411
125 CTGATCTATTTGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCACCACTTAAAA 184
412 CCAATCAATATCAATTCCAACACGTTGTTGAGCTCCAAAGTTTCAATTAATAAAAA 471
185 CCATTAACATAATGCTGAGACGAATTAATACGTATGAGGCTATTTGATCCCTTCA 244
472 CCATCAACATTAAGCTGAGACGAATTAATGATGATGAGGTTATTTGATCCCTTTC 531
245 ATGGCAATTAAGTGTGCTTACATATTAATTAATTAACCAACCGAACGACGTATG 304
532 AAACCAATTAATGCTGTTACCATATCTTAATGATATCTCAGATACGAACGCAAGATG 591
305 TGGAGAAATCTCTTTGCTGAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
592 TAAAGACTACTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
365 GCTTATATCCGACCATGAAAGAAAGACAGAAATTAATCAAGAAATCAATGCTCAAT 424
652 GTGATATTCACATTTGATGATCAAAAGCGGAGTAAATCAAAAGTCAAGTCCAACTG 711
425 GAATTAATATCTCAGAGTGAATGGAATTAATCTCTGAGTTGATTCCTCTGTAA 484
712 GAATTAATATCTCAGAGTGAATGGAATTAATCTCTGAGTTGATTCCTCTGTAA 484
485 AAACCTGAGGCTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
772 AAACCGAAGCGAATCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
545 AGTACATAGAGAACCAAGTCAAGTAAATTTTATAGAGATTTACCTGATCCCAAG 604
832 AGTACATAGAGAACCAAGTCAAGTAAATTTTATAGAGATTTACCTGATCCCAAG 891
605 TAAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 664
892 TACTTAATTTGCAAGAGACATGGGTTAGATTTCAACAGCAATTCATGATGCCAAGAT 951
665 GGGCTTACCCAAACCACTTGAAGTATGATGATGATGATGATGATGATGATGATGATGAT 724
952 GAGTTTACCCAAACCTCTGAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1011
725 GAGTGAATTAATCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
1012 GAGTGAATTAATCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1071

QY 785 CAACTTA 791
Db 1072 CAACTTA 1078

RESULT 10
US-09-005-273-3
Sequence 3, Application US/0905273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nigun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

Query Match 66.8%; Score 529.4; DB 3; Length 1379;
Best Local Similarity 79.5%; Pred. No. 5.5e-149;
Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

5 TAAATACGATCACCCTTGTGATGCTGGAATGCGACCATTAACAATATGCCACCTTTATG 64
292 TGAATCAATCACTACATCTTGAAGTACCACTTACCAATACGCCACTTTTCGGA 351
65 AATCTCTTGTATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
352 ATGATCTTGTATGAAGCAAGATCCAGTTTAAATGCTATGGAATCAATGCTGC 411

QY 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTACAGATGCCAAGATG 664
DB 659 TACTTATATTGACGAGACATGGGGTAAGATTCTTCAGGAATTCATGGTCCAGGATG 718
QY 665 GGGCTTTACCCCAACCACTTGAAGTATGATGCGCAAGATGCAAGTATGTTCTTA 724
DB 719 GAGTTTACCCCAATCCTCTCAAGCTAGTGCATGCGCAATGTCGCAATGATGTTGTA 778
QY 725 GAGTGAATGAATCAATCGATGATGTCGACTCTTAAGTACGTTAATGGAACCTGTGGA 784
DB 779 GAGTGAATGAATCAACCTGATGTGTCACTTTAACTAGCTTATGGAGCTGCCAGA 838
QY 785 CAACCTTA 791
DB 839 GAACCTTA 845

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/0A445

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7700

TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 918 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULAR TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Phytolacca insularis* Nakai

TISSUE TYPE: leaf

IMMEDIATE SOURCE:

CLONE: PIP

US-08-319-622A-1

Query Match 58.2%; Score 460.6; DB 2; Length 918;
Best Local Similarity 76.7%; Pred. No. 2,3e-128;
Matches 604; Conservative 0; Mismatches 174; Indels 9; Gaps 3;

QY 5 TAAATGATCACCTTGTATGCTGAAATGCCAATTAACAATATGCCACCTTATGG 64
DB 68 TGAATACATCATCTTACATCTTGTGAAGTACCAATTAAGAACTATGCAACTTTTGAT 127
QY 65 AATCTCTGTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGGCATACCAATGTAC 124
DB 128 A-----CTTGCTACTGAAGCGGAAGATCCAAG--TTATGTGCTATGGAATACATGTGTC 181
QY 125 CTGATCTAATTTGACCCCTTACTATGTTATGTTAAGTCCAAAGTGCAAACTTAAAA 184
DB 182 CCAATATGGAATCAATTCCAAAATACATATGTTGATGCTCCAGGCTTCAAAAGAAGAG 241
QY 185 CCATTAACATTAATGCTGAGACGAATTAATTAACGATGAGGCTATTCATCCCTTCA 244
DB 242 GCATCACATTAATGCTTAAGACGAACAAATTAATGTGATGGGCTATTCATCCCTACA 301
QY 245 ATGGCAATTAAGTGTCTTACCATTAATTAATGATTAACAAGCACGAACGACGTATG 304
DB 302 A---CAATAGGTGTGCTTTCATCTCTTAAGGCTATTCAGGTACTGAACGGAGATG 358
QY 305 TGGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTGTGCAATGTCATTAACAATA 364
DB 359 TAGAGACTACTCTTTCGCCAAATGCCGATTCGTGTGTAAACATTAACATATGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAACTGAAGAAATCAAGTCCAAATTTG 424
DB 419 GTGATATTCGAATGGAATGGAATCAAAAGCAGAGATTAATCAAGATCGAGTCCACTG 478
QY 425 GAAATCAATATCTGACAGTGAATGGAAGAAATCTGTGAGTTGATTCCTGTGA 484
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QY 485 AATGAGGCTTTTCTTCTGATGTCATCCAAATGTTTCAGAGGACGCGCATTC 544
DB 539 GAACCGAAGCTGAATCTTACGTGTAGCCATTAAGATGATCAGGACGAAGATTC 598
QY 545 AGTACATAGAGACCAAGTCAAGACTAATTTTATAGACATTCACCTGATCCCAAG 604
DB 599 AGTACATAGAGATCAAGTGAAGAACTTAATTTAAGACATTCACCTTAATCCCAAG 658
QY 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTGTAGGCAATTCGAATGCCAAGATG 664
DB 659 TACTTATATTGACGAGACATGGGGTAAAGATTCTTCACCAATTCATGGTCCAGGAATG 718
QY 665 GGGCTTTACCCCAACCACTTGAAGTATGATGCGCAAGATGCAAGTATGTTCTTA 724
DB 719 GAGTTTACCCCAATCCTCTCAAGCTAGTGCATGCGCAATGTCGCAATGATGTTGTA 778
QY 725 GAGTGAATGAATCAATCGATGATGTCGACTCTTAAGTACGTTAATGGAACCTGTGGA 784
DB 779 GAGTGAATGAATCAACCTGATGTGTCACTTTAACTAGCTTATGGAGCTGCCAGA 838
QY 785 CAACCTTA 791
DB 839 GAACCTTA 845

RESULT 13

US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Whan

APPLICANT: Lee, Kwan Ho

APPLICANT: Kim, Man Keun

TITLE OF INVENTION: No. 5723326el Genome Coding *Phytolacca* Antiviral

TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: DARBY & DARBY

STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 58.2%; Score 460.6; DB 2; Length 918;
Best Local Similarity 76.7%; Pred. No. 2.3e-128;
Matches 604; Conservative 0; Mismatches 174; Indels 9; Gaps 3;
QY 5 TAAATGATCACCTTGTGATGCTGGAATGCAACATTAACAATATGCCCTTTATGG 64
DB 68 TGAATACCATCATCTACATGTTGGAAGTACACCATTAAGAACTATGCACTTTTGAT 127
QY 65 AATCTCTTGTATCAAGCGAAGATCCAAACTAAATGCTATGCAATACCAATGCTAC 124
DB 128 A----CTTCGTACTGGAAGCGAAGATCCAG--TTATGTGCTATGGAATCCAAATGCTGC 181
QY 125 CTGATCTAATTCGACCCCTAAGTACTTATTTGTTAGTCCAGGTCGAAAGCTTAAAA 184
DB 182 CCAATATTGATCAAAATCCAAATATGTTGTTGAGCTCCAGGTTCAATTAAGAG 241
QY 185 CCAATCACTAATGCTGAGAGCAAAATTAATGATGAGGCTATTCGATCCCTTCA 244
DB 242 GCATCACACTTAATGCTAAGCAAGAAACAATTAATGATGAGGCTATTCGATCCCTACA 301
QY 245 ATGGCAATAGTGTGCTTACCATTAATTAATGATTAACAAGACCGACCTGATG 304
DB 302 A---CAATAGGTGTGCTTACCATTCCTTTAAGGCTACTCAAGTACGAACGCGAATG 358
QY 305 TGAAGATACTCTTGTGCTAAGTCTAAGTCTGTGTTGCAATGTCATTAACATACATA 364
DB 359 TAGAGACTACTCTTGTGCTCAATGCGCAATTCGTGTGTTGTAAGAAACATTAATGATA 418
QY 365 GCTTAATTCGACCAAGGAAAAAGAGCAAGTAATCAAGAAATCAAGTCCAAATGCG 424

DB 419 GTGATATCCAACTTGGAATCAAAAGCAGAGATTAATTCAGAAAGTGCAGTCACTG 478
QY 425 GAATTCAAATATCTCAGAGTGCAGTTCGAAAAATCTTGAAGTGAATCATTCCTGTAA 484
DB 479 GAATTCAAATATCTCAGAGTGCAGTTCGAAAAATCTTGAAGTGAATCATTCCTGTAA 538
QY 485 AAATGAGGCTTTTCTCTAGTGTGATGCTCAATTCGAAATGTTTCAAGAGCGCGATTC 544
DB 539 GATCGAAGCTGAATTCCTCTGTGATGCTCAATTCGAAATGTTTCAAGAGCGCGATTC 598
QY 545 AGTACATAGAGAACCAAGTCAAGCTAATTTAATGAGCAATTCATCCGATCCCAAG 604
DB 599 AGTACATAGAGAACCAAGTCAAGCTAATTTAATGAGCAATTCATCCGATCCCAAG 658
QY 605 TAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGATG 664
DB 659 TACTTAATATTCAGAGACATGGGTGAAGATTTCTTCAGCAATTCATGAGGCCAGATG 718
QY 665 GGGCTTACCCCAACCACTTGAAGTGAATGCAAGGACCAAGTGAATGATGTTCTTA 724
DB 719 GAGTTTACCCCAATCTCTCTAGTGTGATGCTCAATTCGAAATGATGATGTTGA 778
QY 725 GAGTGAATGAATCAATGATGATGCTCACTCTTAAGTACGTTAATGAACTGTGAGA 784
DB 779 GAGTGAATGAATCAATGATGATGCTCACTCTTAAGTACGTTAATGAACTGTGAGA 838
QY 785 CAACCTTA 791
DB 839 GAACCTTA 845

RESULT 14
PCT-US91-05766-1
Sequence 1, Application PC/ITS9105766
GENERAL INFORMATION:
APPLICANT: Rosenblum, Michael
APPLICANT: Kohr, William Jack
APPLICANT: Agarwal, Bharat
TITLE OF INVENTION: Protein Structure of the Plant Toxin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pulbright & Jaworski Patent Department
STREET: 1301 McKinney #5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05766
FILING DATE: 19910814
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/567,220
FILING DATE: 14-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5195 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-3634
TELEFAX: (713) 651-5246
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown

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/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Gelonium multiflorum
/ DEVELOPMENTAL STAGE: Seed
/ TISSUE TYPE: Nut
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..774
PCT-US91-05766-1

Query Match
Best Local Similarity 11.1%; Score 88.2; DB 6; Length 774;
Matches 155; Conservative 75; Mismatches 234; Indels 3; Gaps 1;

QY 308 AGAATCTCTTTCCTCAAGTTCTAGTTCCTGCTTTCGATTCATTAACATAAGTCT 367
DB 296 ABAATACNATHAABAAYCCNVTNTTTCGNGNABACMGNVTTCATTTTGNGN 355
QY 368 TATATCCGACCATGAAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAAATGGGA 427
DB 356 SNTAYCCNMSNTYNGARGNGABARAGCTAYMGNGABACNACNGAYTTNGNATGARC 415
QY 428 TTCAATATCTCAGCATGACATTCGAAAAATCTCTGAGTTGATTCATTCCTGTAAAA 487
DB 416 CATTNNGNATHGNATHAABAAYTNGAYGARAAYGCAATGAYAAATYTAABCCNACNG 475
QY 488 CTGAGCCTTTTCTTCTACTGCTAGTCCATCCAAATGGTTTCAGAGCGAGCGCATTCAGT 547
DB 476 AATATCCNMSNNTYNTNGTNGTATTCATTCATGTTNNGARGCNGCMGTTTACNT 535
QY 548 ACATAGAGAACCAAGTCAAGACTAATTTTATAGAGCATTCACCTGATCCCAAGTAA 607
DB 536 TATATGABAAYCARATHMGNAAYAAATYTCARCAFMGNATHMNCNGCNAAYAAACNA 595
QY 608 TTAACCTTGAGAGAGTGGGCGCAAAATCTCTGAGCAATTCACA--ATGCCAAGATG 664
DB 596 THMSNTNGARAAYARATGGGNAARYTMSNTTTCARATHMGNACNMSGNGCNAAYG 655
QY 665 GGGCTTTACCAACCACTTGAGTATGATGTCACCAAGGTACCAAGTGTATGTTCTTA 724
DB 656 GNATGTTTWSNGARGCNGTNGARYTNGABWNGCNAAYGNAABATATYATGTAACNG 715
QY 725 GAGTGATGAATCAATCTGTATGTGGCACTCTTAAAGTCACTTAAT 771
DB 716 CNGTNGAYCARGTNARCCNAARATGCVTNTTNAATYTGNGAY 762

RESULT 15
US-08-718-904-80
/ Sequence 80, Application US/08718904
/ Patent No. 6037329
/ GENERAL INFORMATION:
/ APPLICANT: Baird, J. Andrew
/ APPLICANT: Chandler, Lois Ann
/ APPLICANT: Sosnowski, Barbara A.
/ TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/718,904
/ FILING DATE: 24-SEP-1996
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/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6037329enbunrg Ph. D., Carol
/ REGISTRATION NUMBER: 39,317
/ REFERENCE/DOCKET NUMBER: 760100.415C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1233 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1230
/ OTHER INFORMATION: /product= "E. coli codon optimized
/ OTHER INFORMATION: FGF-SAP"
US-08-718-904-80
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Query Match
Best Local Similarity 10.4%; Score 82; DB 3; Length 1233;
Matches 349; Conservative 0; Mismatches 380; Indels 9; Gaps 3;

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DB 469 ATGTCATCTTATATACGCTGATCTGTCAACCGACCGCTGTGATACACTGCTTT 528
QY 61 ATGGAATCTCTTCTGATATGAGGAAATCCAAATCTAATATGATAGGATACCAATG 120
DB 529 GTCTGATAGATTCGTATATATGTAAGATCCGAATTTAAATACGCTGACGATAT 588
QY 121 CTACCTGATATTAATTCGACCCCTTAAGTACTATGTTAAGTCCAAAGTCAACCTTA 180
DB 589 GCAATGATTCGCCCCCGCTTAAAGAAAGTCTTCCATTAATCTTAAAGCTTCCG 648
QY 181 AAAACATTATACATTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCGATCC 240
DB 649 GGCATGTCCTCTGCTGGCTTAAAGCGATTAATTTGATGTTGATACGTAACCTGGAG 708
QY 241 TTCAATGCAAT--AAGTGTTCATCAATATTAATGATATTAACAACCGAATCC 297
DB 709 GATTAATCAACATTAACCGTCTTATCTATTTCAAAAGGAAATTAATCTGCTGAATG 768
QY 298 ACTGATGTAAGATATCTTTGCTCAAGTTCATGTTCTGATGCAATATGTCATTAAC 357
DB 769 ACTGATTAATTCGCGAAGCGACTATGCAATCAGAAACCTGGAATATACCAAGAT 828
QY 358 TACAATAGCTTATATCCACATGAAAGAAAGAAAGATTAATCAAGAAATCAAGTC 417
DB 829 TATACATGATTAAGAAAAACGGGCAATTAACCGAGGAGCAAAATCGGCAAAAGTTG 888
QY 418 CAATTGGGAATTCATATCTACAGAGTACATTTGAAAAATCTCTGAGTTGATTCATTC 477
DB 889 GGTCTGGTATTTGACCTGCTGCTGACGTTATAGAGCGGCTCAACAAAAGTCTGTC 947
QY 478 CCGTAAATAGAGGCTTTTTCATCTGTAGCATCAATATGTTTCAAGGAGGAGG 537
DB 948 --AGTGAATAAGAGCTGCTTTTCTGCTGATGCTATTAATGATCTCTGAAGTTGCT 1005
QY 538 CGATTCAATAGATAGAGAACCAAGTCAAGATTAATTTAATAGACATTTACCTGAT 597
DB 1006 CGTTTCGTTACATTCAGAACTTGTGTTACTAAGAACTTTCCGAAACAAATTCAGCTCCGAT 1065
QY 598 CCAAAAGTATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTC--CAAT 654
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QY 655 GCCAAGAAATGGGCTTTTACCAAAACCATGAGCTAGTGGAGCCAAAGSTACCAAGTGG 714
DB 1126 GCCAAAACGCGGATTTTAAACAAAGATTATGACTTGGTTTGGCAAGGTTGCTCAGGTG 1185
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Qy 715 ATAGTCTTAGAGTGAT 732
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GenCore version 5.1.7
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OM protein - nucleic search using frame p2n model

Run on: April 9, 2006, 01:20:32 ; Search time 6004.59 Seconds
(without alignments)
2489.732 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357
Sequence: 1 MINITPDAGNATINKYATP.....DEINRDVALKYNVGTQTT 263

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-Q=/abs/RASSWEB.spool/US09978274/runat_07042006_173032_28388/arp_query.faeta.1
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-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs04
-USRR=US09978274.@CGN_1.1.5548.@runat_07042006_173032_28388 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV -TIMEOUT=120
-WARN -TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_pn:*
8: gb_pr:*
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10: gb_sts:*
11: gb_by:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	792	6	AX427704 Sequence
2	1352	99.6	945	6	AX427702 Sequence
3	1352	99.6	1249	15	PAPAPSRIP X98079 P.americana

4	1332	98.2	786	15	AB071855
5	1312	96.7	1092	6	AX427720
6	1099.5	81.0	783	15	AB071854
7	1052	77.5	882	6	A67183
8	1050	77.4	942	15	AY547315
9	1050	77.4	942	15	AY572976
10	1050	77.4	1164	15	PAPAP
11	1050	77.4	1195	6	A42103
12	1050	77.4	1195	6	I43835
13	1050	77.4	1195	6	I55866
14	1050	77.4	1379	6	AR009535
15	1050	77.4	1379	6	AR136704
16	1050	77.4	1379	6	AX427731
17	1047	77.2	1379	6	AR141172
18	1045.5	77.0	939	15	AY327475
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39	701	51.7	1226	15	CAANTIPR
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41	564	41.6	333	6	AX427708
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44	452	33.3	902	15	AF533516
45	425.5	31.4	1180	15	MCU80072

ALIGNMENTS

RESULT 1
AX427704
LOCUS
DEFINITION Sequence 3 from Patent WO0233107.
ACCESSION AX427704
VERSION AX427704.1 GI:21537816
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1
Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A.3 25-APR-2002;
CAMBRIDGE
FEATURES
LOCATION/Qualifiers
source
1..792
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
1..79
/note="Binding site for primer PS1BP"
misc_feature
1..3
/note="Initiation codon added via PCR primer"
misc_feature
complement(436..462)

misc_feature /note="Binding site for primer PS1SR"
463..492
/note="Binding site for primer PS2BP"
612
variation /note="Nucleotide change from published sequence"
681..686
misc_feature /note="Sequence replacing removed XbaI site"
complement(765..792)
misc_feature /note="Binding site for primer PS2SR"
790..792
/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 1,03e-110 Length: 792
Score: 1357.00 Matches: 263
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-09-978-274A-4 (1-263) x AK427704 (1-792)

QY 1 MetTlaaThrlleThrPheAaPAlaGlyAaAAlaThrlleAaAlyTyTAlaThrPhe 20
DB 1 ATGATTAATACGATCACCCTTGTGATGCTGAAATGCCACATTAACAATATGCCACCTTT 60
QY 21 MetGluSerLeuArgAaGlnAlaLyAaPProLyLeuLyCyTyTgLyileProMet 40
DB 61 ATGGAATCTTGTGTATCAAGCGAAGATCCAAATCAATTAAGCTATGGCATGCCATG 120
QY 41 LeuProAaPThraAaSerThrProLyTyTleuLeuValLyLeuGlnAlaAaAaLeu 60
DB 121 CTACCTGATGATCTAATTCGACCCCTTAAGTACTTATGTGTTAGCTCCAAAGTGCAACTTA 180
QY 61 TyTThrlleThrlleuWetleuAArgAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 80
DB 181 AAAACCAATTACCTTAATGCTGAGACGAATTAACCTTAACGTGAGGCTATTCGATCCC 240
QY 81 PheAaGlyAaAaLyCyAaTgTyThrllePheAaAaPrlleThraAaPrlleThraAaAa 100
DB 241 TTCAATGGCAATAGTATGCTTACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
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DB 301 GATGTGGAGAAATCTCTTGTCTCAAGTTCTGTTCTGTTGCAATGTCATTAACTAC 360
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QY 141 LeuGlyTlleglnleuAaSerAaPrlleGlyTyTllegSerGlyValAaPSePhePro 160
DB 421 TTGGGAATTCAAATACCTCAGCAGTGAATGGAATTAATCTCTGAGTGTGATCTTCCCT 480
QY 161 ValLyThrcGluAaPhePheLeuLeuValAlaTlleglmeTyAaSerGluAaAaAaAaAa 180
DB 481 GTAAAAAATGAGGCTTTTCTTCTAGCTGAGCATCAATGGTTTCAGAGGACGGCGA 540
QY 181 PheLyTyTlleglmeGlnGlnValLyThraAaPheAaAaAaAaAaAaAaAaAaAaAaAa 200
DB 541 TTCAAGTACATAGAAACCAAGTCAGAACTAATTTTAATAGACATTCTACCTGATCCC 600
QY 201 TyAaValTllegAaAaGluGluTyTgLyTyTllegSerGluAaTllegAaAaAaAaAa 220
DB 601 AAAGTAATTAATCTTGAAG 660
QY 221 AaAaGlyAa 240
DB 661 AATGGGAGCTTACCCAAACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
QY 241 LeuAa 260

DB 721 CTAGAGTGAATGAATCAATCGATGTCGACCTCTTAAGTACGTTAATGAACCTGT 780
QY 261 GlnThrThr 263
DB 781 CAGACAACT 789

RESULT 2
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 1 from Patent WO0233107.
DEFINITION AX427702
ACCESSION AX427702.1 GI:21537815
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.AUTHORS
TITLE
JOURNAL
CAMBRIDGE ADVANCED TECH (GB)
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variation /note="Binding site for primer PSXDP"

misc_feature /note="Sequence replacing removed XbaI site"

/note="Binding site for primer PS2SR"

ORIGIN

Alignment Scores:

Pred. No.: 3.46e-110 Length: 945
Score: 1352.00 Matches: 262
Percent Similarity: 100.0% Conservative: 0
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Query Match: 99.6% Indels: 0
DB: Gaps: 0

US-09-978-274A-4 (1-263) x AK427702 (1-945)

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DB 133 GAATCTCTGTAATCAAGGAAAGATCCAAATCAATTAATGCTATGCAATCAATGCTTA 192
QY 42 ProAaPThraAaSerThrProLyTyTleuLeuValLyLeuGlnGlnAlaAaAaAaAa 61
DB 193 CCGAATACATTAATTCGACCCCTTAAGTACTTAATGTTTAACTCCAAAGTGCAGAAACCTTA 252
QY 62 ThrlleThrlleuWetleuAArgAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 81
DB 253 ACCATTACATTAATGCTGAGCAAGAAATTAATTAATGCTGATGAGTATCTGATCCCTTC 312
QY 82 AaAaGlyAa 101
DB 313 AATGGCAATAGTGTGTTACCATATATTTAATGATATTACAAAGCACCGAAGCACTGAT 372
QY 102 ValGluAaAaThrlleuCyAaSerSerSerSerSerAaAaAaAaAaAaAaAaAaAa 121
DB 373 GTGGAGAAATACCTTGTGCTCAAGTTCTAGTTCGTGTTGCAATGTCATTAACTCAAT 432

QY 122 SerLeuTYrProThrMetGluIuYleYValaGluValaAsnSerArgAsnGluValGlnLeu 141
DB 433 AGCTTATTCGACCATGAGAAAGAAAGAAAGTAACTCAAGAAATCAAGTCCAAATTG 492
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyIleYsIleSerGlyValaAspSerPheProVal 161
DB 493 GGAATTCAAATACATCAGCAGTGAACATTCGAAAAATCTCTGGAGTTGATTCAATCCCTGTA 552
QY 162 LysThrGluValaPhePheLeuLeuValaIleGlnMetValSerGluValaAlaArgPhe 181
DB 553 AAAACGTAGGCTTTTCTTCTACTGTCAGTCAATCCAAATGTTTCAGAGCGACGGGATTC 612
QY 182 LysTrilIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheTYrProAspProlys 201
DB 613 AAGTACATAGAACCAAGTCAAGCTAATTTTAATAGCATTTTCACTGATCCCAAA 672
QY 202 ValIleAsnLeuGluGluIuYleTYrPGLyIleYsIleSerGluValaIleHisAsnAlaIysAsn 221
DB 673 GTAATTAAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCAAAATGCCAAGAT 732
QY 222 GlyValaLeuProIysProLeuGluLeuValaAsnAlaIysGlyThrIleTYrTrpIleValLeu 241
DB 733 GGGGCTTTACCAACCACTGAGCTAGTGAATGCCAAAGTACCAAGTGAATGTTCTT 792
QY 242 ArgValaAspGluIleAsnArgAspValaIleLeuLeuIleTYrValaAsnGlyThrCysGln 261
DB 793 AGAGTGCATGAAATCAATCGTAGTGTGCACTCTTAAAGTACGTTAAAGAACCTGTGAG 852
QY 262 ThrThr 263
DB 853 ACAACT 858

RESULT 3

PAPASRIP

LOCUS PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005

DEFINITION P. americana mRNA for pokeweed antiviral protein.

ACCESSION X98079.1 GI:1707648

VERSION X98079.1 GI:1707648

KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating

SOURCE Protein.

ORGANISM Phytolacca americana (American pokeweed)

Phytolacca americana; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;

Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

AUTHORS

TITLE

Poyet, J.L. and Hoeveler, A.
cDNA cloning and expression of pokeweed antiviral protein from

seeds in Escherichia coli and its inhibition of protein synthesis

in vitro
FRBS Lett. 406 (1-2), 97-100 (1997)

JOURNAL

PUBMED

9109394
2 (bases 1 to 1249)

REFERENCE

AUTHORS

TITLE

Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Moléculaire, UFR Sciences et Techniques, 16

route de Gray, 25030 Besancon Cedex, FRANCE
Revised by author 20-SEP-1996

REMARK

FEATURES

SOURCE

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CDS

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ORIGIN

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polya_site

sig_peptide

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Alignment Scores:

Pred. NO.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-978-274A-4 (1-263) x PAPASRIP (1-1249)
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DB 178 ATAAATACGATCACTTGTGATGCTGGAAGGCCACCAATTAACAATATGCACTTATATG 237
QY 22 GluSerLeuArgAsnGlnAlaIysAspProIleLeuIleCysTYrGlyIleProMetLeu 41
DB 238 GAATCTCTTGATATCAAGGAAAGATCCAAACTTAAATGCTTAGGCAATACCAATGCTA 297
QY 42 ProAspThrAsnSerThrProIleTYrLeuLeuValIleSLeuGlnGlyAlaAsnIleIys 61
DB 298 CCGATATCAATATGACCCCTTAAGTCTTAATGTTAAGCTCCAAAGTGCAAACTTAA 357
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTYrValMetGlyTYrSerAspProPhe 81
DB 358 ACCATTACACTTAAGTGAAGCAAGAAATTAATTAATGATGGCTATTCTGATCCCTTC 417
QY 82 AsnGlyAsnIleCysArgTYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 418 AATGGCAATTAAGTGTCTGATACCATTAATTTAATGATATTAACACACGAAAGCACTGAT 477
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValaIleMetSerIleAsnTYrAsn 121
DB 478 GTGAGAAATACCTTCTGCTCAAGTTCAATGTTCTCGTTCGAATGTCATTAACTACAT 537
QY 122 SerLeuTYrProThrMetGluIuYleYValaGluValaAsnSerArgAsnGlnValGlnLeu 141
DB 538 AGCTTATTCGACCATGAGAAAGAAAGAAAGTAACTCAAGAAATCAAGTCCAAATTG 597
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyIleYsIleSerGlyValaAspSerPheProVal 161
DB 598 GGAATTCAAATACATCAGCAGTGAACATTCGAAAAATCTCTGAGTTGATTCAATCCCTGTA 657
QY 162 LysThrGluValaPhePheLeuLeuValaIleGlnMetValSerGluValaAlaArgPhe 181
DB 658 AAAACGTAGGCTTTTCTTCTACTGTCAGTCAATCCAAATGTTTCAGAGCGACGGCATTC 717
QY 182 LysTrilIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheTYrProAspProlys 201
DB 718 AAGTACATAGAACCAAGTCAAGCTAATTTTAATAGACATTTCACTGATCCCAAA 777
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Qy 222 G|A|A|LeuProLybProLeuG|u|LeuVal|AspAla|ArgG|Y|Thr|Y|StrP|I|LeuVal|Leu 241
Db 838 GGGGCTTTACCAAACTCTAGAGCTAGTGAGATGCCAAAGGTACCAAGTGATAGTTCTT 897
Qy 242 ArgVal|AspG|u|I|LeuAsnArgAspVal|Ala|LeuLeu|Y|StrY|Val|AsnG|Y|Thr|Cy|Gln 261
Db 898 AGAGTGATGAATCAATCGATGATGTGGCACTCTTAAGTACGTTAATGGAACCTGTCAAG 957
Qy 262 ThrThr 263
Db 958 ACAACT 963
RESULT 4
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana pap2 gene for PAP-S2, partial cds.
DEFINITION
AB071855
AB071855.1 GI:19570839
VERSION
KEYWORDS
SOURCE .
ORGANISM Phytolacca americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS 1.
Honojo, E. and Matanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
JOURNAL 2 (bases 1 to 786)
AUTHORS Matanabe, K. and Honojo, E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Matanabe, Saga University,
Department of Applied Biological Sciences, Honojo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watakei@cc.saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)
FEATURES
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Query Match: 98.2% Indels: 0
DB: 15 Gaps: 0
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Qy 262 ThrThr 263
Db 781 GCCACT 786
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AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION
AX427720
AX427720.1 GI:21537829
VERSION
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1.
Neelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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 DEFINITION Phytolectase americana papai gene for PAP-S1, partial cds.
 ACCESSION AB071854
 VERSION AB071854.1 GI:19570837
 SOURCE
 ORGANISM
 . Phytolecta americana (American pokeweed)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolectaceae; Phytolecta.
 REFERENCE
 AUTHORS 1
 TITLE Honjo, E. and Watanabe, K.
 JOURNAL Cloning of genomic DNA encoding two types of pokeweed antiviral
 REFERENCE protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
 AUTHORS their recombinant proteins with other PAP isoforms
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 783)
 REFERENCE Watanabe, K. and Honjo, E.
 AUTHORS Direct Submission
 TITLE Submitted (19-SRP-2001) Keiichi Watanabe, Saga University,
 JOURNAL Department of Applied Biological Sciences, Honjo-machi, Saga city,
 Department of Applied Biological Sciences, Honjo-machi, Saga city,
 Saga 840-8502, Japan (E-mail: wateke@cc.saga-u.ac.jp,
 Tel:81-952-28-8774, Fax:81-952-28-8774)
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 ORIGIN
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 Best Local Similarity: 83.2% Mismatches: 30
 Query Match: 81.0% Indels: 1
 DB: 15 Gaps: 1
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 Oy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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QY 62 ThrIleThleuMeleuArgArgaanaenLeuTyValMeclYTySerAapProPhe 81
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QY 262 ThrThr 263
DB 778 GCCACT 783

RESULT 7
LOCUS A67183 882 bp DNA linear PAT 05-MAY-1999
DEFINITION Sequence 1 from Patent EP0808902.
ACCESSION A67183
VERSION A67183.1 GI:4756167
KEYWORDS
SOURCE Phycolacca insularis
ORGANISM Phycolacca insularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 882)
REFERENCE
AUTHORS Moon,Y., Choi,J., Yun,Y., Jin,J., Hong,B., Lee,J., Choi,K., Lee,J.,
Song,S., Choi,Y., Kim,C. and Kim,M.
Novel genes encoding antiviral proteins of Phytolacca insularis
Nakai and recombinant microorganisms expressing the same proteins
J. JINRO LTD (KR)
Other publication JP 9308489 19971202
Other publication CA 2186303 19971123
Other publication AU 6570696 19971127.
FEATURES
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ORIGIN

Alignment Scores:
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Score: 1052.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.5% Indels: 0
DB: 6 Gaps: 0
US-09-978-274A-4 (1-263) x A67183 (1-882)

QY 1 MetIleAsnThrIleThrPheAspAlaGLyAsnAlaThIleAsnLysTyValaThrPhe 20
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QY 21 MetGLuSerLeuArgaenGLuAlaLysAapProLysLeuLysCyAArgTyHsIlePcomet 40
DB 61 CTGGATATCTTCTGTATATAGCAAAAGATCCAAAGTTTAAATGCTATAGCAATCCAAATG 120
QY 41 LeuProAapThrAasnerThrProLysTyLeuLeuValyLysLengluAlaAsnLeu 60
DB 121 TTGCCCAATACCAATCAATCAATGATGCTGTTGCTTAAGCTCAAGTTCAAATGAA 180
QY 61 LysThrIleThleuMeleuArgArgaanaenLeuTyValMeclYTySerAapPro 80
DB 181 AAAACCATCACTAATGCTGAGACGAAACAAATTTGTATGATGAGGCTAATCTGATCCC 240
QY 81 PheAsnGLyAsnLysCyAArgTyHsIlePheAsnAspIleThSerThrgIuAgtTn 100
DB 241 TTTGATACCAATAGTGTGCTTACATCTTTAATGATATCTACAGTCTGACCCCA 300
QY 101 AspValGLuAsnThreLeuCySerSerSerSerSerArgValAlaMeSerIleAenTy 120
DB 301 GATGTAGACATCACTCTTGCCCAATCCCAATTCCTCGTGTATGATTAACATTAATCTAT 360
QY 121 AasnSerLeuTyProThMetGluValyValaGLuValaAsnSerArgaenGLuValGln 140
DB 361 GATAGCATATCCCAATTTGAAATCCAAAGCGGAGTAAATTCAGAAAGTCAAGTTCA 420
QY 141 LeuGLyIleGLIleuSerSerAepIleGLyValIleSerGLyValaAspSerPhePro 160
DB 421 CTGGGAATTCAAATCTCGACAGTGCATTTGAAAGATTTCTGGGTGACGTCATTCCT 480
QY 161 ValyLysThrGLuAlaPhePheLeuValAlaIleGlnMeValSerGLuAlaAlaArg 180
DB 481 GAGAAAGTCGAAGCTGAATTCCTAGCTGATGACATCAATGATGATCAAGGAGCAAGA 540
QY 181 PheLysTyTlleGLuBenglnValyLysThrAenPheAsnArgAlaPheTyProAapPro 200
DB 541 TTCAGTACATAGAGATAGGTGAGAAAGAAATTTTAACAGAGCATTCAACTTAATCCC 600
QY 201 LysValIleAsnLengluGLuLysTyTPGIlyLysIleSerGLuAlaIleHsAsnAlaLys 220
DB 601 AAAGTACTTAATTTGGAAAGACATGGGTGAATTTCTACAGCAATTCATGATGCCAAG 660
QY 221 AasnGLyAlaLeuProLysProLeuGLuLeuValaAspAlaLysGLyThrySTPleVal 240
DB 661 AATGAGTTTACCCCAACCTCGAGTATGAGATGCAAGTGTGCCAATGAGTGGT 720
QY 241 LeuArgValaAspGLuIleAsnArgaPheValAlaLeuLysTyValaBengIyThrCyGln 260
DB 721 TTGAGGTGTAGATATCAAGCTGATGACCTTAACACTTAAGTATGATGAGAGCTGC 780
QY 261 GlnThr 262
DB 781 CAAACA 786

RESULT 8
LOCUS AY547315 942 bp DNA linear PLN 13-JUL-2005
DEFINITION Phytolacca americana antiviral protein gene, complete cds.
ACCESSION AY547315
VERSION AY547315.1 GI:44889055

Alignment Scores:

Pred. No.: 1,66e-83 Length: 942
 Score: 1050.00 Matches: 200
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 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.4% Indels: 0
 DB: 15 Gaps: 0

US-09-978-274A-4 (1-263) x AY572976 (1-942)

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DB 127 AATGATCTTCGTATGAGCGAAAGATCCAGTTTAAATGCTATGAAATACCAATCTG 186

QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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DB 187 CCCAATACAAATACAAATCCAAAGTACGTGTGGTTCAGCTCCAAAGTTCAAATTAATAAAA 246

QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
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DB 247 ACCATCACTAATGCTGAGACGAAACAAATTTGATGTGATGGTATTCGATCCCTTT 306

QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
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DB 307 GAACCAATTAATATGCTGTTCCATATCTTTATGATATCTCAGGTACTGAACCGCAAGAT 366

QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
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DB 367 GTGAGACACTACTCTTGGCCCAATGCTGATTCGTGTAGTAAACATTAACCTTGAT 426

QY 122 SerLeuTyrProThrMetGlyLysValGluValAsnSerArgAsnGlnValGlnLeu 141
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DB 427 AGTCGATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAACTCAAGTCCAACTG 486

QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
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DB 487 GGAATTCAAATATCTCCACAGATATATTGGAAGATTTCTGAGTGAATCATCACTGAG 546

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DB 727 GAGGTTTATCCCAAACTCTCGAGTAGTGATGCCAGTGTCCAAAGTGATAGTGTG 786

QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
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QY 262 ThrThr 263
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DB 847 ACAAAT 852
  
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RESULT 10

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
 LOCUS PAPAP
 DEFINITION P. americana PAP gene for anti-viral protein.
 ACCESSION X55383
 VERSION X55383.1 GI:20421

KEYWORDS

antiviral protein; cell wall protein; PAP gene; ribosome
 inactivating protein.

SOURCE

Phytolacca americana (American pokeweed)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 (bases 1 to 1164)
 Ian O., Chen Z.C., Antoniw J.F. and White R.F.
 Isolation and characterization of a cDNA clone encoding the
 anti-viral protein from Phytolacca americana
 Plant Mol. Biol. 17 (4), 609-614 (1991)

JOURNAL

1912488

PUBMED

2 (bases 1 to 1164)

AUTHORS

Antoniw J.F.

TITLE

Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops
 Research, Dept. of Plant Pathology, Rothamsted Experimental
 Station, Harpenden, Herts, AL5 2JQ, UK

FEATURES

source

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gene

CDS

ORIGIN

Alignment Scores:

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 Query Match: 77.4% Indels: 0
 DB: 15 Gaps: 0

US-09-978-274A-4 (1-263) x PAPAP (1-1164)

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QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
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DB 128 AATGATCTTCGTATGAGCGAAAGATCCAGTTTAAATGCTATGAAATACCAATGCTG 187

QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
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DB 248 ACCATCACTAATGCTGAGACGAAACAAATTTGATGTAGTGGTATTCGATCCCTTT 307

QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
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DB 308 GAACCAATTAATGCTGTTACCAATATCTTTAATGATATCTCAGGTACTGAACGCAAGAT 367
  
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Qy 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrIleTyrIleValLeu 241
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Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuIleTyrValAsnGlyThrCysGln 261
Db 819 AGAGTGAATGAAATCAACCTGATGTAGCACTTAACCTAGTTGGTGGAGCTGTGAG 878
Qy 262 ThrThr 263
Db 879 ACAACT 884

RESULT 14
AR009535 1379 bp DNA linear PAT 04-DEC-1998
LOCUS AR009535
DEFINITION Sequence 1 from patent US 5756322.
ACCESSION AR009535
VERSION AR009535.1 GI:3968340
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.B.
TITL Pokedeod antiviral protein mutants
JOURNAL Patent: US 5756322-A 1 26-MAY-1998;
FEATURES
source location/Qualifiers
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Alignment Scores:
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Score: 1050.00 Matches: 200
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Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AR009535 (1-1379)

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Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIlePheMetLeu 41
Db 351 AATGATCTTCGTATGAAAGCAAGATCCAACTTAAATGCTATGGAATCCAAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTAATGCTGAGACGAAACAAATTTGATGAGGGGTTATCTGATCCCTT 530
Qy 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATAAATGCTGATACCAATATCTTAAATGATCTCAAGTACGAAACGCAAGAT 590
Qy 102 ValGluAsnThrLeuLysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 591 GTAAAGCTACTCTTCTCCCAAAAGCCAAATCTGCTGTAGTAAACATTAACCTTGAT 650
Qy 122 SerLeuTyrProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTGAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 710
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyValIleSerGlyValAspSerPheProVal 161

Db 711 GGAATCAAAATACTCGACATTAATATGAAAGATTTCTGAGATGATGATCATTCAGTAC 770
Qy 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
Db 771 AAAACCAAGCCGAATTCCTAATGGTAGCCATCAAAATGGATCAAGGACGAAGATTC 830
Qy 182 LysTyrIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheTyrProAspProLys 201
Db 831 AAGTACATAGAGATCAAGTGAAGAACTAATTTTAACAGAGCTTCAACCTTAATCCCAA 890
Qy 202 ValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 891 GTACTAATTTGCAAGACAGATGGGTTAAGATTTCAACAGCAATTCATGATGCCAAGAT 950
Qy 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrIleTyrIleValLeu 241
Db 951 GGAGTTTAAACCAACCTCTGAGCTATGATGCACTTAAACCTAGTTGGTGGAGCTGTGAG 1010
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuIleTyrValAsnGlyThrCysGln 261
Db 1011 AGAGTGAATGAAATCAACCTGATGTAGCACTTAAACCTAGTTGGTGGAGCTGTGAG 1070
Qy 262 ThrThr 263
Db 1071 ACAACT 1076

RESULT 15
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LOCUS AR136704
DEFINITION Sequence 1 from patent US 6137030.
ACCESSION AR136704
VERSION AR136704.1 GI:14477376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.B.
TITL Pap mutants that exhibit anti-viral and/or anti-fungal activity in
JOURNAL plants
FEATURES
source location/Qualifiers
1..1379
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/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.54e-83 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AR136704 (1-1379)

Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleTyrAlaThrPheMet 21
Db 291 GTGAATCATCATCTACATCAATGTTGGAAGTACCACTTACCAATACGCACTTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIlePheMetLeu 41
Db 351 AATGATCTTCGTATGAAAGCAAGATCCAACTTAAATGCTATGGAATCCAAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTAATGCTGAGACGAAACAAATTTGATGATGAGGGTATCTGATCCCTT 530

GenCore version 5.1.7
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Run on: April 9, 2006, 00:56:13 ; Search time 697.998 Seconds
(without alignments)
2511.204 Million cell updates/sec

Title: US-09-978-274A-4
Perfect score: 1357
Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALKYVNGTCQTT 263

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: genesegn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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9	1047	77.2	1378	12	ADG76061	ADG76061 American
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11	1044	76.9	1164	11	ADM74765	ADM74765 HIV-1 inh
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13	1042	76.8	1378	6	AAD42739	AAD42739 Pokeweed
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17	1014.5	74.8	2472	2	AAQ34967	AAQ34967 Pokeweed
18	977.5	72.0	2369	2	AAT99557	AAT99557 PhytoIacc
19	977.5	72.0	2369	2	ABA96543	ABA96543 PhytoIacc
20	862.5	63.6	918	2	AAQ64893	AAQ64893 Antiviral
21	862.5	63.6	918	2	AAT04782	AAT04782 DNA pJMC2
22	793	58.4	465	6	AAD42717	AAD42717 Pokeweed
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26	349	25.7	765	3	AAD61131	AAD61131 DNA encod
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38	341	25.1	804	9	ACD67205	ACD67205 Common so
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ALIGNMENTS

RESULT 1
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ID AAD42716 standard; DNA; 792 BP.
XX
AC AAD42716;
XX
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed mature PAP-S protein encoding DNA.
XX
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW gene; ds.
XX
OS PhytoIacca americana.
XX
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XX 14-OCT-2000; 2000GB-00025217.
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XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25919.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 2; Page 76; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is pokeweed mature PAP
XX CC -S protein encoding DNA
XX
XX Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2.03e-141 Length: 792
XX Score: 1357.00 Matches: 263
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-978-274A-4 (1-263) x AAD42716 (1-792)
XX
XX 1 MetIleAsnThrIleThrPheAspAlaGluValAsnSerArgAsnGlnValGln 20
XX 1 ATGATTAATATGATGATCCTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60
XX
XX 21 MetGluSerLeuArgAsnGlnAlaValAspProLysLeuLysCysTyrGlyIleProMet 40
XX 61 ATGAAATCTCTTGTGATATCAAGGAGAAAGATCAAAATCAAAAGCTATGACATACCAATG 120
XX
XX 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
XX 121 CTACCTGATCTATATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAAACTTA 180
XX
XX 61 LysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
XX 181 AAAACCATTAACATAATGCTGAGACGAAATTAATCTTAAGTGGCTATTTCTGATCCC 240
XX
XX 81 PheAsnGlyValAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
XX 241 TTCATATGGCAATATAGTGTCTTACCATATATTTAATGATATTTCAAGCACCGAAGCACT 300
XX
XX 101 AspValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyr 120
XX 301 GATGTGAGAAATATCTTGTCTCAAGTTCTAGTTCTCGTGTGCATGTCATTAACTAC 360
```

```
QY 121 AsnSerLeuTyrProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTATATTCGACCATGAGAAAGCAAGGATTAATCTCAAGAAATCAAGTCCAA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro 160
DB 421 TTGGGAATTCAAATACCTACGACGATGACATGAGAAATCTCTGAGATTTGATTCCTCC 480
QY 161 ValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
DB 481 GTAAAACTGAGCTTTTCTTACTGTGATGCCATCCAAATGATTTCAAGGACGCGCA 540
QY 181 PheLysTyrIleGluLeuAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspPro 200
DB 541 TTCAGATACATAGAGAACCAAGTCAGACATTAATTTAATGACATTCCTGATCCC 600
QY 201 LysValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 220
DB 601 AAAGTATTAATCTTGAGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCAAATGCCAAG 660
QY 221 AsnGlyValAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTyrIleVal 240
DB 661 AATGGGCTTTACCCAAACCATTTGAGCTAGTGAGTCCAAAGTATCCAAAGTGAATGTT 720
QY 241 LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCys 260
DB 721 CTAGAGTGAATGAATCAATGCTGATGTCGACTCTTAAAGTAACTTAATGAGAACTGT 780
QY 261 GlnThrThr 263
DB 781 CAGACAACT 789
XX
XX RESULT 2
XX AAD42715
XX ID AAD42715 standard; DNA; 945 BP.
XX
XX AC AAD42715;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE pokeweed pro-PAP-S protein encoding DNA.
XX
XX KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX gene; ds.
XX
XX OS Phytolacca americana.
XX
XX FH Key
XX FH Location/Qualifiers
XX FT 1..945
XX FT /*tag= a
XX FT /product= "Pro-PAP-S protein"
XX FT primer_bind
XX FT 1..24
XX FT /*tag= b
XX FT /bound_moiety= "Primer PS1BF"
XX FT complement(735..776)
XX FT /*tag= c
XX FT /bound_moiety= "Primer PSXDR"
XX FT primer_bind
XX FT 736..777
XX FT /*tag= d
XX FT /bound_moiety= "Primer PSXDF"
XX FT m18c_feature
XX FT 750..759
XX FT /*tag= e
XX FT /note= "Sequence replacing removed XbaI site"
XX FT primer_bind
XX FT complement(922..945)
XX FT /*tag= f
XX FT /bound_moiety= "Primer PS28R"
XX
XX PD MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
```

XX 14-OCT-2000; 2000GB-00025217.
PR (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PA Thomas CUR, Mcpherson MJ, Atkinson HU, Neelam A;
PI WPI; 2002-489891/52.
XX P-PSDB; AAE25918.
DR
XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 24; Page 73-74; 87pp; English.
PS
XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC protein encoding DNA
XX
SQ Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 9.36e-141 Length: 945
Score: 1352.00 Matches: 262
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.6% Indels: 0
DB: 6 Gaps: 0
US-09-978-274a-4 (1-263) x AAD42725 (1-945)
QY 2 IleanthrilethrpheaspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
Db 73 ATAAATCGATCAGCTTGTGATGCTGAAATGCCACCTTAACAAATATGCGACCTTATG 132
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
Db 133 GAATCTCTGCTATCAAGGAAAGATCCAAATTAATCTATGGCATTCCAATGCTA 192
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 193 CCTGATCTAATTCGACCCCTTAAGTACTTATGGTTAAGCTCCAAAGTGCAAACTTAAA 252
QY 62 ThrIleThrMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 253 ACCATTACACTAATGCTGAGACGAATTAATTAACGATGGCTATTCGATCCCTTC 312
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 313 AATGCAATAGTCTGCTACCATATATTAATGATTAACAACACCGAAGCACTGAT 372
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 373 GTGAGAAATCTCTTCTCTCAAGTTCTAGTCTCGTGTGCAATGTCATTAACTACAAAT 432
QY 122 SerLeuTyrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
Db 433 AGCTTAATATCCGACATGAGAAAGAAAGCAAGATTAATCAAAATATCAAGTCCAAATG 492
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
Db 493 GGAATTCAAATATCTCAAGATGACATTCGAAATATCTCTGAGATGATTCATTCCTGTA 552
QY 162 LysThrGluLysPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
Db 553 AAAACTGAGGCTTTTCTTACTGTGATCCATTCAAATGTGTTTCAGAGGCGCGCATTC 612

QY 182 LysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
Db 613 AAGTACATAGAGAAACCAAGTCGAATTAATTTATAGACATCTACCTGATCCAAA 672
QY 202 ValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 673 GTATTAATTTGAGGAGGAGAGTGGGCAAAATCTCTAGGCAATTCACATGCCAAGAT 732
QY 222 GlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
Db 733 GGGGCTTTACCCCAACCACTTGACCTGATGATCCAAAGGTACCAAGTGGATGTTCTT 792
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
Db 793 AGAGTGAATGAAATCAATCGATGTGGCACTCTTAAGTACGTTAATGGAACCTGTGCG 852
QY 262 ThrThr 263
Db 853 ACAACT 858
RESULT 3
AAD42729 standard; DNA; 1092 BP.
ID AAD42729
XX
AC AAD42729;
XX
DT 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DE Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW chimeric; rice; cystatin delta D86; N1a protease cleavage site; PCS; ds.
XX
XX Phytolacca americana.
OS Oryza sativa.
OS Tobacco; Etch virus.
OS Chimeric.
OS
XX
FH Key
FT primer_bind
FT 1..29 Location/Qualifiers
FT /tag= a
FT /bound_moiety= "Primer PS1BF"
FT misc_feature
FT 681..686
FT /tag= b
FT /note= "Modified XbaI site"
FT primer_bind
FT 766..786
FT /tag= c
FT /bound_moiety= "Primer PCS-PAPSR"
FT primer_bind
FT 766..806
FT /tag= d
FT /bound_moiety= "Primer PCS-Delta86P"
FT misc_feature
FT 766..786
FT /tag= e
FT /note= "TEV N1a protease cleavage site"
FT primer_bind
FT complement (1066..1092)
FT /tag= f
FT /bound_moiety= "Primer SYNPORTDelta86P"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-G8004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HU, Neelam A;
XX
XX WPI; 2002-489891/52.
DR

XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 PS Disclosure, Page 83; 87pp; English.
 XX
 CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is a fusion DNA. This
 CC sequence comprises pokeweed pro-PAP-S DNA, rice cytosolic delta D86 DNA,
 CC and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
 CC on 29-AUG-2003 to standardise OS field)
 SQ Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,29e-136 Length: 1092
 Score: 1312.00 Matches: 255
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 96.7% Indels: 0
 DB: 6 Gaps: 0
 US-09-978-274a-4 (1-263) x AAD42729 (1-1092)
 QY 1 MetIleAnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPhe 20
 DB 1 ATGATTAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60
 QY 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrTgLyIleProMet 40
 DB 61 ATGGAATCTCTTGATATCAAGCGAAGAAATCCAAATGAATGCTATGCGATACCATG 120
 QY 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
 DB 121 CTACCTGATCTATATTCGACCCCTTAAGTACTTATGTTAGCTTCAAGGTCGCAACCTTA 180
 QY 61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
 DB 181 AAACACCTTACACATAATGCTGAGCGAATAATACGTAATGAGGCTATTTCTGATCCC 240
 QY 81 PheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
 DB 241 TTCAAATGGCAATAGTGTCTTACCATATTTATATGATATTTACACGACCGAAGCACT 300
 QY 101 AspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyr 120
 DB 301 GATGTGGAAATATCTCTTCTCTCAAGTTCTAGTCTCTGCTTGCAATGTCATTAATAC 360
 QY 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
 DB 361 AATAGCTTATATCCGACCATGAAAGAAAGCAAGAAATTAATCAAGAAATCAAGTCCA 420
 QY 141 LeuGlyTyrIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro 160
 DB 421 TTGGGAATTCMAATATCTACAGACGACATTCGAAAAATCTCTGAGTGTGATTCATCCCT 480
 QY 161 ValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
 DB 481 GTTAAATCTAGAGCTTTTCTTACTGCTGAGCCATTCMAATGGTTTCAAGGCGACCGCA 540
 QY 181 PheLysTyrTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspPro 200
 DB 541 TTCAGATCATATAGAACCAAGTCAAGACTAATTTTATATGAGGATTCATCCGATGCC 600
 QY 201 LysValIleAsnLeuGluGlyTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 220

DB 601 AAGTAAATTAATCTTGAGAGAGAAAGTGGCGCAAAATCTCTGAGCAATTCACAAATGCCAAG 660
 QY 221 AsnGlyValAlaLeuProLysPheLeuGluLeuValAspAlaLysGlyThrLysTyrIleVal 240
 DB 661 AATGGGGCTTATACCAACCACTTGAAGTGAATGCGCAAAAGTACCAAGTGAATGTT 720
 QY 241 LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyr 255
 DB 721 CTTAGAGTGAATGAATTCATGCTGATGTCGACTCTTAAATGATAC 765
 RESULT 4
 AAT99556
 ID AAT99556 standard; DNA; 882 BP.
 XX
 AC AAT99556;
 XX
 DT 17-OCT-2003 (revised)
 DT 08-JUN-1998 (first entry)
 XX
 DE Phytoacca insularis antiviral protein gpi2 gene.
 XX
 KM Antiviral protein; gpi2 gene; virucide; transgenic plant;
 KM virus resistance; immunoconjugate; AIDS; cancer; therapy; ss.
 XX
 PH Phytoacca insularis; Nakai.
 FH
 FT Key Location/Qualifiers
 FT CDS 1..882
 FT /tag= a
 FT /trans_except= (pos:715..717, aa:11e)
 FT
 XX
 XX EP808902-A2.
 XX
 XX 26-NOV-1997.
 PD
 XX
 XX 30-SEP-1996; 96EP-00307159.
 PF
 XX
 XX 22-MAY-1996; 96KR-00017404.
 PR
 XX
 PA (JINR-) JIN RO LTD.
 XX
 XX Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J;
 PT Song S, Choi Y, Kim C, Kim M;
 PT
 PT WPI; 1998-001788/01.
 DR
 DR P-PSDB; AAW6773.
 XX
 XX
 PT Antiviral proteins of Phytoacca insularis Nakai and their genes - useful
 PT in plant antiviral agents and immunoconjugates for the treatment of AIDS
 PT and cancer.
 XX
 PS Claim 2; Page 10-12; 26pp; English.
 XX
 CC This polynucleotide comprises the coding region of the Phytoacca
 CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
 CC designated gpi2 (see AAW6773). The gpi2 gene was isolated from leaf
 CC genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
 CC AAT99557), encoding a 35.7 kDa protein (see AAW6774) designated gpi50,
 CC has also been isolated from P. insularis Nakai. Also claimed are vectors
 CC encoding these antiviral proteins and host cells transformed or
 CC transfected with these vectors. E. coli XL1-Blue MRF' gpi2 (KCM-10080)
 CC host cells are claimed, as is a process for preparing antiviral protein
 CC by culturing these cells and purifying the protein from inclusion
 CC bodies. The antiviral proteins and recombinant proteins inhibit protein
 CC synthesis. They can be used as active ingredients of antiviral agents of
 CC plant viruses, and employed in the manufacture of immunoconjugates for
 CC the treatment of AIDS and cancer. The isolated genes can be used in the
 CC breeding of transgenic plants having viral resistance. (Updated on 17-OCT
 CC -2003 to standardise OS field)
 XX
 SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;
 Alignment Scores:

Pred. No.: 2.41e-107 Length: 882
 Score: 1052.00 Matches: 200
 Percent Similarity: 87.0% Conservative: 28
 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.5% Indels: 0
 DB: 2 Gaps: 0

US-09-978-274A-4 (1-263) x AAT99556 (1-882)

QY 1 MetIleAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleuYrValaThrPhe 20
 1 ATGGTGAATACATCAATCAATGTTGAAGTACCAATTAACCAATTAACCAATTAACCAATTTT 60
 QY 21 MetGluSerLeuAAGAsnGlnAlaIleAspProIleuYsCyTYrGlyIleProMet 40
 61 CTGATATATCTCTCTTAATGAAGCAAAAGATCCAAAGTTAAATGATAGAAATCCAAATG 120
 QY 41 LeuProAspThrAsnSerThrProIleuYrIleuValIleuGlnGlyValaAsnIleu 60
 121 TTGCCCAATCAAAATCCAAATCCAAAGTACGTTGGTTAAGTCCAAAGTTCAATGA 180
 QY 61 LysThrIleThrIleuMetIleuArgAsnAsnIleuYrValaMetGlyYrSerAspPro 80
 181 AAAACCAATCACTAAATGCTGAAGCAAAATTTGATGATGGCTATTCGATCC 240
 QY 81 PheAsnGlyAsnIleuYsYrGlyIleIlePheAsnAspIleThrSerThrGluArgThr 100
 241 TTGATATCAATATAGTCTGTTACCAATATCTTAATATCTCAAGTACCAAGCCCA 300
 QY 101 AspValaGluAsnThrIleuYsSerSerSerSerSerArgValaIleMetSerIleAsnYr 120
 301 GATGTAGAGACTACTCTTGGCCAAATCCCAATCTCGTTAGTAAACATTAATCAT 360
 QY 121 AsnSerLeuYrProThrMetGluIleuValaGluValaAsnSerArgAsnGlnValaGln 140
 361 GATATGATCAATCAATCAATGGAATCAAAAGCGGAGTAAATCAAGAACGCAAGTTCAA 420
 QY 141 LeuGlyIleGlnIleuSerSerAspIleGlyIleIleSerGlyValaAspSerPhePro 160
 421 CTGGGATTCATTAATCTCGACAGTACATTTGGAAGATTTCTGGGGTGACCTCATCT 480
 QY 161 ValIleThrGluAlaPhePheIleuValaIleGlnMetValaSerGluValaAlaArg 180
 481 GAGAAAGTCCAGAGCTGAATCTTACTGTGTAGCCATCAATGATCAAGGCGACAGAGA 540
 QY 181 PheIleYrIleGluAsnGlnValaIleThrAsnPheAsnArgAlaPheYrProAspPro 200
 541 TTCAGATCAATGAAGATCAAGGTGAAAACGAATTTTAAACAGAGATTCACCCCTAATCCC 600
 QY 201 LysValaIleAsnLeuGluGluIleuYrGlyIleSerGluAlaIleHISAsnAlaIle 220
 601 AAAGTACTTAATTTGGAGAGACATGGGGTGAAGTTCTTACAGCAATTCATGATGCCAG 660
 QY 221 AsnGlyValaLeuProIleuYrProLeuGluIleuValaAspAlaIleYsGlyIleThrIleVal 240
 661 AATGAGATTTTAACTCGAAACCTCTGAGTTAGTATCCAGTGTGCAATTTGATGATG 720
 QY 241 LeuArgValaAspGluIleAsnArgAspValaIleuLeuYrYrValaAsnGlyIleThrCys 260
 721 TTGAGAGTGTATATCAAGCTGATGTAGCACTTTAAATCACTTATGAGGAGCTGC 780
 QY 261 GlnThr 262
 781 CAAACA 786
 DB
 RESULT 5
 AA245197 standard; DNA; 1379 BP.
 XX
 AC AA245197;
 XX
 DT 29-FEB-2000 (first entry)
 XX

DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
 XX
 KW Pokeweed antiviral protein; PAP, PAP II; antifungal; transgenic plant;
 KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
 KW potato virus X; cucumber mosaic virus; CMV; ss;
 KW tomato yellow leaf curl virus.
 XX
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "PAP"
 FT /note= "Pokeweed antiviral protein"

W09960843-A1.

02-DEC-1999.

21-MAY-1999; 99WC-US011301.

22-MAY-1998; 98US-0086374P.

(RUTP) UNIV RUTGERS STATE NEW JERSEY.

Turner NE, Wang P;

WPI; 2000-062555/05.

P-PSDB; AAY58025.

New antiviral DNA useful for generating transgenic plants resistant to

viruses and/or fungi.

Example, Page 4-5; 43pp; English.

XX
 PS This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
 CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
 CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
 CC catalytically removes a specific adenine residue from a highly conserved
 CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
 CC antiviral protein II (PAP II) protein confers antiviral and or antifungal
 CC activities to plants. A DNA molecule encoding a PAP II protein with an
 CC intact catalytic active site amino acid residue (E102) is useful for
 CC generating transgenic plants. PAP II DNA is useful for generating
 CC transgenic plants (especially cereal crops) through transforming a
 CC protoplast or introducing the DNA directly into a plant part prior to
 CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
 CC activity thus have increased resistance to viruses and/or fungi. Viruses
 CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
 CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
 CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
 CC other plants pests including insects, bacteria and nematodes. PAP II DNA
 CC is also useful for identifying a PAP II protein having reduced
 CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
 CC unlike PAP transgenic plants which are stunted and sterile, PAP II
 CC transgenic plants have a normal and fertile phenotype
 XX

SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.43e-107 Length: 1379
 Score: 1050.00 Matches: 200
 Percent Similarity: 87.0% Conservative: 28
 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.4% Indels: 0
 DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x AA245197 (1-1379)

QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleuYrValaThrPheMet 21
 291 GTGAAATACATCATCTACATATGTTGAAGTACCAATTAACCAATTAACCAATTTCTG 350

```
QY 22 GUSerLeuArgaNglnAlaIyAspProLyLeuIyCyArTygIyIleProMetLeu 41
DB 351 AATGATCTTGGTATGAGGAAAGATCCAAAGTTAAATGATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLySerIleuLeuValIleuGlnIleValIleuLeu 61
DB 411 CCNATPACAAATACAAATCCAAAGTACGTGTGGTGAAGCTCCAAAGTTCAAAATAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
DB 471 ACCATCAGCTATGCTGAGACGAAACAAATTGTATGTATGCTTATCTGATCCCTTT 530
QY 82 AsnGlyAsnLyCyArGtyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATAAATGCTGTTACCATCTTAAGATATCTCAGGTCTGAACCCCAAGAT 590
QY 102 ValGluAsnThrLeuCySerSerSerSerSerValAlaMetSerIleAsnTyraen 121
DB 591 GTRAGACTACTCTTTGGCCCAATGCGATTCTCGTGTATGTAATAAACAATAACTTTGAT 650
QY 122 SerLeuTyProThrMetGluLybAlaGluValAsnSerArgaNglnValGlnLeu 141
DB 651 AGTCGATATCCAAATCGAATGGAATCAAAAGCGAGTAAATCAAGAAGTCAAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLybIleSerGlyValAspSerPheProval 161
DB 711 GGAATTCAAATACTCCACAGTAATATTTGAAAGATTTCTGAGTATGTCATTCACCTGAG 770
QY 162 LybThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 181
DB 771 AAAACCGAAGCCCAATTCCTATTGTAGCATCAATGATATCAAGGCGCAAGATTC 830
QY 182 LybTyriIleGluAsnGlnValIySerThrAsnPheAsnArgAlaPheTyProAspProLy 201
DB 831 AAGTACATGAGAGATCAGGTGAAACCTAATTTTAAACAGACATTCACCTATCCCAAA 890
QY 202 ValIleAsnLeuGlnGluLybTyriIleSerGlnAlaIleHisAsnAlaIyAsn 221
DB 891 GATCTTAATTTTGCAGAGACATGGGGTAAAGATTTCACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLybProLeuGlnIleuValAspAlaIyGlyThrIySerPheIleValLeu 241
DB 951 GGAATTTCACCAACCTCTCGAGTATGAGATGCCAGTGTGCCAAGTGAATAGTGTG 1010
QY 242 ArgValAspGlnIleAsnArgAspValAlaIleuLeuLybTyriValAsnGlyThrCySgln 261
DB 1011 AAGGTGATGAAATCAAGCTGATGTAGACCTCTTAACCTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076
RESULT 6
AAZ59220
ID AAZ59220 standard; cDNA; 1379 BP.
XX
XX AAZ59220;
XX
XX 20-APR-2000 (first entry)
XX
XX Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX Phycolacca americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
```

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XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS ) MONSANTO CO.
XX
XX Kanlewbaki WK, Turner NE, Lodge JK,
XX
XX WPI; 2000-126326/11.
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 6; Fig 4; 30pp; English.
XX
XX This is the coding sequence for the spring leaf form of the pokeweed
XX antiviral protein (PAP) which is used to generate transgenic potato
XX plants. PAP is able to confer resistance to infection by potato virus X
XX (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
XX potato plant or tuber expressing PAP
XX
XX SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 7,43e-107 Length: 1379
XX Score: 1050.00 Matches: 200
XX Percent Similarity: 87.0% Conservative: 28
XX Best Local Similarity: 76.3% Mismatches: 34
XX Query Match: 77.4% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-978-274A-4 (1-263) x AAZ59220 (1-1379)
QY 2 ILeAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLybTyriAlaThrPheMet 21
DB 291 GGAATACATCATCTACATGTTGGAAGTACCAACATACCAATACCAATCTTTCTG 350
QY 22 GUSerLeuArgaNglnAlaIyAspProLyLeuIyCyArTygIyIleProMetLeu 41
DB 351 AATGATCTTGGTATGAGGAAAGATCCAAAGTTAAATGATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLySerIleuLeuValIleuGlnIleValIleuLeu 61
DB 411 CCNATPACAAATACAAATCCAAAGTACGTGTGGTGAAGCTCCAAAGTTCAAAATAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
DB 471 ACCATCAGCTATGCTGAGACGAAACAAATTGTATGTATGCTTATCTGATCCCTTT 530
QY 82 AsnGlyAsnLyCyArGtyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATAAATGCTGTTACCATCTTAAGATATCTCAGGTCTGAACCCCAAGAT 590
QY 102 ValGluAsnThrLeuCySerSerSerSerSerValAlaMetSerIleAsnTyraen 121
DB 591 GTRAGACTACTCTTTGGCCCAATGCGATTCTCGTGTATGTAATAAACAATAACTTTGAT 650
QY 122 SerLeuTyProThrMetGluLybAlaGluValAsnSerArgaNglnValGlnLeu 141
DB 651 AGTCGATATCCAAATCGAATGGAATCAAAAGCGAGTAAATCAAGAAGTCAAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLybIleSerGlyValAspSerPheProval 161
DB 711 GGAATTCAAATACTCCACAGTAATATTTGAAAGATTTCTGAGTATGTCATTCACCTGAG 770
QY 162 LybThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 181
DB 771 AAAACCGAAGCCCAATTCCTATTGTAGCATCAATGATATCAAGGCGCAAGATTC 830
QY 182 LybTyriIleGluAsnGlnValIySerThrAsnPheAsnArgAlaPheTyProAspProLy 201
DB 831 AAGTACATGAGAGATCAGGTGAAACCTAATTTTAAACAGACATTCACCTATCCCAAA 890
QY 202 ValIleAsnLeuGlnGluLybTyriIleSerGlnAlaIleHisAsnAlaIyAsn 221
```


DB 891 GTACTTAATTGCAGAGACATGGGGTAAAGATTTCACACGCAATTCATGATGCCAAGAT 950
QY 222 GAlaAlaLeuProlysProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241
DB 951 GGAATTATACCAAACTCTGAGCTAGAGATGCGACGTGGCCAAAGGATTAATGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsnGlyThrCysGln 261
DB 1011 AGAGTGATGAATCAAGCTGATGTAGCACTTTAACTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076

RESULT 7
AAD42738
ID AAD42738 standard; DNA; 1379 BP.

XX AAD42738;

DT 15-NOV-2002 (first entry)

DB Pokeweed PAP' DNA #1.

KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.

XX Phytolacca americana.

PH Key Location/Qualifiers

FT msc_feature 290..1076

/*tag= a

PN WO200233107-A2.

XX 25-APR-2002.

PF 15-OCT-2001; 2001WO-GB004593.

PR 14-OCT-2000; 2000GB-00025217.

PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

PI Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;

DR WPI; 2002-489891/52.

PT Inducing necrotic effect in specific cells of plant by transforming plant

PT with a chimeric gene encoding pokeweed antiviral protein and a promoter

PS which acts in response to application of specific stimulus to plant.

XX Claim 5; Page 86; 87pp; English.

CC The invention relates to a method of inducing a necrotic effect in

CC specific cells of a plant. The method involves transforming the plant

CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely

CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts

CC in response to the application of a specific stimulus to the plant so as

CC to facilitate expression of the pokeweed antiviral protein in specific

CC cells of the plant. The method is useful for inducing a necrotic effect

CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA

SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.43e-107

Score: 1050.00

Percent Similarity: 87.0%

Best Local Similarity: 76.3%

Query Match: 77.4%

Length: 1379

Matches: 200

Conservative: 28

Mismatches: 34

Indels: 0

Gaps: 0

US-09-978-274A-4 (1-263) x AAD42738 (1-1379)

QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTrpAlaThrPheMet 21

DB 291 GTGAATACCAATCACTTCAATGTTGGAAGTACCAATTCACCAATTAATAGCCACTTTTCG 350

QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTrpGlyIleProMetLeu 41

DB 351 AATGATCTCTTAATGAAGCCAAAGATTCAGATTAAATCTATGAAATACCAATGCTG 410

QY 42 ProAspThrAsnSerThrProLysTrpLeuValLysLeuGlnGlyAlaAsnLeuLys 61

DB 411 CCCAATACAAATACCAATCCAAAGTACGTTGGTGGATCTCCAAAGTTCCAAATAA 470

QY 62 ThrIleThrLeuMetLeuArgAspAsnLeuTrpValMetGlyTrpSerAspProPhe 81

DB 471 ACCATCACTAAATGCTGAGAGCAAAATTTGATGATGAGGGTTATTCGATCCCTTT 530

QY 82 AsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101

DB 531 GAAACCAATTAATGTCGTTACCATATCTTTAATGATATCTCAGGATCTGAACGCCAAGT 590

QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTrpAsn 121

DB 591 GTAGAGACTACTCTTGGCCAAATGCCAATCTCGTGTAGTAAATAACATTAACCTTTGAT 650

QY 122 SerLeuTrpProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGlnLeu 141

DB 651 AGTCGATATCAATGATGGAATCAAAAGCGGAATGAAATCAAGAGTCAGTCCACATCG 710

QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161

DB 711 GGAATTCAATATCTCGACAGTATATGGAAGATTTCTGAGATGATCTCACTCACTGAG 770

QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181

DB 771 AAACCCAAAGCCGAATCTCTATGTTGTTAGCCATACAAATGATATCAGAGGCAAGATTC 830

QY 182 LysTrpTrpIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTrpProAspProLys 201

DB 831 AAGTACATGAGATCAAGTGAATCAAAATTTTAAACAGATCAACCCCAATCCCAAA 890

QY 202 ValIleAsnLeuGluGluLysTrpGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221

DB 891 GTACTTAATTGCAGAGACATGGGGTAAAGATTTCACACGCAATTCATGATGCCAAGAT 950

QY 222 GAlaAlaLeuProlysProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241

DB 951 GGAATTATACCAAACTCTGAGCTAGAGATGCGACGTGGCCAAAGGATTAATGTGTG 1010

QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsnGlyThrCysGln 261

DB 1011 AGAGTGATGAATCAAGCTGATGTAGCACTTTAACTACGTTGGTGGAGCTGTGAG 1070

QY 262 ThrThr 263

DB 1071 ACAACT 1076

RESULT 8

AD105787

AD105787;

15-APR-2004 (first entry)

DNA encoding the wild-type pokeweed antiviral protein.

ribosome depurination; antifungal; antiviral; virocid; anti-HIV;

cytostatic; immunosuppressive; agricultural biotechnology; pharmaceuticals;

medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;

B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;

ds.

XX PhytoIacca americana.
OS
XX
XX Key Location/Qualifiers
FH 225..1166
FT CDS //tag a
FT /product= "wild-type pokeweed antiviral protein"
XX
XX MO200262952-A2.
XX
XX 15-AUG-2002.
XX
XX 01-FEB-2002; 2002MO-US002792.
XX
XX 02-FEB-2001; 2001US-0266396P.
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Turner NE, Hudak KA, Parikh B;
XX
XX WPI; 2003-15656/15.
XX
XX P-PSDB; ADI05788.
XX
XX
XX New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT type PAP, useful in agricultural biotechnology or in the fields of
PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
PT or autoimmune disease.
XX
XX
XX Disclosure; SEQ ID NO 1; 51bp; English.
XX
XX The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
CC that is less toxic than wild-type PAP and exhibits ribosome depurination
CC activity, where the mutant is a central domain mutant or N-terminal
CC domain mutant. The PAP mutants have the following activities: antifungal,
CC antiviral, virecidic, anti-HIV, cytostatic and immunosuppressive. The PAP
CC mutants are useful in agricultural biotechnology as well as in the fields
CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
CC treating mammals with cancer, AIDS, viral infection or autoimmune
CC diseases associated with proliferations of unwanted T-cells or B-cells.
CC The transgenic plants are useful in exhibiting resistance to a broad
CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC sequence represents the DNA encoding the wild-type pokeweed antiviral
CC protein of the invention.
XX
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 7.43e-107 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 10 Gaps: 0
US-09-978-274A-4 (1-263) x ADI05787 (1-1379)
QY 2 IleasnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaTrpPheMet 21
DB 291 GTGAATACATCATCTACATGTTGGAAACCACTTGCAAAATACGCACTTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB 351 AATGATCTTCGTAAATGAAGCAAGATCCAAAGTTTAAAGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 411 CCCAATACAAATACCAATCCAAAGTACGTGTGCTGAGCTCCAAAGTTTCAAAATAAAAA 470
QY 62 ThrIleThrLeuLeuLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACCATCACACTAATGCGAGACGAACAATTTGATGTGATGGGTTATTCGATCCCTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluAlaGlnAsp 101

DB 531 GAAACCAATAAATGCTTACCATATCTTAATGAATCTCAGGTACTGAACCCCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACTCTTTCGCCAATTCGCGTGTAGTAAGAAACATTAACCTTGGAT 650
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCATATATCAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAAGTCCAGTCACTG 710
QY 142 GlyTlleGlnTleuSerSerSerArgLysLysIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATACTCCACAGTAATATGGAAAGATTTCTGAGTGAATGTCATTCAGTGA 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 181
DB 771 AAAACCGAAGCCCAATTCCTATTGTGTAGCCATACAAATGATACAGAGCGCAAGATTC 830
QY 182 LysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATAGAGATCAGGTGAAGAACTAATTTTAAACAGAGCATTCAAACCTAATCCAA 890
QY 202 ValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGCATGGGGTAAAGATTTCAAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
DB 951 GAGCTTTTACCCAAACCTCTCGAGCTAGTGAGCCAGTGCGTCCAAATGAGATGCTTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTGAGTGAATCAAGCTGATGTAGCACTTTAAACTAGCTGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076
RESULT 9
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
AC
AC ADG76061;
XX
XX 11-MAR-2004 (first entry)
XX
XX
XX American pokeweed antiviral protein (PAP) DNA Segid 1.
XX
XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
XX nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX American pokeweed; retroviral.
XX
XX
XX PhytoIacca americana.
XX
XX
XX MO2003106479-A2.
XX
XX 24-DEC-2003.
XX
XX 17-JUN-2003; 2003MO-US019141.
XX
XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.


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Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuYrYValaEnglyThrCyegln 261
Db 819 AGAGTGGATGAATCAAGCTGATGTAGCACTTTAACTACGTTGGTGGAGCTGTCAAG 878
Qy 262 ThrThr 263
Db 879 ACAACT 884

RESULT 13
AAD42739
AAD42739 standard; DNA; 1378 BP.
XX
AC AAD42739;
XX
DT 15-NOV-2002 (first entry)
XX
DE Pokeweed PAP' DNA #2.
XX
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS Phytoacca americana.
XX
FH Key Location/Qualifiers
FT misc_feature 290..1076
FT /tag= a
FT /note= "Mature PAP' sequence"
XX
PN MO200233107-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001MO-GB004593.
XX
PR 14-OCT-2000; 2000GB-00025217.
XX
PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI Thomas CUR, Mepherston MJ, Atkinson HU, Neelam A;
XX
DR WPI; 2002-489891/52.
XX
PT Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
PS Claim 5; Page 86-87; 87pp; English.
XX
CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5 79e-106 Length: 1378
Score: 1042.00 Matches: 199
Percent Similarity: 86.6% Conservative: 28
Best Local Similarity: 76.0% Mismatches: 35
Query Match: 76.8% Indels: 0
DB: Gaps: 0

US-09-978-274A-4 (1-263) x AAD42739 (1-1378)
Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnYrYrAlaThrPheMet 21
Db 291 GTGAAATACATCATCTACATGTTGGAGACCAACCATTTAGCAAAATACGCACTTTCCG 350
Qy 22 GluSerLeuArgAsnGlnAlaValAspProLeuLeuYrYrGlyIlePrometLeu 41

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Db 351 AATGATCTTGTATGAAGCGAAGATCCAAAGTTTAAATGCTATGCAATACCAATCTG 410
Qy 42 ProAspThrAsnSerThrProlyrYrLeuLeuValIleLeuGlnGlyAlaAsnLeuYs 61
Db 411 CCCAATACAAATCAAAATCCAAAGCAGTGTGTGATGAGCTCCAAAGGTTCAAAATAAAAA 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuYrYrValMetGlyYrSerAspProPhe 81
Db 471 ACCATCACTAATGCTGAGACCAAACTTTGTATGTATGGTTTATTTCTGATCCTTT 530
Qy 82 AsnGlyAsnYrCyAspArgYrHsiIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATAAATGCTGTACCATATCTTAATGATATCTCAGGTAAGTCAAGCAAGAT 590
Qy 102 ValGluAsnThrLeuYrYrSerSerSerSerSerSerYrYrAlaMetSerIleAsnYrAsn 121
Db 591 GTAGAGACTACTCTCTTGGCCCAATGCCAATTCGTGTGTAGTAAACATMAACTTTGAT 650
Qy 122 SerLeuYrProThrMetGluYrSlyAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCATATTCCAATTCGATGGAATCAAAAGCGAGTAATCAAGAACTCAGTCCAACTG 710
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyYrYrIleSerGlyYrAlaAspSerPheProVal 161
Db 711 GGAATTCAAATFACTCCACAGTAAATATTGGAAAGATTCTCGAGTGAATGTCATTCACCTGAG 770
Qy 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetYrYrSerGlyAlaIleAspPhe 181
Db 771 AAAACCGAAGCCCAATTCCTATTGTGTAGCCATCAAAATGATCAAGGCAAGCAAGTTC 830
Qy 182 LysYrIleGluAsnGlnValIleYrThrAsnPheAsnArgAlaPheYrProAspProYs 201
Db 831 AAGTACATGAGATCAGATCAGGTAACCAATTTTAACAGAGCATTCAAACCTTAATCCAA 890
Qy 202 ValIleAsnLeuGluGluYrYrGlyYrYrIleSerGluAlaIleHisAsnAlaYrAsn 221
Db 891 GTACTTAATTTGCAGAGACATGGGTAAGATTTCACAGCAATTCATGATGCCAAGAT 950
Qy 222 GluAlaLeuProlyAspProLeuGluLeuValAspAlaYrGlyYrYrYrPheIleValLeu 241
Db 951 GAGGTTTACCCAAACCTCTCGAGCTAGTGAGCCAGTGAGTCCAAAGTGAATAGTTTG 1010
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuYrYrYrValaEnglyThrCyegln 261
Db 1011 AGAGTGGATGAATCAAGCTGTATGTAGCACTTTAACTACCTGTGTGGAGCTGTCAAG 1070
Qy 262 ThrThr 263
Db 1071 ACAACT 1076

RESULT 14
AAZ59221
AAZ59221 standard; cDNA; 1379 BP.
XX
AC AAZ59221;
XX
DT 20-APR-2000 (first entry)
XX
DE Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
KM Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KM resistance; potato virus X; potato virus Y; potato leaf roll virus;
KM tuber; ss.
XX
OS Phytoacca americana.
XX
PN US6015940-A.
XX
PD 18-JAN-2000.
XX
PF 07-APR-1992; 92US-00865169.
XX

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PR 07-APR-1992; 92US-00865169.
XX
XX (MONS ) MONSANTO CO.
XX
XX Kaniewski WK, Turner NE, Lodge JK;
XX WPI; 2000-126326/11.
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 7; Fig 5; 30pp; English.
XX
XX This is the coding sequence for a variant spring leaf form of the
XX pokeweed antiviral protein (PAP') which is used to generate transgenic
XX potato plants. PAP' is able to confer resistance to infection by potato
XX virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
XX the potato plant or tuber expressing PAP'. PAP' varies from PAP
XX (AAZ59220) by mutations L20R and Y49H
XX
SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.8e-106 Length: 1379
Score: 1042.00 Matches: 199
Percent Similarity: 86.6% Conservative: 28
Best Local Similarity: 76.0% Mismatches: 35
Query Match: 76.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x AAZ59221 (1-1379)
QY 2 ILEAATHTTLETHRPHASPAALAGLYASNAATHRIIEASNYTYRVALATHRPHMET 21
DB 291 GTGAAATCAATCATCTCAATGTTGAAAGTCCACCAATACCAATACGCACTTTTCGG 350
QY 22 GUSELEUARGANGINALALYASPPROLYSEULYSYCYTYGTYLLEPROMETLEU 41
DB 351 AATGATCTTCGTATGAAAGCAAGATCCAAAGTTTAAATCTATGGAATCCAAATGCTG 410
QY 42 PROAAPHTRHNSERTHRPROLYSEULYSEULYVALYSEULENGINGLYALASNEULYS 61
DB 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
QY 62 THRIETHEUETLEUARGASASNAASNEUTYRVALMETGYTYRSEATSPROPH 81
DB 471 ACCATCACTAATCTGAGACGAAACAATTTGATGAGGTATTCGATCCCTTT 530
QY 82 ASNGLYASNYSCYATGYTHLSILEPHASNAAPILLETHRSETHRGUARGTTHRASP 101
DB 531 GAAACCAATAAATGCTGTTACCAATATCTTTATGATATCTCAAGTACGAAAGCAAGAT 590
QY 102 VALGLUASANTHRIEUCYSESESESESESESESESESESESESESESESESESESE 121
DB 591 GTAGAGACTACTCTTTGCCCAATGCAATCTCGTGTAGTAAACATTAACCTTGAT 650
QY 122 SETLEUHYRPROTHMETGLULYVALAGLVALASNESEARGANGINVALGLEU 141
DB 651 AGTCGATATCCAAATGAAATCAAAAGCGGAGTAATAAACAAGTCAGTCAACTG 710
QY 142 GLYILEGINILEUSESESESESESESESESESESESESESESESESESESESESE 161
DB 711 GGAAATCAAAATCACTCGCAAGTAATATGAAAGATTTCTGAGAGATGATCACTCAGAG 770
QY 162 LYETHRGUVALAPHEPELEULEUVALALALEGIMETVALSERGUVALAALAPHE 181
DB 771 AAAACCAAGCCGAATTCCTAATGCTAGCCATCAAAATGATATGAGGCGCAAGATTC 830
QY 182 LYETRTILEGLUANGINVALYETHRASNPHASNAAPILAPHETYRPROASP 201
DB 831 AAGTACATTAAGATTCAGTCAAAATCAATTTTAAAGAGATTCAAACCTTAATCCAAA 890
QY 202 VALLEASNEUGLUGLYUTRPGLYLSEISERGLUALAILEHISASNAALALYASN 221

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```

DB 891 GTACTTAATTTGCAAGAGACATGGGTRAAATTTCAACAGCAATTCATGATCCAGAT 950
QY 222 GLVALALEUPROLYSPROLEUGLULEUVALASPAALAYSGLYTHRYSTPILYALU 241
DB 951 GGAGTTTACCCAAACTCTCGAGCTAGTGCAGTGTGCCAAGTGCATGATGTTG 1010
QY 242 ARGVALASPGIUILEASNAASPAVALALEULEUSYTYRVALAANGLYTHRCYAGLN 261
DB 1011 AGAGTGAATGAAATCAAGCCCTGATGTAGCACTTTAAACTAGTGTTGGAGCTGTGAG 1070
QY 262 THRTHR 263
DB 1071 ACAACT 1076

RESULT 15
ADM74751
ID ADM74751 standard; cDNA; 1164 BP.
XX
AC ADM74751;
XX
DE 03-JUN-2004 (first entry)
XX
DE HIV-1 inhibition activity related cDNA.
XX
KW human immunodeficiency virus; HIV-1; tumour; plant;
KW Chinese phytoacta leaf; trans-acting activation factor; Tac; mutant;
KW gene; ss.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT CDS 1..1164
FT /*tag= a
FT /product= "HIV-1 related protein"
XX
PN CN1400220-A.
XX
PD 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
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XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX Peng X, Bai L, Yin B;
XX
XX WPI; 2003-469263/45.
XX
XX P-PSDB; ADM74752.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
XX its expression, separation and purification method in protokaryon.
XX
XX Example 8; Page 9-10; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
XX human immunodeficiency virus (HIV-1) activity, including separation clone
XX of two kinds of cDNA, external mutation, fusion expression in prokaryons
XX and application of the cDNA in preparation of preparation for curing the
XX virus and tumours. One of the described cDNAs is obtained by separation
XX and cloned from a plant Chinese phytoacta leaf, and one from the trans-
XX acting activation factor (Tac) mutant coded by human immunodeficiency
XX virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
XX the HIV-1 inhibition activity of the invention.
XX
SQ Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.94e-106 Length: 1164
Score: 1041.00 Matches: 198
Percent Similarity: 87.0% Conservative: 30
Best Local Similarity: 75.6% Mismatches: 34

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Query Match: 76.7% Indels: 0
DB: 11 Gaps: 0

US-09-978-274A-4 (1-263) x ADM74751 (1-1164)

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DB      289 GTAAATACAAATCAATCTACAAATGTTGGAAAGTACCACCAATGACAAATAGCCACATTTCTG 348
QY      22  GluSerleuArgAsnGlnAlaLysAspProLysleuLysCysTyrglyIleProMetLeu 41
DB      349 GATATATTTCTGTATGAGGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGTTG 408
QY      42  ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB      409 CCCAATACAAATCCAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCCAAATATAAAAA 468
QY      62  ThrIleThrIleuMetLeuArgAsnAsnLeuTyrValMetGlyTyrsAspProPhe 81
DB      469 ACCATCACACTAATGCTGAGACGAAACAAATTTGTATGTATGGCTATTCGATCCCTTT 528
QY      82  AsnGlyAsnLysCysArgTyrglyIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB      529 GATACCAATAAAGTGTCTTACCATATCTTTAGTATCTCAGGTTGAAAGCCAAAGAT 588
QY      102 ValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyAsn 121
DB      589 GTAGAGCTACTGTTGCCCAATCCCAATTCCTGTTAGTAAACATTAATGAT 648
QY      122 SerLeuTyrrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
DB      649 AGTCGATATCCAAATCTGGAATCAAAAGCGGAGTAAATCAAGAACTCAAGTTCAACTG 708
QY      142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
DB      709 GGAATTCAAATTAATCTCCACAGATTAATTTGAAAGATTTCTGAGTGAAGTCACTGAG 768
QY      162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAsnArgPhe 181
DB      769 AAAACCGAAGCCGAATTCCTACTGTTAGCATCAAAATGTTATCAGAGCGAGCAAGATTC 828
QY      182 LysTyrrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrrProAspProLys 201
DB      829 AAGTACATAGGGGAAATCAGGTGAAACTTAATTTTAACAGACATTCATCTTAATCCCAA 888
QY      202 ValIleAsnLeuGluGluLysTyrrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
DB      889 GTACTTAATTTGAAAGAGACATGGGGTAAGATTTCTACAGCAATTCATGATGCCAAGAAAT 948
QY      222 GlyAlaLeuProLysPProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241
DB      949 GGAATTTTACCCAAACCTCTGAGCTAGTGATGCCAGTGCCAAAGTGATAGTGTG 1008
QY      242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrrValAsnGlyThrCysGln 261
DB      1009 AAGAGTGAAATGATCAAGCTGATGTAAGCACTCTTAACATACGTGTGGAGACTGCCAA 1068
QY      262 ThrThr 263
DB      1069 ACAACT 1074
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Search completed: April 9, 2006, 02:22:32
Job time : 703.998 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 4779.97 Seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357

Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALTKYVNGTCQTT 263

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=sh807
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_est2: *
3: gb_est3: *
4: gb_hlc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_ges1: *
10: gb_ges2: *
11: gb_ges3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335.5	24.7	829	7	CN782289 EST00385
2	266.5	19.6	993	2	BR035039 MM02A03 M
3	266.5	19.6	1021	2	BR036639 MP03B03 M
4	263.5	19.4	1033	2	BR036541 MP01B07 M
5	256.5	18.9	816	2	BR035038 MM02A01 M
6	251.5	18.5	639	2	BR037217 MP18B02 M
7	248.5	18.3	837	1	AM053634 L30-1401T

8	245	18.1	649	6	CA838757	CA838757 MCT020B02
9	245	18.1	649	6	CA839330	CA839330 MCT026C11
10	245	18.1	661	6	CA835532	CA835532 MCS038A11
11	245	18.1	671	6	CA839511	CA839511 MCT028D04
12	245	18.1	689	6	CA833333	CA833333 MCS021A09
13	245	18.1	689	6	CA833383	CA833383 MCS021F04
14	239	17.6	841	7	CO121195	CO121195 GR_EB02B
15	235	17.3	903	7	CO103587	CO103587 GR_EB02B
16	225	16.6	639	6	CA838555	CA838555 MCS004G12
17	217.5	16.0	1038	2	BR035546	BR035546 MP03A09 M
18	187	13.8	498	5	BQ588134	BQ588134 E012337-0
19	172.5	12.7	811	2	BE0304055	BE0304055 MG04C05 M
20	171.5	12.6	489	2	BR130330	BR130330 L48-484T3
21	164.5	12.1	662	6	CF227047	CF227047 IH215 sub
22	164	12.1	661	6	CF227046	CF227046 IH202 sub
23	152	11.2	698	6	CA838926	CA838926 MCT021H09
24	151	11.1	405	8	T24255	T24255 CR81345 1am
25	150.5	11.1	267	1	AA856221	AA856221 L30-242T3
26	149.5	11.0	665	6	CF227084	CF227084 IHSBP22 8
27	149	11.0	671	7	CN846973	CN846973 PG07022B0
28	142	10.5	659	7	CN848288	CN848288 PG07019B0
29	140.5	10.4	658	5	BQ583480	BQ583480 E011975-0
30	138.5	10.2	603	5	BQ590856	BQ590856 E012599-0
31	134	9.9	601	6	CA198032	CA198032 SCEZAD107
32	130.5	9.6	659	5	BQ584743	BQ584743 E013262-0
33	128	9.4	1094	4	AY105813	AY105813 Zee maye
34	126	9.3	420	6	CF227009	CF227009 IH149 sub
35	126	9.3	678	6	CA840373	CA840373 MCT03G003
36	125.5	9.2	677	6	CA174183	CA174183 SCJFST100
37	125.5	9.2	680	6	CA198271	CA198271 SCCFEL300
38	124	9.1	546	5	BQ588856	BQ588856 E012534-0
39	124	9.1	667	6	CA838446	CA838446 MCT016F04
40	123	9.1	497	5	BQ488214	BQ488214 31-B8143
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42	120	8.8	644	4	CA838401	CA838401 MCT016B04
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44	117.5	8.7	614	7	CN846558	CN846558 PG07003F0
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ALIGNMENTS

RESULT 1
CN782289 829 bp mRNA linear EST 21-MAY-2004
LOCUS CN782289
DEFINITION EST00385 cgseed Chenopodium quinoa cDNA clone S02022 5' similar to
antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.
ACCESSION CN782289
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
Coles,N.D., Coleman,C.E., Christensen,S.A., Jellian,E.N.,
Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and
Maughan,P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
225 WTDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward

JOURNAL COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

High quality sequence stop: 829.

FEATURES	Location/Qualifiers
source	1. .829

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ORIGIN

Alignment Scores:

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Score:	335.50	Matches: 92
Percent Similarity:	53.5%	Conservative: 39
Best Local Similarity:	37.6%	Mismatches: 95
Query Match:	24.7%	Indels: 19
DB:	7	Gaps: 8

US-09-978-274A-4 (1-263) x CN782289 (1-829)

QY	13	ThrIleAsnLysYrVrlaTrPheMetGluSerLeuAsgAlaGlnAlaLysAspProLys	32
Db	122	ACACAGAAATCTTAAACACCTTTCTGCAAAGTAAACGACCAATCAAGATCAAGC	181
QY	33	LeuLysCyEtyrGlyIleProLeuLeuProAspThrAsnSerThrProLysTyrLeuLeu	52
Db	182	TTTGATGTATAGAAAGAAATCCCAATGATGACCAACCAACCAAGATACATATCTTTTG	241
QY	53	ValLysLeuGlnGlyAlaAsnLeuLysThr-----IleThrLeuMetLeuArgArg	69
Db	242	GTTGACCTTGAACTTAAAAAGATTAAGAAATGAGATTTTCATTACCTTGCTTAAAGTGA	301
QY	70	AsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsnLysCyEaGrTyrHis	89
Db	302	AACGACTTGATGTAGTGGCGCTTCTGCTGAATAATTT---GAGAGCAAGTTCCGGCCGAT	351
QY	90	IlePheAsnAspIleThrSerThrGluAlyThrAspValGluAsnThrLeuCySerSer	109
Db	359	TTCTTTTCCATCTTAAACATT-----GACACCATGTAAGGCAAGAAAGTTT	408
QY	110	SerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLys	129
Db	410	CCAGAAGTTACAGTTTTCATTAATATATACGTATGGGAAAGTTACAGTCAATATGAAAGC	469
QY	130	LysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAsp	149
Db	470	AATGCTGGTACAAAC--CGATTAAAGTTTCCGTGGGGTTTGATTAACCTTAAAACTTAC	529
QY	150	IleGlyLysIleSerGlyValAspSerPhePro-----ValIleThrGluAlaPhe	169
Db	527	ATGCAAAAGGCTATAGGAGATGATCTAAGGCCAAAGATTATAGCAAAATGAAAGCTCG	586
QY	167	PheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsn	186
Db	587	TTCTCTACTACCGAATTCATAATAGTTGGTGGAGAGGCGGACGTTTAAATGATCATCGAGGA	646
QY	187	Gln-----ValLysThrAsnPheAsnArgAlaPheTyrProArgProLysValIleAsn	206
Db	647	AGAGCTATGCTTATCTACAAATCTTAAAC-----AATTATTAATATCTGCG	696
QY	205	LeuGlnGluLysTyrGlyLysIleSerGluAlaIleIleValAsnAlaLysAsnGlyAlaLeu	224
Db	692	TTTGAGAACAAACAGGGAGACTATTTTGCAAAGGCATTCCGAAGCGCTTTAAGAAAGTCAT	751
QY	225	ProLysProLeuGlnLeuValAspAla---LysGlyThrIleTyrTrpIleValLeuArgAla	244
Db	752	CAATCTCGGCTTAANTTTTACATATACCTTAAATGGGATCAACATGGACAGTTTACATCAACATGG	811

Qy	244	AspGluIleAsnArg	248
		::: :::	
Db	812	AGTGATATAAAAAA	826

RESULT 2	
BE035039/c	
LOCUS	993 bp mRNA linear EST 07-JUN-2000
DEFINITION	MMO2A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
ACCESSION	BE035039
VERSION	BE035039
KEYWORDS	BE035039.1 GI:8330048
SOURCE	EST.
ORGANISM	Mesembryanthemum crystallinum (common iceplant)
	Mesembryanthemum crystallinum

ORIGIN

Alignment Scores:

Pred. No.:	3,38e-22	length:	6
Score:	266.50	Matches:	6
Percent Similarity:	56.8%	Conservative:	2
Best Local Similarity:	41.4%	Mismatches:	5
Query Match:	19.6%	Indels:	1
DB:	2	Gaps:	1

US-09-978-274A-4 (1-263) x BE035039 (1-993)

[illegible]

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Db 341 TGTGACACAAATGGAAGGTGATTAAGATTGCCACATTAACCTGACTTGGGATTAATCA 282
Qy 254 sTyR 255
Db 281 GTTC 278

RESULT 3
BE036639
LOCUS BE036639 1021 bp mRNA linear EST 07-JUN-2000
DEFINITION MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:8331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alceaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 1021)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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ORIGIN
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Score: 266.50 Matches: 92
Percent Similarity: 52.28 Conservative: 38
Best Local Similarity: 36.94 Mismatches: 95
Query Match: 19.64 Indels: 26
DB: 2 Gaps: 11

US-09-978-274A-4 (1-263) x BE036639 (1-1021)

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Qy 23 SerleuArgAsnGlnAlaValAspProlyLeuLeuCystrGlyIlePrometLeuPro 42
Db 273 TCTCTCCGAGCTCAACTCTCTGCGC---ACAACCGCAATG-----CAAAATCCC 317
Qy 43 AspThrAsnSerThr-----ProlystrleuLeuVallyLeuGlnGlyAla 58

Db 318 GTGACAGCTCAACCGGACCGGATCTCCAAAGATTGCTGCTGCGACCTCAAAACAAC 377
Qy 59 AsnleuLystrIleThrleuMetleuArgArgAsnleuLytrValMetGlyTrSer 78
Db 378 TCGCAAAAGACCAACACACTCGCAATGACAGTGAACAACCGCTATGTCGTGGCTTACCGC 437
Qy 79 AspProheAsnGlnAlaValleuArgValAspGluIleAsnArgAspValAlaLeuLy 98
Db 438 GACAAAGCT---GGCGAAAAGACCTGCGCAACTCTTACAGATGCTCCACCGTGGT 494
Qy 99 ArgThrAspValGluAsnThrleuCyserSerSerSerSerArgValAlaMetSerIle 118
Db 495 AGG-----AACCACTCTTCAAGGCGCGACGTTGCG-----AACAT 533
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Db 650 ATTAATGAGGACATGTGAGGCGCAAAATCTTGCTGATCTCTATACAGATGTTCTGAGCA 709
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Db 770 CCCGACCCGAAAGTCTGAGTTTGGAGAACATGCGGAAAGATTTCGCAAAATTAATA 829
Qy 217 HisAsnAlaLyAsnGlnAlaLeuProLy-----ProleuGluLeuValAspAlaLy 234
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Qy 235 GlyThrlystrpIleValleuArgVal 243
Db 889 TGTTCACATGGAAGGTGATTAAGGTG 915

RESULT 4
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DEFINITION MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION BE036541
VERSION BE036541.1 GI:8331550
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alceaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 1033)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Location/Qualifiers
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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

ORIGIN

/cissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

Alignment Scores:

Pred. No.:	8,56e-22	Length:	1033
Score:	263.50	Matches:	69
Percent Similarity:	54.1%	Conservative:	36
Best Local Similarity:	35.6%	Mismatches:	68
Query Match:	19.4%	Indels:	21
DB:	2	Gaps:	7

US-09-978-274a-4 (1-263) x BE036541 (1-1033)

```

QY 71 AsnLeuTyValMetGlyTyrSerAspProPheAsnGlyAsnLysCysArgTyrHisIle 90
DB 47 AGCGTCATGTCGTGGCTACCGCGACACACTT--GGCGAAGAACCGTGCACACTTC 103
QY 91 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 110
DB 104 CTAGAGGATGCTCCACAGCTCGCTAGG-----AACAACTCTTCAAGGGGCG 151
QY 111 SerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysLys 130
DB 152 ACGGTTCCG-----AACATTCGCTCGAGGAGGAGTTACATAGCCTTAGAAGAGCT 202
QY 131 AlAGluValAsnSerArgAsnGluValGluLeuGlyIleGluIleLeuSerSerAspIle 150
DB 203 GCAAG--CAAGCCGAAATGCAATAGAGTTAGGTGAATTAACATAGATTGGCATC 259
QY 151 GlyLysIleSerGlyValAspSerPheProValIleThrGluAlaPhePheLeuVal 170
DB 260 GAGTCGGTTTGTGTAAGAACCCGATTAATGGGAGGTTAGGCAAACTTCTGCTAT 319
QY 171 AlaIleGluMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGluVal--Lys 189
DB 320 GCTATACACATGTTCTGTAAGCAGCACGCTTAAGATATTTGTAAGTAAGTGACCA 379
QY 190 ThrAsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyr 209
DB 380 AGTGGGTACATGCTGCTTCATACCCGACCCGAAAGTCTGAGTTGGAGAACATGG 439
QY 210 GlyLysIleSerGluAlaIleAsnAlaLysAsnGlyAlaLeuProLysPro----- 227
DB 440 GGGAAAGTTTCGAGAGATTCATATGACA-----CTTGGCGGAAACCTGCTTGT 450
QY 228 -----LeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
DB 491 ACGAATATTTACCGCGGATTAAGTTACAAATGCTGATGTTCAACATGGAAGTGGAT 550
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyr 255
DB 551 GATGTTGCCACTTAAACCTGATTTGGGATATCAACTTC 592

RESULT 5
BE035038/c 816 bp mRNA linear EST 07-JUN-2000
LOCUS MM02001 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION anti-viral protein, mRNA sequence.
ACCESSION BE035038
VERSION BE035038.1 GI:8330047
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 816)
Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
Perrera,H., Kawasaki,S., McCollough,A., Michaelowski,C.B.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
REFERENCE
AUTHORS

```

TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michaelowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu.

FEATURES
source Location/Qualifiers
1..816
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"
/clone_lib="WM"
/note="Vector: Bluescript SK⁺; Site 1: EcoRI; Site 2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Alignment Scores:

Pred. No.:	4.57e-21	Length:	816
Score:	255.50	Matches:	65
Percent Similarity:	54.4%	Conservative:	28
Best Local Similarity:	38.0%	Mismatches:	59
Query Match:	18.9%	Indels:	19
DB:	2	Gaps:	4

US-09-978-274a-4 (1-263) x BE035038 (1-816)

```

QY 103 GluAsnThrLeuCysSerSerSerSerArg----- 113
DB 786 CAAATTCCTTAAGCATCTTCTACAGTGCATTAAGAAACCTTCTTAAGAGAGCG 727
QY 114 ---ValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysLys 132
DB 726 CCGGTGCAAAACATTCCTCCATTTGGGTGAATATCATAGCTTGAGAAACCTGCGGT 667
QY 133 ValAsnSerArgAsnGluValGluLeuGlyIleGluIleLeuSerSerAspIleGlyLys 152
DB 666 ---CAAGCCGAAACAGTATGACGTGGGGCTGTGTAATAGATTGCCATCGATCA 610
QY 153 IleSerGlyValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIle 172
DB 609 ATTATGTGTAATAAAACGATCGATCGAGAAACCTGAGCCAAATCTTACGATTCGATC 550
QY 173 GluMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGluVal--LysThrAsn 191
DB 549 CAGATGTTTCAGAACACACGCGTTCATTATATGAACTAAGGTGCCGAAAGTGGG 490
QY 192 PheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyrIleVal 211
DB 489 TCACATGCTTCTTCAACCCGATCCGAAAGTATTAATCTTGAGAAACAACTGGGAAAG 430
QY 212 IleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro----- 225
DB 429 ATTTCGATGAGATTCATTAAGTCAGTTACGTCGAAACCACTGCTAATTGTACGAACAT 370
QY 226 ---LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAsp 244
DB 369 TCCCTCGCATTAATCAATGCTGATGTGACCAATGAAAGGTGATTAAGATTGCC 310
QY 245 GluIleAsnArgAspValAlaLeuLeuLysTyr 255
DB 309 ACTATTAACCTGACTTGGGATATCAACTTC 277

RESULT 6
BE037217 639 bp mRNA linear EST 07-JUN-2000
LOCUS MP1802 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein/anti-viral protein, mRNA sequence.
ACCESSION BE037217
VERSION BE037217.1 GI:8332233

```


REFERENCE 1 (bases 1 to 649)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR Primers
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 026 row: C column: 11
 Seq primer: T3 20mer
 High quality sequence stop: 649.
 Location/Qualifiers

FEATURES
 SOURCE 1..649

/organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCT026C11"
 /tissue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="ice plant lambda Uni-Zap XR expression
 library, 5 days 0.5 M NaCl treatment, Crassulacean acid
 metabolism, phase IV (5:30 PM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. NO.: 9.1e-20 Length: 649
 Score: 245.00 Matches: 62
 Percent Similarity: 53.4% Conservative: 24
 Best Local Similarity: 38.5% Mismatches: 61
 Query Match: 18.1% Indels: 14
 DB: Gaps: 4

US-09-978-274A-4 (1-263) x CA839330 (1-649)

QY 103 GluAnthrleuCySerSerSerSerSerValAlaMetSerIleAsnTYrAsnSer 122
 DB 25 GAGAAATCTCTTTCATGAGCAACAGTTGGAACCTTGCTTCMAAGGACCTTACACATCC 84
 QY 123 LeuTYrProThrMetGluValylValAGluValAlaAnSerArgAnGlnValGlnLeuGly 142
 DB 85 TTA-----GAGAAATCTCTTTCATGAGCAACAGTTGGAACCTTGAAGTTAGGG 129
 QY 143 IleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProValys 162
 DB 130 GTGATTAACATGAGTTGCGATCGATCGGTTATGTATGTAAGCATGCACCAAGTCAGAGA 189
 QY 163 ThrGluAlaPhePheLeuLeuValAlaIleGlnMetValIleSerGluAlaAlaArgPheLys 182
 DB 190 AATAGAGGCAAAATCTTGCTGATGATGCAATGATGTTTCTGAAAGCGAAGTTCAG 249
 QY 183 TyrIleGluAnGlnValIleThrAsnPhe-----AsnATGAlaPheTYrProAspPro 200
 DB 250 TATATTGAGATGAGTACAGTACCAAAAGTCGTTAGATTATGAAATGCTTTACCCGACCG 309
 QY 201 LysValIleAsnLeuGlnGluLysIleTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 220
 DB 310 AAATATGCTGCTTTGAGACCAATTTGGGGAAAGATTTCGACGAGATTCAATGAGAGTCT 369
 QY 221 AsnGlyAlaLeuPro-----LysPProLeuGluLeuValAspAlaLys 234
 DB 370 ---GGGGGAAACCTGCTTGTATGAAATCTTCACTCGAATTCGTTAAAGAAACCAAT 426

QY 235 GlyThrLysTyrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 254
 DB 427 GGTGATTCATGACGCTGATGATGATGACTTATGACCTGAAATGGGATCTCAAG 486
 QY 255 Tyr 255
 DB 487 TTC 489

RESULT 10

CA835532 661 bp mRNA linear EST 12-DEC-2002
 LOCUS MCS038A11 160572 ice plant lambda Uni-Zap XR expression library, 5
 DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
 AM). Mesembryanthemum crystallinum cDNA clone MCS038A11 5, mRNA
 sequence.

ACCESSION CA835532
 VERSION CA835532.1 GI:26563297
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum

REFERENCE 1 (bases 1 to 661)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR Primers
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 038 row: A column: 11
 Seq primer: T3 20mer
 High quality sequence stop: 661.
 Location/Qualifiers

FEATURES

SOURCE

1..661
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS038A11"
 /tissue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="ice plant lambda Uni-Zap XR expression
 library, 5 days 0.5 M NaCl treatment, Crassulacean acid
 metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. NO.: 9.35e-20 Length: 661
 Score: 245.00 Matches: 62
 Percent Similarity: 53.4% Conservative: 24
 Best Local Similarity: 38.5% Mismatches: 61
 Query Match: 18.1% Indels: 14
 DB: Gaps: 4

US-09-978-274A-4 (1-263) x CA835532 (1-661)

QY 103 GluAnthrleuCySerSerSerSerSerValAlaMetSerIleAsnTYrAsnSer 122
 DB 36 GAGAAATCTCTTTCATGAGCAACAGTTGGAACCTTGCTTCMAAGGACCTTACACATCC 95
 QY 123 LeuTYrProThrMetGluValylValAGluValAlaAnSerArgAnGlnValGlnLeuGly 142


```

Db      96 TTA-----GAGAAATGCTGCAAAACGACGAGCAAGCATGAGTGGG 140
      143 11leGlnIleuSerSerAapIleGlyLysIleSerGlyValAspSerPheProValys 162
      Db 141 GTGATTAACCTAGAGTTTGCATGCAAGTGGTTTATGTAAAGACATGCAAGTCAGGA 200
      Qy 163 ThrGluAaPhePheLeuValAlaIleGlnMetValSerGluAlaAaArgPheLys 182
      Db 201 AATGAGGCCAAATCTTGCTGATTCATGACATAGAGTTTGAAGAGCAAGGTTCAAG 260
      Qy 183 TyrIleGlnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 200
      Db 261 TATATTGAGGTAAAGGTGAACCAAGTCGCTTAGATTATGATGATGCTTACCCGACCG 320
      Qy 201 LysValIleLeuLeuGlnGluLysTyrPGLyLysIleSerGluAlaIleHisAsnAlaLys 220
      Db 321 AATATGCTGCTTTGGAGACCAATTTGGGGAGAGATTTCGACAGATTCATGAGAGTCT 380
      Qy 221 AsnGlyAlaLeuPro-----LysProLeuGlnLeuValAspAlaLys 234
      Db 381 ---GGGGCGAAACCTGCTGTATGATGATCTTACCTCCGATTCGTTAAAGAAACCAAT 437
      Qy 235 GlyThrLysTyrPLeuValLeuArgValAlaIleGlnMetValAspValAlaLeuLys 254
      Db 438 GGTATTCATGACGCGGTGATTAAGTTGACACTATTAGACCTGAATGGGAGTATCTCAAG 497
      Qy 255 Tyr 255
      Db 498 TTC 500

```

```

RESULT 11
LOCUS      CA839511      671 bp      mRNA      linear      EST 12-DEC-2002
DEFINITION MCT028D04 172117 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5,
mRNA sequence.
ACCESSION  CA839511
VERSION    CA839511.1  GI:26567276
KEYWORDS   EST.
SOURCE     Mesembryanthemum crystallinum (common iceplant)
ORGANISM   Mesembryanthemum crystallinum

```

```

REFERENCE 1
AUTHORS   Cushman, J.C.
TITLE     An expressed sequence tag database for the common ice plant,
          Mesembryanthemum crystallinum
JOURNAL   Unpublished (1997)
COMMENT   Contact: Cushman JC
          Department of Biochemistry
          University of Nevada
          MS200, Reno, NV 89557-0014, USA
          Tel: 775-784-1918
          Fax: 775-784-1650
          Email: jcushman@unr.edu
          PCR Primers
          FORWARD: T3 20mer
          BACKWARD: T7 21mer
          Plate: 028 row: D column: 04
          Seq primer: T3 20mer
          High quality sequence stop: 671.

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FEATURES
source
1..671
location/Qualifiers

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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_idb="Ice plant Lambda Uni-Zap XR expression

```

ORIGIN

library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."

note=vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1: EcoRI, Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.56e-20	245.00	53.4%	38.5%	18.1%	6	671	62	24	61	14	4

US-09-978-274A-4 (1-263) x CA839511 (1-671)

```

Qy      103 GluAsnThrLeuCySerSerSerSerArgValAlaMetSerIleAsnTyrAsnSer 122
      25 GAGATCTCTTTCATGAGGACAGCATTCGACCTTGCTTCAAGGACCTTACACATCC 84
      Db 123 LeuTyrProThrMetGluLysLysAlaGlnValAsnSerArgAsnGlnValGlnLeuGly 142
      Db 85 TTA-----GAGAAATGCTGCAAAACCAACGACGAGAGAGCCATGAGTTAGGG 129
      Qy 143 11leGlnIleuSerSerAapIleGlyLysIleSerGlyValAspSerPheProValys 162
      Db 130 GTGATTAACCTAGAGTTTGCATGCAAGTGGGAGAGATTTCGACATGACATGACAGGA 189
      Qy 163 ThrGluAaPhePheLeuValAlaIleGlnMetValSerGluAlaAaArgPheLys 182
      Db 190 AATGAGGCCAAATCTTGCTGATTCATGACATAGAGTTTCTGAAGCAGCAAGGTTCAAG 249
      Qy 183 TyrIleGlnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 200
      Db 250 TATATTGAGGTAAAGGTGAACCAAGTCGCTTAGATTATGATGATGCTTACCCGACCG 309
      Qy 201 LysValIleLeuLeuGlnGluLysTyrPGLyLysIleSerGluAlaIleHisAsnAlaLys 220
      Db 310 AATATGCTGCTTTGGAGACCAATTTGGGGAGAGATTTCGACAGATTCATGAGAGTCT 369
      Qy 221 AsnGlyAlaLeuPro-----LysProLeuGlnLeuValAspAlaLys 234
      Db 370 ---GGGGCGAAACCTGCTGTATGATGATCTTACCTCCGATTCGTTAAAGAAACCAAT 426
      Qy 235 GlyThrLysTyrPLeuValLeuArgValAlaIleGlnMetValAspValAlaLeuLys 254
      Db 427 GGTATTCATGACGCGGTGATTAAGTTGACACTATTAGACCTGAATGGGAGTATCTCAAG 486
      Qy 255 Tyr 255
      Db 487 TTC 489

```

```

RESULT 12
LOCUS      CA833333      689 bp      mRNA      linear      EST 12-DEC-2002
DEFINITION MCS021A09 151944 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA
sequence.
ACCESSION  CA833333
VERSION    CA833333.1  GI:26561098
KEYWORDS   EST.
SOURCE     Mesembryanthemum crystallinum (common iceplant)
ORGANISM   Mesembryanthemum crystallinum

```

```

REFERENCE 1
AUTHORS   Cushman, J.C.
TITLE     An expressed sequence tag database for the common ice plant,
          Mesembryanthemum crystallinum

```


JOURNAL
COMMENT

Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 021 row: A column: 09
Seq primer: T3 20mer
High quality sequence stop: 689.

FEATURES

source

location/Qualifiers

1. 689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021A09"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.: 9.94e-20 Length: 689
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 18.1% Indels: 14
DB: 6 Gaps: 4

US-09-978-274A-4 (1-263) x CA833333 (1-689)

QY 103 GluAnThrIeuCySserSerSerSerSerArgValAlaMetSerIleAsnTYrAsnSer 122
DB 36 GAGATCTCTTTCATGAGCAAGTTCCGAACTTCGATTCGAAAGGACTTACACATCC 95
QY 123 LeuTYrProthMetGluYsAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
DB 96 TTA-----GAGAAATGCTGCACAAACCAACGACGAGAGCCATGAGTTAGGG 140
QY 143 IleGlnIleuSerSerAspIleGlyIleSerGlyValAspSerPheProValLys 162
DB 141 GTGATTAATCTAGAGTTGCGATCGAGTCGCTTATGATTAAGACATGACAACTCAGAGA 200
QY 163 ThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLys 182
DB 201 AATGAGGCCAAATCTTGCCTGATTCGATTCAGATGTTCTTGAAGCAGAGTTTCAAG 260
QY 183 TYrIleGluAsnGlnValYsThrAsnPhe-----AsnArgAlaPheTYrProAspPro 200
DB 261 TATATTGAGAGTAAAGTGAACCAAAAGTCCTTATGATTAAGATGTTCTTACCCGAGCCCG 320
QY 201 LysValIleAsnLeuGluGluYsTYrGlyIleSerGlyValAlaIleAsnAlaLys 220
DB 321 AAAATGCTGCTTTGGAGACCAATTTGGGGAAAGATTTCGAGGAGATTCAAGAGTGTCT 380
QY 221 AsnGlyAlaLeuPro-----LysPheLeuGluLeuValAspAlaLys 234
DB 381 ---GGGGCGAAACCTGCTGATGATTCCTTCACTCCGATTCGTTAAAGAAACCAAT 437
QY 235 GlyThrIleTYrPheIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 254
DB 438 GGTGATCATGAGACGGTGAATTAAGTTGACACTATTAGACCTGAATGGGGATTAATCAAG 497

QY 255 Tyr 255
DB 498 TTC 500

RESULT 13
LOCUS
DEFINITION

CA833383 689 bp mRNA linear EST 12-DEC-2002
MCS021F04 152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

CA833383
CA833383
GI:26561148

ORGANISM

Mesembryanthemum crystallinum (common iceplant)
Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alceaceae; Mesembryanthemum.

REFERENCE

1 (bases 1 to 689)
Cushman, J.C.

AUTHORS

An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum

JOURNAL
COMMENT

Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

source

location/Qualifiers

1. 689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021F04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.: 9.94e-20 Length: 689
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 18.1% Indels: 14
DB: 6 Gaps: 4

US-09-978-274A-4 (1-263) x CA833383 (1-689)

QY 103 GluAnThrIeuCySserSerSerSerSerArgValAlaMetSerIleAsnTYrAsnSer 122
DB 36 GAGATCTCTTTCATGAGCAAGTTCCGAACTTCGATTCGAAAGGACTTACACATCC 95
QY 123 LeuTYrProthMetGluYsAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
DB 96 TTA-----GAGAAATGCTGCACAAACCAACGACGAGAGCCATGAGTTAGGG 140
QY 143 IleGlnIleuSerSerAspIleGlyIleSerGlyValAspSerPheProValLys 162

```

Db      141 GTGATTAACCTAGAGTTTGCATCGACTCGCTTATGCTAGACATCGACACAGTCAAGACA 200
      163 ThcGluAlaPhePheLeuValAlaIleGluMetValSerGluAlaIleArgPheLeu 182
      201 AATGAGCCCAATTTCTTCTGCTGATTCATTCAGATGATTTCTTGAGGACGAGAGTTCAAG 260
      261 TATATTGAGAGTAAAGGACCAAGAGCGCTTAGATTATGATGATGCTTACCGGACCCG 320
      321 AATATGCTGCTTTTGGAGACCAATGGGGAGATTTCGAGAGATTCATGAGAGTCT 380
      381 ---GGGGCAAACTGCTGTTATGATATCTTACCTCCGATTCGTTAAAGAAACCAAT 437
      438 GGTGATTCATGACGCGGTGATTAAGTTGACACTATTGACCTGAATGGGAGTACTCAG 497
      498 TTC 500

QY      221 AasnGlyAlaLeuPro-----LysProLeuGluLeuValAlaPheAlaLeu 234
      234 381 ---GGGGCAAACTGCTGTTATGATATCTTACCTCCGATTCGTTAAAGAAACCAAT 437
      438 GGTGATTCATGACGCGGTGATTAAGTTGACACTATTGACCTGAATGGGAGTACTCAG 497
      498 TTC 500

QY      235 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgPheValAlaLeuLeuLys 254
      438 GGTGATTCATGACGCGGTGATTAAGTTGACACTATTGACCTGAATGGGAGTACTCAG 497
      498 TTC 500

QY      255 Tyr 255
      498 TTC 500

Db      498 TTC 500

RESULT 14
LOCUS   CO121195 841 bp mRNA linear EST 16-JUN-2004
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            mRNA sequence.
ACCESSION CO121195
VERSION   CO121195.1 GI:48819882
KEYWORDS EST.
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ORGANISM Gossypium raimondii
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          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
          1 (bases 1 to 841)
REFERENCE Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
          Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
          Wang,R.A.
          Global assembly of Cotton ESTs
          Unpublished (2004)
          Contact: Rod A. Wang
          Arizona Genomics Institute
          The University of Arizona
          Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: rtwing@genome.arizona.edu
          Plate: 02 row: E column: 11.
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            /clone_lib="GR_Eb"
            /note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
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            Wendle lab. Directional cloned into NotI-EV. Clones
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ORIGIN
Alignment Scores:
Pred. No.: 7.6e-19 Length: 841
Score: 239.00 Matches: 73

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Percent Similarity: 47.0%
Best Local Similarity: 29.3%
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DB: 7
Gaps: 9
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DEFINITION GR_Eb0032E01.r GR_Eb Gossypium raimondii cDNA clone GR_Eb0032E01
            3' mRNA sequence.
ACCESSION CO103587
VERSION   CO103587.1 GI:48802273
KEYWORDS EST.
SOURCE    Gossypium raimondii
ORGANISM Gossypium raimondii
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
          1 (bases 1 to 903)

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GenCore version 5.1.7
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/08373858
; Patent No. 5631155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytoacta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dard & Dard
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
TISSUE TYPE: Leaf
US-08-373-858-1

Alignment Scores:

Pred. No.:	2,936-123	Length:	1195
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Query Match:	77.4%	Indels:	0
DB:	2	Gaps:	0

US-09-978-274a-4 (1-263) x US-08-373-858-1 (1-1195)

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RESULT 2

US-08-342-786B-1
Sequence 1, Application US/08342786B

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana* L.
IMMEDIATE SOURCE:
CLONE: PAP

US-08-342-786B-1

Alignment Scores:

Pred. No.:	2,936-123	Length:	1195
Score:	1050.00	Matches:	200
Percent Similarity:	87.0%	Conservative:	28

Best Local Similarity: 76.3%
Query Match: 77.4%
DB: 2
Matches: 34
Indels: 0
Gaps: 0

US-09-978-274A-4 (1-263) x US-08-342-786B-1 (1-1195)

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QY 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnTYraSP 121
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DB 399 GTAGAGCTACTCTTGGCCCAATGCCAATCTCGTGTATGATTAATAAACATTAACCTTGAT 458
QY 122 SerleuTYrProThrMetGluLysAlaGlyAlaAsnSerArgAsnGlnValGlnleu 141
   ::::::::::::::::::::
DB 459 AGTGAGATTCACATTCATGGAATCAAAAGCGGAGTAAATCAAGAACATGCTCAACTG 518
QY 142 GlylleGlnlleuSerSerAspIleGlylySylleSerglyValaAspSerPheProVal 161
   ::::::::::::::::::::
DB 519 GGAATTCGAATATCTCGACAGTAATATTGGAAGATTTCTGGAGATGATCATTCATCTGAG 578
QY 162 lyethrGlnAlaPhePheleuValAlaIleGlnmetValSerglyAlaAlaArgPhe 181
   ::::::::::::::::::::
DB 579 AAAACCAAGCGCAATTCCTATGTTGATGACCATCAAAATGATGAGGCGCAAGATTC 638
QY 182 lyethrIleGlnGlnVallyleThraSPnAsnArgAlaPheTYrProAspProlys 201
   ::::::::::::::::::::
DB 639 AAGTACATAGAGATCAGTGAATACATATTTTAAAGAGATTCACACCTCAATCCCAA 698
QY 202 ValIleasnleuGlnGlylySTYgylleSerglyAlaIleHisAsnAlaLysaSP 221
   ::::::::::::::::::::
DB 699 GTACTTAATTTGCAAGAGACATGGGATTAAGATTTCAACAGCAATTCATGATGCCAAGAT 758
QY 222 GlyAlaAsnProlySPProleuGlnleuValaAspAlaLysGlyThrlleTPlleValleu 241
   ::::::::::::::::::::
DB 759 GAGATTTCACCAAACTCTGACATGATGATGCCAGTGTGCAAGTGTATGTTG 818
QY 242 ArgValaAspGlnIleAsnArgAspValAlaAsnleuYsTYrValaAsnGlyThrCyGln 261
   ::::::::::::::::::::
DB 819 AGAGTGAATGAATCAAGCCTGATGATGACCTTTAAATCTGATGGTGGAGCTGTGAG 878
QY 262 ThrlleThr 263
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DB 879 ACAACT 884
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RESULT 3

US-08-500-611-1
Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lerner, David, Littleberg, Krumholz & Wentlik
STREET: 600 South Avenue West

```
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Alignment Scores:
Pred. No.: 3.66e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
Gaps: 0
US-09-978-274A-4 (1-263) x US-08-500-611-1 (1-1379)
QY 2 ILeaenThrlleThrPheaspAlaGlyAsnAlaThrlleasnlySTYAlaThrPheMet 21
   ::::::::::::::::::::
DB 291 GTGAATCAATCACTACATGTTGGAGAGTACCAACCTTACCAATGACCACTTTCTG 350
QY 22 GluSerleuArganGlnAlaLysaSPProlyleuYsCySTYgyllePromeleu 41
   ::::::::::::::::::::
DB 351 AATGATCTTCGTATGAAGCAAGATCCAAAGTTCATGATGATGATGATGATGATGATG 410
QY 42 ProAspThraenSerThrProlySTYleuVallyleuGlnGlyAlaAsnleuYs 61
   ::::::::::::::::::::
DB 411 CCCAATCAATCAATCAATCCAAAGTACGTGTGTGAGCTCCAAAGTTCAAATTAATAA 470
QY 62 ThrlleThreumetleuArgaAsnleuThYValmetGlyTYrSerAspProPhe 81
   ::::::::::::::::::::
DB 471 ACCATCACTAAATGCTGAGCAAGAACATTTGTATGATGATGATGATGATGATGATGAT 530
QY 82 AsnGlyAsnlyCySaTgTYrHislePheAsnAspIleThrSerThrgluArgThraSP 101
   ::::::::::::::::::::
DB 531 GAAACCAATTAATGCTGATCCATATCTTTAAATGATGATGATGATGATGATGATGATG 590
QY 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnTYraSP 121
   ::::::::::::::::::::
DB 591 GTAGAGCTACTCTTGGCCCAATGCCAATCTCGTGTATGATTAATAAACATTAACCTTGAT 650
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QY 122 SerLeuTyRProThrMetGluValylsAlaIAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCAATCGAATCAAAAGCGAGTAAATCAAGAAAGTCAGGTCAACTG 710
QY 142 GLYTILEGlnIleLeuSerSerAspIleGlyIleSerGlyValAspSerPheProval 161
DB 711 GGATTCAAATCTCCAGACATGATATTGGAAGATTTCTGGAGATGATCATTCACGTAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATTCAGAGCGACGAAGTTTC 830
QY 182 LysTyrTILEGlnAsnGlnValIleThrAsnPheAsnArgAlaPheTyrProAspProlys 201
DB 831 AAGTACATAGAGATCAAGGTGAAGAACTAATTTTAAACAGACATTCACCTTAATCCCAA 890
QY 202 ValIleAsnLeuGlnGluValylsTyrGlyIleSerGluAlaIleHisAsnAlaIleValAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTGAAGATTTCAACGCAATTCATGATGCCAAGAAAT 950
QY 222 GlyAlaLeuProLysPheLeuGlnLeuValAspAlaIleGlyThrIleValIleValLeu 241
DB 951 GGAGTTTACCAAACTCTCGAGCTAGTGATGCCAGTGTGCCAAGTGGATAGTCTTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaIleLeuLeuTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTCGATGAATCAAGCTGATGTAGCACTTAAACTACGTTGGTGGAGCTGTGAC 1070
QY 262 ThrThr 263
DB 1071 ACAAAT 1076
RESULT 4
US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun B.
; TITLE OF INVENTION: DNAs Encoding Fokweed Antiviral Protein
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,694
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; TELEX: 139-125
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

LOCATION: 225..1163
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
US-08-500-694-1
Alignment Scores:
Pred. No.: 3,66e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 2 Gaps: 0
US-09-978-274A-4 (1-263) x US-08-500-694-1 (1-1379)
QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
DB 291 GTGAATACATCAATCTTACAAATGTTGAGAGTACCAACATTAAGCAATACCCACTTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB 351 AATGATCTTCGTATTAAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValIleLeuGlnIleAlaAsnLeuLys 61
DB 411 CCCAATACAAATACAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAATTAATAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACCATCACTATATGTGAGACCAACAAATTTGTATGTATGGTTATTCCTGATCCCTTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATATGCTTACCATATCTTAATGATATCTGAAGTCAAGCCCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACACTCTTGGCCCAATGCAATTCCTGTTAGTAAACATAAATTGAT 650
QY 122 SerLeuTyRProThrMetGluValylsAlaIleValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCAATCGAATCAAAAGCGAGTAAATCAAGAAAGTCAGGTCCAAACG 710
QY 142 GLYTILEGlnIleLeuSerSerAspIleGlyIleSerGlyValAspSerPheProval 161
DB 711 GGATTCAAATCTCCAGACATGATATTGGAAGATTTCTGGAGATGATCATTCACGTAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATTCAGAGCGACGAAGATTC 830
QY 182 LysTyrTILEGlnAsnGlnValIleThrAsnPheAsnArgAlaPheTyrProAspProlys 201
DB 831 AAGTACATAGAGATCAAGGTGAAGAACTAATTTTAAACAGACATTCACCTTAATCCCAA 890
QY 202 ValIleAsnLeuGlnGluValylsTyrGlyIleSerGluAlaIleHisAsnAlaIleValAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTGAAGATTTCAACGCAATTCATGATGCCAAGAAAT 950
QY 222 GlyAlaLeuProLysPheLeuGlnLeuValAspAlaIleGlyThrIleValIleValLeu 241
DB 951 GGAGTTTACCAAACTCTCGAGCTAGTGATGCCAAGTGTGCCAAGTGGATAGTCTTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaIleLeuLeuTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTCGATGAATCAAGCTGATGTAGCACTTAAACTACGTTGGTGGAGCTGTGAC 1070

QY 262 ThrThr 263
Db 1071 ACAAAT 1076

RESULT 5

US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kanlewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
US-07-865-169-1

Alignment Scores:
Pred. No.: 3.66e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x US-07-865-169-1 (1-1379)

QY 2 ILeahThrlleThrPheAspAlaGlyAsnAlaThrIleAsnLysrYrAlaThrPheMet 21
Db 291 GTGAATACATCATCTCAATGTTGGAAGTACCAACCATATGCAATACGCACTTTCTG 350
QY 22 GluserleuArganglnAlaAspProlyseuLysCysrYrGlyIlePheMetleu 41
Db 351 AATATCTTCCTAATGAGCGAAGATCCAGTTTAAATCTTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysrYrIleuValIysleuGlnGlyAlaAsnleuLys 61
Db 411 CCCAATACCAATATACCAATCCAAAGTACGTGTGTTGAGCTCCAAAGGTTCAATATAAAAA 470
QY 62 ThrIleuMetleuArgAspAsnleuYrValMetGlyrYrSerAspProPhe 81
Db 471 ACGATCACTAATGCTGAGCAAGCAATTTGTATGTATGATGGGTATTCTGATCCCTTT 530

QY 82 AengIAsnLysCysArgYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAACCAATATATATGTCGTACCATATCTTTATATGATATCAAGTACGAACGCCAAGAT 590
QY 102 ValGluSerThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnYrAsn 121
Db 591 GTAGAGACTACTCTTTGCGCAAAATGCCAATCTCGTGTATGTAATAAACAATTAACCTTGAT 650
QY 122 SerLeuYrProThrMetGluLysleuAlaGluValAsnSerArgAsnGlnValGluLeu 141
Db 651 AGTCGATATCCCAACATTTGGAATCAAAACCGGAGATAAATCAAGAGTCAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
Db 711 GGAATTCAAATCTCGACAGTATATTTGGAAGATTTCTGAGATGATGTCTTCACTGAG 770
QY 162 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
Db 771 AAACCGAAGCCGAATTCCTATGTGTAGCCATACAAATGATCAGAGCGAAGCAATTC 830
QY 182 LysYrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheYrProAspProLys 201
Db 831 AAGTACATATAGAAATCAGTGAAACTAATTTTAAACAGACATTCACCTAATCCCAA 890
QY 202 ValIleAsnLeuGluGluLysrYrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 891 GTACTTATTTGCAAGACATGGGGTATGATTTCAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysrYrIleValLeu 241
Db 951 GGAGTTTATCCCAACCTCTGAGCTAGTGATCCAGTGATGCCAAGTATGATGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysrYrValAsnGlyThrCysGln 261
Db 1011 AGAGTGTATGAAATCAAGCCCTGATGTAGCACTTTAAACTAAGTGTGGAGCTGTCTAG 1070
QY 262 ThrThr 263
Db 1071 ACAAAT 1076

RESULT 6

US-09-005-273-1
Sequence 1, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
NUMBER OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33, 071
REFERENCE/DOCKET NUMBER: OICRS 3.3-0334
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290

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Score: 1050.00 Matches: 200
 Percent Similarity: 87.0% Conservative: 28
 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.4% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x PCT-US96-11546-1 (1-1379)

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QY 2 ILeasnthrllethrpheaspalaglyasna1aThrileasnytyrAlaThrpheMet 21
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DB 291 GTGAATCAATCATCTACATGTTGGAAGTACACACATTTGCAAAATACGCCACTTTTCTG 350
QY 22 Gluserleuarganginalalyaspprolyseulyscysyrglyileprometleu 41
   |||.....|
DB 351 AATGATCTTCGTATGAGCGAAGATCCAGTTTAAATGCTAATGCAATCCATCTG 410
QY 42 ProasphtrnsenrthrpolystryleuVallyseuInglyalaasnylys 61
   |||.....|
DB 411 CCCAATCAATCAATCAATCCAAAGTACCTGTTGAGCTCCAAAGTTCAATTAATAA 470
QY 62 ThrillethruetleuargargasnaasnytyrValmetglytyrserasprophe 81
   |||.....|
DB 471 ACCATCACTAATGCTGAGAGCAAAATTTGATGATGAGGTTATTCGATCCCTTT 530
QY 82 Asnglyasnylyscysyrglyrhie1lephasnaaspi1ethrserthrgluargThrasp 101
   |||.....|
DB 531 GAAACCAATAAATGCTTACATATCTTTAATGATNTCTCAGATCCGAAAGCCCAAGAT 590
QY 102 ValgluasanthrleuCyserSerSerSerSerSerArgValAlametsertleasnytrasn 121
   |||.....|
DB 591 GTAGAGCTACTCTTTGCCCCAAATGCCAATCTCGTTTAAATAACATTAACCTTGAT 650
QY 122 SerleutyrrprothrmecglulysalaglyValasnseryarganglnValgluleu 141
   |||.....|
DB 651 AGTCGATATCCAAATTCGAAATCAAAAGCGGAGTAAATCAAGAAGACAGCTCCAACTG 710
QY 142 GlylleqnlleleuserSerasp1leglylyrileserglyValasppropheProVal 161
   |||.....|
DB 711 GGAATTCAAATATCTCGACATATTTGGAAGATTTCTGAGATGATCTCATTCAG 770
QY 162 lyethrqlualaphetheleuValAlaleglnmetValserglualAlaargphe 181
   |||.....|
DB 771 AAAACCAAGCCGAATTCATTTGTTAGCCATACAAATGATATCAGAGGCGCAAGATTC 830
QY 182 lyethrlllegluasnglnVallyethrasnphasnaargAlaBheityrProaspProlys 201
   |||.....|
DB 831 AAGTACATTAAGAGATGAGTGAATAAATTTTAAACAGATTCACACCCCTAACCCAA 890
QY 202 ValilleasneugluglulysrlyrlyrileserglualAlaleh1asnaAlalyasn 221
   |||.....|
DB 891 GTACTTAATTTGCAAGAGACATGCGGTAAAGTTTCAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyValaleuProlyspProleugluValasphAlalyseglythrllystrlyleValleu 241
   |||.....|
DB 951 GGAAGTTTACCCAAACCTCTGAGCTAGTGATGCCAGTGGTCCAAAGTGAATGTGTG 1010
QY 242 ArgValaspp1u1leasnaargasvalAlaleuuleuysrtyrValasnglythCyegl 261
   |||.....|
DB 1011 AGAGTGATGAATCAAGCCCTGATGTAGCACTTTAAACTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
   |||
DB 1071 ACAACT 1076

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RESULT 8
 US-08-501-253A-1

; Sequence 1, Application US/08501253A

; Patent No. 6146628

; GENERAL INFORMATION:

; APPLICANT: Uckun, Patih

; APPLICANT: Turner, Nilgun

; TITLE OF INVENTION: Biotherapeutic Agents Comprising

; TITLE OF INVENTION: Recombinant Pap and Pap Mutants

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: Merchant & Gould

STREET: 90 South 7th Street, 3100 No. 6146628west Center

CITY: Minneapolis

STATE: MN

COUNTRY: US

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/501.253A

FILING DATE: 11-JUL-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kettleberger, Denise M.

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 600.323US01

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 225..1163

US-08-501-253A-1

Alignment Scores:

Pred. No.: 8.81e-123

Score: 1047.00

Percent Similarity: 87.0%

Best Local Similarity: 76.0%

Query Match: 77.2%

DB: 3

Length: 1379

Matches: 199

Conservative: 29

Mismatches: 34

Indels: 0

Gaps: 0

US-09-978-274A-4 (1-263) x US-08-501-253A-1 (1-1379)

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QY 2 ILeasnthrllethrpheaspalaglyasna1aThrileasnytyrAlaThrpheMet 21
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DB 291 GTGAATCAATCATCTACATGTTGGAAGTACACACATTTGCAAAATACGCCACTTTTCTG 350
QY 22 Gluserleuarganginalalyaspprolyseulyscysyrglyileprometleu 41
   |||.....|
DB 351 AATGATCTTCGTATGAGCGAAGATCCAGTTTAAATGCTAATGCAATCCATCTG 410
QY 42 ProasphtrnsenrthrpolystryrleuVallyseuInglyalaasnylys 61
   |||.....|
DB 411 CCCAATCAATCAATCAATCCAAAGTACCTGTTGAGCTCCAAAGTTCAATTAATAA 470
QY 62 ThrillethruetleuargargasnaasnytyrValmetglytyrserasprophe 81
   |||.....|
DB 471 ACCATCACTAATGCTGAGAGCAAAATTTGATGATGAGGTTATTCGATCCCTTT 530
QY 82 Asnglyasnylyscysyrglyrhie1lephasnaaspi1ethrserthrgluargThrasp 101
   |||.....|
DB 531 GAAACCAATAAATGCTTACATATCTTTAATGATNTCTCAGATCCGAAAGCCCAAGAT 590
QY 102 ValgluasanthrleuCyserSerSerSerSerSerArgValAlametsertleasnytrasn 121
   |||.....|
DB 591 GTAGAGCTACTCTTTGCCCCAAATGCCAATCTCGTTTAAATAACATTAACCTTGAT 650
QY 122 SerleutyrrprothrmecglulysalaglyValasnseryarganglnValgluleu 141
   |||.....|
DB 651 AGTCGATATCCAAATTCGAAATCAAAAGCGGAGTAAATCAAGAAGACAGCTCCAACTG 710

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QY      142 GYIIIEGNIIELEUSERSERAPIEGILYSRIIESERGIVALAASerPheoval 161
DB      711 GGAAITTCMAATNCTCGACGTATATTGGALAGATTCTTGGAGVATGCATTCATCACTGAG 770
QY      162 LysThrGluAlaphPheLeuleValAlallegImetValIsergIuaIalAargPhe 181
DB      771 AAAACCAGAAGCCGAATTCCTTAGTTAGTGCATTAACAATGGTATCGAAGGCCAAGATTC 830
QY      182 LysTYRILEGLIAserGIvalLysrThrasnPheAnaIGalaPhETyrProAsPrOlys 201
DB      831 AAGTACATATGAGAAATCAGGTGAAAACTATAATTTTAAACAAGCATTCMACCTTAATCCCAAA 890
QY      202 ValIIeaenLeuGlunLUlsTrOpJLYsrIlEsErGIuaIalEHLISanaIalyasEn 221
DB      891 GTACTTAATTTTGCAAGAGACATGGGGGTAAAGTTTCAAACGCAATTCATGATGCCAAGAT 950
QY      222 GIyAlaleuPLoLyseProleuglInleuValaspAlalySGlythrLYeSTrpIleValIeu 241
DB      951 GGAGGTTTACCCAACCTCTCGAGCTAGTGATGCCAGTGGTGCACGATGTAGTATGTGTTG 1010
QY      242 ArgValaspGluIIeaAsnArgspValAlaleuLeuSYTyrrValaSerGIYTHCyagln 261
DB      1011 AGAGGATGAGAAATCAAGCCTGATGTAGCACCTTTAAACTAGTGTGGAGGCTGTCTAG 1070
QY      262 ThrThr 263
DB      1071 ACAACT 1076

RESULT 9
US-07-865-169-2
; Sequence 2, Application US/07865169
; Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kantlewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940Ch
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865.169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-865-169-2

Alignment Scores:          3.8e-122           Length:         1379
Pred. No.:

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSEE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCTRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig peptide
LOCATION: 225..230
US-09-005-273-3
Alignment Scores:
Pred. No.: 3.8e-122 Length: 1379
Score: 1042.00 Matches: 199
Percent Similarity: 86.6% Conservative: 28
Best Local Similarity: 76.0% Mismatches: 35
Query Match: 76.8% Indels: 0
Gaps: 0
US-09-978-274A-4 (1-263) x US-09-005-273-3 (1-1379)
QY 2 ILeaenThrlerThrPheAspAlaGlyAsnAlaThrlleasnlyrYrAlaThrPheMet 21
DB 291 GTGAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCG 350
QY 22 GluserleuArGaenGlnAlaLeuAspProlyseuLeuCyeyrYrGlylePrometleu 41
DB 351 AATGATCTTCGTATGAGGCAAGATCAAGTTTAAATGCTATGGAATACCAATCTG 410
QY 42 ProAspThrAsnSerThrProlyrYrleuLeuValylsleuGlnGlyAlaAsnleuLys 61
DB 411 CCCAATACCAATACCAATACCAATACCAATGCTGTGCTGAGCTCCCAAGTTCAAATRAAAA 470
QY 62 ThrlleuThrlleuThrlleuThrlleuThrlleuThrlleuThrlleuThrlleuThrlleu 81
DB 471 ACCATCACTAATGCTGAGGCAAGCAATTTGATGATGAGGCTTATTTCTGATCCCTTT 530

QY 82 AsnGlyAsnLysCyeyrGlyrHislePheAsnAspIleThrSerThrlGluArGThrAsp 101
DB 531 GAAACCAATCAATGCTGTACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 590
QY 102 ValGluBenthrlleuCySerSerSerSerSerArgValAlaMetSerleAsnTyraen 121
DB 591 GTAGAGACTACTCTTGGCCCAATGCCAATCTCTGTGTAGTAAATAAATCAATCTTGCAT 650
QY 122 SerleuTyrrProthMetGluLysAlaGluValAsnSerArgAsnGlnValGlnleu 141
DB 651 AGTCGATATCCAAATTCGATGAAACCGGCAATTAATCAAGAGTCAGGTCCAACTG 710
QY 142 GlylleGlnleuLeuSerSerAspIleGlyLysleSerGlyValAspSerPheProVal 161
DB 711 GAAATTCAAATCAATCTGACAGTAATATGAAAGATTTCTGAGATGATCTTCACTGAG 770
QY 162 LysThrlGluAlaPhePheleuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACCGAGCCGAATTCCTATTGTTAGCCATACAAATGATCAAGGCGAGCAAGATTC 830
QY 182 LysTyrrlleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrrProAspProLys 201
DB 831 AAGTACATGAGGAATCAGGTGAAAATTAATTTTAAAGAGCATTCACCTTAATCCCAA 890
QY 202 ValIleAsnleuGlnGluLysTrpGlyLysleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGACATGAGGTGAAGATTTTCAACAGCAATTCATGAGCCAAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrlLysTrpIleValleu 241
DB 951 GGAATTTTACCAAACTCTCTGAGCTAGTGAATCCAGTGTGCAAGTGAATAGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrrValAsnGlyThrCysGln 261
DB 1011 AGAGTGTATGAATCAAGCTGATGTAGCACTTAAACTACATGTTGTGGAGGTGTGAG 1070
QY 262 ThrlThr 263
DB 1071 ACAACT 1076
RESULT 11
US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 5348865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5348865e1 Genome Coding PhytoIacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Alignment Scores:
Pred. No.: 1,28e-99 Length: 918
Score: 862.50 Matches: 174
Percent Similarity: 79.4% Conservative: 34
Best Local Similarity: 66.4% Mismatches: 52
Query Match: 63.6% Indels: 4
Gaps: 2

US-09-978-274a-4 (1-263) x US-08-138-636-1 (1-918)

QY 2 11aenThr11eThrPheapAlaGlyAsnAlaThr11eAsn1yTyra1aThrPheMet 21
DB 67 GTGAATACCACTCACTCACTGTTGGAAGTACCACTTGAACCTATGCACTTTGG- 125
QY 22 GluSerLeuArganginala1yAspProlyLeu1yLeu1yLeu1yLeu1yLeu1yLeu 41
DB 126 ---ATACCTTGCTAGTGAAGCGAAGATCCA--GTATGTGCTATGGAATACCAATGCTG 180
QY 42 ProAspThrAsnSerThrProlyTyLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 61
DB 181 CCAATATTTGATCAATCAATCAATCAATTTGTTGAGCTCCAGGTTCAATTAAGAAGAA 240
QY 62 Thr11eThrLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 81
DB 241 GGCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 300
QY 82 AsnGlyAsn1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 101
DB 301 AAC---AATAGGTCGCTTCCATCTCTTAAGGCTATTCAGGTAAGTGAACCGAAGAT 357
QY 102 ValGluAsnThrLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 121
DB 358 GTAGAGACTCACTCTTTGGCCCAATGCCGATTCGTTGTTGTTGTTGTTGTTGTTGTTGTT 417
QY 122 SerLeu1yProThr1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 141
DB 418 AGTCGATATTCACCACTTGAATCAAAAGCGAGTAATCAAGAGTCAAGTCAAGTCAAGT 477
QY 142 Gly11eGlu11eLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 161
DB 478 GGAAATTCGAATCTCCAGCACTGCGCATTTGGAAGATTTCTGAGAGTCAAGTCAAGTCA 537
QY 162 LysThrGlu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 181
DB 538 AGAACCGAAGCTGAATTTCTACTGTTAGTCAATCAATGTTATCAAGAGCGAAGATTC 597
QY 182 LysThr11eGlu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 201
DB 598 AAGTACATAGAGATCAAGTGAAGAACTAATTTAAACGACATCAACCTTAATCCCAA 657
QY 202 Val11eAsn1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 221
DB 658 GTACTTATATTCAGAGACATGAGGATTAAGATTTCTCAAGCAATTCATGTTGCGAAGAT 717

QY 222 GlyAlaLeuProlyProLeuGluLeuVala1yAspGlyThr1yTyra1yLeu1yLeu 241
DB 718 GGAATTTACCAATCTCTCAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 777
QY 242 ArgVala1yGlu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 261
DB 778 AGAGTGAATGAATCAAGCTGATGTGTCACTTAAACTACGTTATTTGGAGCTGCGAG 837
QY 262 ThrThr 263
DB 838 AGAACT 843

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Kyun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08445
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1
Alignment Scores:
Pred. No.: 1,28e-99 Length: 918
Score: 862.50 Matches: 174
Percent Similarity: 79.4% Conservative: 34
Best Local Similarity: 66.4% Mismatches: 52
Query Match: 63.6% Indels: 4
Gaps: 2

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US-09-978-274A-4 (1-263) x US-08-319-622A-1 (1-918)
QY 2 IleaenThrillethPheaspAlaGlyAsnAlaThrIleasnLysTyraLathrPheMet 21
DB 67 GTGAATACCATCATCTACCATGTTGGAAGTACACCACTTAGAACTAGCACTTTGG- 125
QY 22 GluserleuArgasnGlnAlaLysAspProLysleuLysCysTyrglyIlePrometleu 41
DB 126 ---ATACTTCGTAAGTGAAGCGAAGATCCAA--GTTATGTGCTATGGAATACCAATGCTG 180
QY 42 ProasphThrasenSerThrProLysTyrlleuValLysleuGlnGlyAlaAsnleuLys 61
DB 181 CCCAATATGATCAATCAAAATCAAAATGATGTTGAGCTCCAAAGTTCAATGAAGA 240
QY 62 ThrillethleuMetleuArgAsnAsnleuTyraValMetGlyTyrsSerAspProPhe 81
DB 241 GGCACTACACATTAATCTTAAGCAAGAAACAAATTTATATGATGAGGCTATTCGATCCCTAC 300
QY 82 AsnGlyAsnLysCysArgTyrllethPheasnAspIlethSerThrGluArgThrAsp 101
DB 301 AAC---AATAGGTGTCGTTTCATCTCTTAAGGCTATCTCAGTACTGGAAGCGAAGAT 357
QY 102 ValGluAsnThrleuLysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyra 121
DB 358 GTAAGACTACTCTTTGCCAAATGCCAATCTCTGTTGGTAAACATTAATGATGAT 417
QY 122 SerleuTyProthMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnleu 141
DB 418 AGTCGATATCCAACTTGGAATCAAAAGCAAGATTAATTCAGAAAGTCCAACTG 477
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
DB 478 GGAATTCGAATATCTCGACAGTGGCATTTGGAAGATTTCTGAGTACCTCATCTACAG 537
QY 162 LysThrGluAlaPhePheleuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 538 AGAACCGAAGCTGAATTCCTACTGCTAGCCATACAAATGATATCAGAGCGAAGATTC 597
QY 182 LysTyrlleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyProAspProLys 201
DB 598 AAGTACATAGAGATCAAGTAAATCTAATTTTAACAACCACTTAACCTTAATCCCAA 657
QY 202 ValIleAsnleuGluLysTyrlleSerGluAlaIleAsnAlaLysAsn 221
DB 658 GTACTTATATTCAGAGACATGGGGTAAAGATTTCTTCAAGATTCAGTCCAGAT 717
QY 222 GlyAlaLeuProLysProleuGluValAspAlaLysGlyThrLysTyrlleValleu 241
DB 718 GGAGCTTTTAACTCAATCTCTACAGCTAGTCATGCGCAATGATGCAATTTGATAGTGTG 777
QY 242 ArgValAspGluIleAsnArgAspValAlaIleuLysTyraValAsnGlyThrCysGln 261
DB 778 AGAGTGAATGAATCAAGCTGATGTGCTTAACTTAACTAGTTATGGAGCTGCCAG 837
QY 262 ThrThr 263
DB 838 AGAAGCT 843

```

```

ADDRESSER: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1
Alignment Scores:
Pred. No.: 1.28e-99 Length: 918
Score: 862.50 Matches: 174
Percent Similarity: 79.4% Conservative: 34
Best Local Similarity: 66.4% Mismatch: 52
Query Match: 63.6% Indels: 4
DB: Gaps: 2
US-09-978-274A-4 (1-263) x US-08-471-564-1 (1-918)
QY 2 IleaenThrillethPheaspAlaGlyAsnAlaThrIleasnLysTyraLathrPheMet 21
DB 67 GTGAATACCATCATCTACCATGTTGGAAGTACACCACTTAGAACTAGCACTTTGG- 125
QY 22 GluserleuArgasnGlnAlaLysAspProLysleuLysCysTyrglyIlePrometleu 41
DB 126 ---ATACTTCGTAAGTGAAGCGAAGATCCAA--GTTATGTGCTATGGAATACCAATGCTG 180
QY 42 ProasphThrasenSerThrProLysTyrlleuValLysleuGlnGlyAlaAsnleuLys 61
DB 181 CCCAATATGATCAATCAAAATCAAAATGATGTTGAGCTCCAAAGTTCAATGAAGA 240
QY 62 ThrillethleuMetleuArgAsnAsnleuTyraValMetGlyTyrsSerAspProPhe 81
DB 241 GGCACTACACATTAATCTTAAGCAAGAAACAAATTTATATGATGAGGCTATTCGATCCCTAC 300
QY 82 AsnGlyAsnLysCysArgTyrllethPheasnAspIlethSerThrGluArgThrAsp 101
DB 301 AAC---AATAGGTGTCGTTTCATCTCTTAAGGCTATCTCAGTACTGGAAGCGAAGAT 357

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0Y      102 Val1gluaSnrThrluCysserSeserSeserSeserArgVal1laMetSer1leAsnTrAsn 122
Db      358 GTAGAGACACACTCTTGTGCCCAATGGCGAATCTTCGTGTGTGGTAAACATTAACATTAATGAT 411
0Y      122 SerleuTyPProThmetGluYsYlValaGluValaAsnSerArGaenGlnValaGluLeu 141
Db      418 AGTCGATATCCAAACATTTGGATGMAATMAAAGCAGAGATMAATTCAGAAAGTCGATCCAACTG 477
0Y      142 G1Y1leGln1leuSeserSeserAp1leG1YsY1leSerg1YValaAspSerPheProVal 161
Db      418 GGAATTCGAATATCTCAGACAGCTGACATTTGGAGAAGATTTCTGAGTACAGCTCATTTACTGAG 533
0Y      162 LysThrGluAlaPhePheLeuLeuValaAla1leGlnMetValSerg1YValaAlaArgPhe 181
Db      538 AGAACCCGAAGCTGAATTTCTCACTGATAGCCATCAATGGTATTCAGAGCGAGCAAGATTCC 597
0Y      182 LysTr1leG1laSnglnVal1YsTr1ArAsnPhaAsnArgAlaPheTyPProAspProLys 201
Db      588 AGGTATCATAGAGGATCAAGTAAAGTAAACTTAATTTAAACAGACCATTTCAACCTTAATCCCAA 657
0Y      202 Val1leAsn1leuGlnGluGluYsTrPglY1Ys1leSerg1YVala1le1leAsnAla1YsAsn 221
Db      658 GTACTTATATTCGACGAGACATCGGGATAGATTTCTTCACACATTTACATGATGCGCAGAGAT 711
0Y      222 G1YAlaLeuProLysPheLeuGluLeuValaAspAlaYsG1YThrYsTP1leValLeu 241
Db      718 GGAAGTTTATCCCAATCTCTCAACGCTAGTGACATGCCAATGGTGCAAAATTTGGATGTGTG 777
0Y      242 ArgValaAsnG1Y1leAsnArgAspVala1AlaLeuLeuYsTrYValaAsnG1YThrCysGln 261
Db      778 AGAGTGAATGAATCAAGCTGTATGTGTCTCTTAAACTACGTTATTGGAGAGCTGCAG 833
0Y      262 ThrThr 263
Db      838 AGAACT 843

RESULT 14
US-08-356-161-7
: Sequence 7, Application US/08356161
: Patent No. 5916772
: GENERAL INFORMATION:
: APPLICANT: Lappi, Douglas A.
: APPLICANT: Barthelmy, Isabel
: APPLICANT: Baird, J. Andrew
: APPLICANT: Sobnowski, Barbara A.
: TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
: TITLE OF INVENTION: SAPORIN-CONTAINING PROTEINS
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSER: SEED and BERRY LLP
: STREET: 701 Fifth Avenue, 6300 Columbia Center
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/356,161
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/356,161
: FILING DATE: 13-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5916772eburg, Carol
: REGISTRATION NUMBER: 39,317
: REFERENCE/DOCKET NUMBER: 760100.404US
: TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: CDS
LOCATION: 1..804
FEATURES:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G9 in Example 1.B.2."
OTHER INFORMATION: /product= "Saporin"
US-08-356-161-7

Alignment Scores:

Pred. No.:	1.84e-33	Length:	804
Score:	341.00	Matches:	94
Percent Similarity:	55.5%	Conservative:	52
Best Local Similarity:	35.7%	Mismatches:	95
Query Match:	25.1%	Indels:	22
DB:	2	Gaps:	10

US-09-978-274A-4 (1-263) x US-08-356-161-7 (1-804)

OY 2 ILeaenTrilleThrrPheaspAlaglyAsnAlaThrIleasnTyraLathrPhemet 21
Db 46 GTCACTAAATCACATTAGACTGATGTAAATCCGACCGGGCTCAATACTCATCTTTGTG 105
OY 22 GluberleuAgaenGlnAlaLyasppProlyseuleysCytyrGlyIlepromet--- 40
Db 106 GATAAATCCGAACAACAGTAAAGATTCCAAACCTGAAATACCGTGTAACGACATAGCC 165
OY 41 LeudProapThrsenSerThrProlyeTyrlenuValLybleuGlnGlyAlaasnleu 60
Db 166 GTGATAGGCCCACTTCTTAAGAAAATAATCCTTAGAATTAATTTCCAAAGTCCCGA--- 222
OY 61 LysThrIleThrMetLeuArgArgAsnAsnleuTyraImecGlyTyr-----Ser 78
Db 223 GGAACGGCTCACTTGCGCTTAAACGCATTAATCTGTATGTGTCGCGATCTTGCATG 282
OY 79 AspProPheasnGlyAsnLyCyseArgTyriHisIlePheasnApIleThrserThrglu 98
Db 283 GATAAACGATGTTAATCCGGCA---TATTACTTCAAGTACGAATTAATCTTCCCGCAG 339
OY 99 ArgThrAspValGlueanThrleucySeSerSerSerSerSerArgValAlaMetserile 118
Db 340 TTAACC-----GCCCTTTTCCACAGGCGCAACATGCAATCAAGAAGCTTTA 387
OY 119 AsnTyraSenSerleuTyProThrMetcGluLysIleValaglVal-----Asn 134
Db 388 GAATTAACACAGAGATTATCACTCGATTAAGAAAAGTAATCCAGATTAACACAGAGATCAA 447
OY 135 SerArgasnGlnValGlnLeuGlyIleGlnIleleuSerSerAspIleGlyLysIleSer 154
Db 448 AGTGAAGAAAAGAACCTCGGTTGGGGATGTGACTTACTTCAAGTCATGGAACAGATGAAAC 507
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Db 508 ---AAGAAGCACGCTGTGTTAAAGACGAAAGCTGATCTCTTATGCTATTCAGATG 564
OY 175 ValSerGluAlaAlaArgPheLyThrIleGlnIleleuasnGlnValLythrAsnphasnArg 194
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Qy 195 AlAphETyrProAspProLysValIleAsnLeuGluGluTyrGlyLysIleSerGlu 214
Db 625 AAGTTCAACTCGAAGAAACAAAGTATTCAGTTTGAAGTTAACTGAAAAAATTTCTACG 684
Qy 215 AlAlIleHis--AenAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAla 233
Db 685 GCAATATATCGGGAGATCCAAAAACGCGCTTTAATTAAGATTATTCGGGTTTGGGA 744
Qy 234 LysGlyThrIleTyrPleValleuArgValAspGluIleAsnArgAspValAlaLeuLeu 253
Db 745 AAA-----GTAGGCAAGTGAAGACTTG-----CAATGGGACTCCTT 783
Qy 254 LysTyrVal 256
Db 784 ATGTATTG 792

RESULT 15
US-08-718-904-23
Sequence 23, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329Leuburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G9 in Example I.B.2."
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-718-904-23

Alignment Scores:
Pred. No.: 1,84e-33 Length: 804
Score: 341.00 Matches: 94

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Query Match: 25.1% Indels: 22
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US-09-978-274A-4 (1-263) x US-08-718-904-23 (1-804)
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Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuTyrCysTyrGlyIleProMet--- 40
Db 106 GATAAATCCGAAACACAGCTAAAGATCCAACTGAAATACGGTGTACCGACATACCC 165
Qy 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
Db 166 GTGATAGGCCCACTTGAAGAAAAATTCCTTGAATTAATTCNAAGTTCCCGA--- 222
Qy 61 LysThrIleThrLeuMetLeuArgArgAsnLeuTyrValMetGlyTyr-----Ser 78
Db 223 GGAACGGTCTCACTTGGCTTAAACGCGATTAATCTGTATGTGTGCGCGTATCTTGCAATG 282
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Db 283 GATAACAGATGTTAATTCGGCA---TATTACTTCAGATCAGAAATTAATTCGCCGAG 339
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Qy 135 SerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 448 AGTAAAAAGAACTCCGGTGTGGGATGATCACTTTCACAGCTCAGGAAGCAGTAAAC 507
Qy 155 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 174
Db 508 ---AAGAAGGCACTGTGTGTTAAAGACGAGCTAGATTCTTATTCGCTATTCAGATG 564
Qy 175 ValSerGlnAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 194
Db 565 ACGGCTGAGGAGGCGCATTTAGGTACATCAAAACTTGTATCAAGAACCTTCCCAAC 624
Qy 195 AlAphETyrProAspProLysValIleAsnLeuGluGluTyrGlyLysIleSerGlu 214
Db 625 AAGTTCAACTCGAAGAAACAAAGTATTCAGTTTGAAGTTAACTGAAAAAATTTCTACG 684
Qy 215 AlAlIleHis--AenAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAla 233
Db 685 GCAATATATCGGGAGATCCAAAAACGCGCTTTAATTAAGATTATTCGGGTTTGGGA 744
Qy 234 LysGlyThrIleTyrPleValleuArgValAspGluIleAsnArgAspValAlaLeuLeu 253
Db 745 AAA-----GTAGGCAAGTGAAGACTTG-----CAATGGGACTCCTT 783
Qy 254 LysTyrVal 256
Db 784 ATGTATTG 792

Search completed: April 8, 2006, 14:02:09
Job time : 294.08 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 941.609 Seconds
(without alignments)
2309.713 Million cell updates/sec

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Perfect score: 1357
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published.Applications.NA.Main -QWTS=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published.Applications.NA.Main.*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1312	96.7	1092	3	US-09-978-274A-19
4	1050	77.4	1379	3	US-09-978-274A-30
5	1050	77.4	1379	10	US-11-106-187-1
6	1042	76.8	1368	3	US-09-978-274A-31
7	1038.5	76.5	1376	8	US-10-467-009-1

8	793	58.4	465	3	US-09-978-274A-5	Sequence 5, Appl1
9	564	41.6	333	3	US-09-978-274A-7	Sequence 7, Appl1
10	453	33.4	934	3	US-09-978-274A-32	Sequence 32, Appl1
11	453	33.4	934	10	US-11-106-187-3	Sequence 3, Appl1
12	452	33.3	855	10	US-11-106-187-20	Sequence 20, Appl1
13	349	25.7	765	3	US-09-792-793A-66	Sequence 66, Appl1
14	349	25.7	765	6	US-10-375-209A-66	Sequence 66, Appl1
15	349	25.7	984	3	US-09-792-793A-60	Sequence 60, Appl1
16	349	25.7	984	6	US-10-375-209A-60	Sequence 60, Appl1
17	349	25.7	993	3	US-09-792-793A-63	Sequence 63, Appl1
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19	349	25.7	999	3	US-09-792-793A-54	Sequence 54, Appl1
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24	341	25.1	804	6	US-10-189-360-23	Sequence 23, Appl1
25	340	25.1	765	3	US-09-861-257-23	Sequence 23, Appl1
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27	340	25.1	1230	6	US-10-189-360-53	Sequence 53, Appl1
28	340	25.1	1230	3	US-09-861-257-75	Sequence 75, Appl1
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36	340	25.1	1266	6	US-10-189-360-75	Sequence 75, Appl1
37	340	25.1	1269	3	US-09-861-257-81	Sequence 81, Appl1
38	340	25.1	1269	6	US-10-189-360-78	Sequence 78, Appl1
39	340	25.1	1275	3	US-09-861-257-76	Sequence 76, Appl1
40	340	25.1	1275	6	US-10-189-360-73	Sequence 73, Appl1
41	340	25.1	1299	3	US-09-861-257-80	Sequence 80, Appl1
42	340	25.1	1299	6	US-10-189-360-77	Sequence 77, Appl1
43	340	25.1	1320	3	US-09-861-257-76	Sequence 76, Appl1
44	340	25.1	1320	6	US-10-189-360-76	Sequence 76, Appl1
45	337	24.8	804	3	US-09-861-257-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 3
; SOFTWARE: Patentin version 3.1
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-3

Alignment Scores:

Pred. No.: 4,23e-163
Score: 1357.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 792
Matches: 263
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

RESULT 3
US-09-978-274A-19
Sequence 19, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 1092
TYPE: DNA
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:
Pred. No.: 4,19e-157 Length: 1092
Score: 1312.00 Matches: 255
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.7% Indels: 0
DB: 3 Gaps: 0

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QY 21 MetGluSerLeuAArgAnglnAlaLyAspProLyLeuLyCySyrGlyIlePromet 40
DB 61 ATGCAATCTCTTCCTTAATCAAGCAAGATCCAAATCAAAATGCTATGCGATCAATG 120
QY 41 LeuProAspThrAsnSerThrProLySyrLeuLeuValLySleuGlnGlyAlaAsnLeu 60
DB 121 CTACCTTAATCAATTCAGACCCCTTAAGTACTTATGTTAAGCTCCCAAGGTGCAAACTTA 180
QY 61 LysThrIleThrLeuMetLeuAArgAsnAsnLeuTyrrValMetGlyTyrrSerAspPro 80
DB 181 AAAACCATTCACATTAATCTGAGAGCAAAATTAATTAACGATGAGGCTATTCGATCC 240
QY 81 PheAngLyAsnLyCySArgTyrrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGCAATAGATGTCGTTACCATATATTATTAATGATTAACAGACCAAGCACT 300
QY 101 AspValGluAsnThrLeuCySerserSerSerSerArgValAlaMetSerIleAsnTyrr 120
DB 301 GATGTGAGAAATCTCTTGTCTCAAGTTCAAGTCTCGTGTGCAAGTCCATTAACTAC 360
QY 121 AsnSerLeuTyrrProThrMetLeuAArgAsnAsnLeuTyrrValMetGlyTyrrSerAspPro 140
DB 361 AATAGCTTATATCCGACCATGAGAAAAGAAAGCAAGTAATCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLySleSerGlyValAspSerPhePro 160
DB 421 TTGGAAATTCAAATATCTCAGACAGTACATTGAAAATCTCTGAGGTGATTCAATCCCT 480
QY 161 ValLySerThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
DB 481 GTAAATATGAGGCTTTTCTTCTAGTGTACCAATCCAAATGAGTTTCAAGAGCGCGGA 540
QY 181 PheLySyrIleGluAsnGlnValLySerThrAsnPheAsnArgAlaPheTyrrProAspPro 200

DB 541 TTCAATGATCATAAGAGAACCAATCAAGCTAATTTTAAATAGCATTTTACCTGATCC 600
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QY 221 AsnGlyAlaLeuProLySyrProLeuGlnLeuValAspAlaLySgIyThrIleVal 240
DB 661 AATGGGCTTAACTCCAAACCACTTGAGCTAGTGAATGCCAAAGGTACCAAGTGAATAGTT 720
QY 241 LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLySyr 255
DB 721 CTTAGAGTGAATGAATCAATCAATCGTATGTCATCTTAAATGATC 765

RESULT 4
US-09-978-274A-30
Sequence 30, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1379
TYPE: DNA
ORGANISM: Phytiolacca americana
US-09-978-274A-30

Alignment Scores:
Pred. No.: 2,35e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 3 Gaps: 0

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QY 22 GluSerLeuAArgAnglnAlaLyAspProLyLeuLyCySyrGlyIlePrometLeu 41
DB 351 AATGATCTCTGATTAAGAGAAAGATCCAAAGTTAAATGCTAATGAAATCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLySyrLeuLeuValLySleuGlnGlyAlaAsnLeuLyS 61
DB 411 CCCAATCAAAATTAATTCAAAGTACGTTGAGTCCCAAGGTTCAAATTAATAAAA 470
QY 62 ThrIleThrLeuMetLeuAArgAsnAsnLeuTyrrValMetGlyTyrrSerAspProPhe 81
DB 471 ACCATCACTTAATCTGAGAGCAAAATTTGATGATGAGGTTATTCGATCCCTTT 530
QY 82 AsnLyAsnLyCySArgTyrrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGTCCTTAACCAATCTTAAATGATATTCAGGTAATCAAGCAAGAT 590
QY 102 ValGluAsnThrLeuCySerserSerSerSerArgValAlaMetSerIleAsnTyrrAsn 121
DB 591 GTAGAGACTACTCTTGTCCCAAAATTCGATGTTAGTAAACATTAATCTTGTAT 650
QY 122 SerLeuTyrrProThrMetGluLySleValAlaAsnSerArgAsnGlnValGlnLeu 141

US-09-978-274A-31

Alignment Scores:

Pred. No.:	2,46e-122	Length:	1368
Score:	1042.00	Matches:	199
Percent Similarity:	86.6%	Conservative:	28
Best Local Similarity:	76.0%	Mismatches:	35
Query Match:	76.8%	Indels:	0
DB:	3	Gaps:	0

US-09-978-274A-4 (1-263) x US-09-978-274A-31 (1-1368)

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Db 411 CCCAATCAATCAATCAATCAATGCGTGTGGTGGCTCCAGGTTCAAAATAAAAA 470
QY 62 ThrilleuMetleuAArgaAsnleuTyValMetGlyTYrSerAspProPhe 81
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QY 162 LyethrGluAlaPhePheleuValAlaileGlnMetValSerGlnAlaAlaArgPhe 181
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Db 1071 ACAAAT 1076

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US-10-467-009-1

; Sequence 1, Application US/10467009

; Publication No. US20040241673A1

; GENERAL INFORMATION:

APPLICANT: RUTGERS, THE STATE UNIVERSITY
 TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS

FILE REFERENCE: OCSRS 3.4-076

CURRENT APPLICATION NUMBER: US/10/467,009

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: 60/266,396

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1376

TYPE: DNA

ORGANISM: Phytolacca americana

FEATURE:

NAME/KEY: CDS

LOCATION: (225)..(1160)

US-10-467-009-1

Alignment Scores:

Pred. No.:	6,97e-122	Length:	1376
Score:	1038.50	Matches:	200
Percent Similarity:	86.6%	Conservative:	27
Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	76.5%	Indels:	1
DB:	8	Gaps:	1

US-09-978-274A-4 (1-263) x US-10-467-009-1 (1-1376)

```

QY 2 ILeaanthrillethrpheaspalaglYasnalaThrilleasnlySTYrAlaThrPheMet 21
   ::::::::::::::::::::
Db 291 GTGAATCAATCAATCAATCAATGTTGGAAGTACCAACATTAGCAATAGCCACTTTTCTG 350
QY 22 GluSerLeuAArgaEnglnAlaLyAspProlyleuLyScYrTYrGlylleProMetleu 41
   ::::::::::::::::::::
Db 351 AATGATCTTGGTAATGAGCGAAGATCAAGTTAAATGCTAATGGAATACCAATCTG 410
QY 42 ProAspThrAnsSerThrProLySTYrleuValLySerGlnGlyAlaAsnleuLyS 61
   ::::::::::::::::::::
Db 411 CCCAATCAATCAATCAATCAATGCGTGTGGTGGCTCCAGGTTCAAAATAAAAA 470
QY 62 ThrilleuMetleuAArgaAsnleuTyValMetGlyTYrSerAspProPhe 81
   ::::::::::::::::::::
Db 471 ACCATCAACATAAGCTGAGCGAAACAATTTGTATGTGATGGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLyScYrAgtTYrHisllePheAsnAspilleThrSerThrGluArgThraP 101
   ::::::::::::::::::::
Db 531 GAAACCAATAAATGTCTTACCAATATCTTAAATGATCTCAAGTACGAAAGCCAAAGAT 590
QY 102 ValGluAsnThrleuCySerSerSerSerSerArgValAlaMetSerilleAsnTyraSn 121
   ::::::::::::::::::::
Db 591 GTAGAGACTACTCTTTGCC---CCAGCCAATTTCTGTGTAGTAAAAACATAAATCTTGAT 647
QY 122 SerleuTyProThrMetGluLyblyAsnlaGluValAsnSerArgaEnglnValGlnleu 141
   ::::::::::::::::::::
Db 648 AGTGATATCCAAATCAATGGAATCAAAAGCGGAGTAAATCAAGAAGTCAGTCCAACTG 707
QY 142 GlylleGlnlleuSerSerAspilleGlylylleSerGlyValAspSerPheProVal 161
   ::::::::::::::::::::
Db 708 GGAATTCAAATCAATCGACAGTAATATGGAAGATTTCTGAGAGTCAATTCATTCAGTGA 767
QY 162 LyethrGluAlaPhePheleuValAlaileGlnMetValSerGlnAlaAlaArgPhe 181
   ::::::::::::::::::::
Db 768 AAAACCGAAGCCGAATTCCTATGTGTAGCCATACAAATGATGACAGGCGCAAGATTC 827
QY 182 LySTYrilleGluEnglnValLySTYrAsnPheAsnArgAlaPheTYrProAspProLyS 201
   ::::::::::::::::::::
Db 828 AAGTACATAGAGATCGGTGAAAACTAATTTTAAACAGACATTCACACCTTAATCCCAA 887
QY 202 ValilleuAsnleuGluLySTYrGlylylleSerGlnAlaileHAsnAlaLyAsn 221
   ::::::::::::::::::::
Db 888 GTACTTAAATTTGCAAGAGACATGCGGTAAATTTTCAACAGCAATTCATGATGAGCCAAAT 947
QY 222 GlyAlaLeuProLySProleuGluLeuValAspAlaLySgLYrThrlySTPilleValleu 241

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Db 948 GGAGTTTACCCAACTCTGAGCTGATGCCAGTGCTGCCAAGTGATAGTGTG 1007
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuYsYrValangIyThrCysGln 261
Db 1008 AGAGTGTATGAATCAAGCCGATGATGACCTTTAACTAGTGGTGGAAGCTGTGAG 1067
Qy 262 ThrThr 263
Db 1068 ACAACT 1073
RESULT 8
US-09-978-274A-5
; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-5

Alignment Scores:
Pred. No.: 3,47e-91 Length: 465
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 58.4% Indels: 0
Gaps: 0

US-09-978-274A-4 (1-263) x US-09-978-274A-5 (1-465)

Qy 1 MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnYsYrAlaThrPhe 20
Db 1 ATGATAAATAGCATCACTTGTGATGCTGGAATCCACCATTAACAATATGCCACTTT 60
Qy 21 MetGluSerLeuArgAsnGlnAlaIleAspProIleLeuYsYrGlyIleProMet 40
Db 61 ATGGAATCTCTGCTATCAAGCGAAGATCCAAATGCTATGGCATACCAATG 120
Qy 41 LeuProAspThrAsnSerThrProIleYrIleLeuValIleLeuGlnGlyAlaAsnLeu 60
Db 121 CTACCTGATCAATATGAGCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCAAACTTA 180
Qy 61 LysThrIleThrIleuMetLeuArgAsnAsnLeuYrValMetGlyYrSerAspPro 80
Db 181 AAAACCATTAACATTAAGCTGAGAGCGAATTAACCTTAACGTATGCTGATCCC 240
Qy 81 PheAsnGlyAsnYsCysArgYrHisIlePheAsnAspIleThrSerThrgluArgThr 100
Db 241 TTCAATGGCAATAGTCTGTTACCATATATTAATGATATTAACAAGCACCGAAGCACT 300
Qy 101 AspValGluAsnThrIleuYsSerSerSerSerSerSerIrgValAlaMetSerIleAsnYr 120
Db 301 GATGTGAGAAATCTCTTGCTCAAGTTCTAGATTCCTGCTGTGCAATGTCATTAACTAC 360
Qy 121 AsnSerLeuYrProThrMetGluYsValGluValAlaIleAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTATATCGAATCGAAGAAAGAAAGAAAGCAAAATTAACCTCAAGAAATCAAGTCCA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyYsIleSer 154

Db 421 TTGGAAATCAATACTCAGCAGTACATGAAATATCTCT 462

RESULT 9
US-09-978-274A-7
; Sequence 7, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 333
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-7

Alignment Scores:
Pred. No.: 4,54e-62 Length: 333
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
Gaps: 0

US-09-978-274A-4 (1-263) x US-09-978-274A-7 (1-333)

Qy 155 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 174
Db 4 GGAGTGTATCATTCCTGTAAATCTGAGGCTTTTCTACTAGTGATCCAAATG 63
Qy 175 ValSerGluAlaIleArgPheIyYrIleGluAsnGlnValIyThrAsnPheAsnArg 194
Db 64 GTTTCAGAGCAGCGGATTCAGATGAGAACCAAGTCAGACTAATTTAATAG 123
Qy 195 AlaPheTyProAspProIleValIleAsnLeuGluIlyTrpGlyYsIleSerGln 214
Db 124 GCATTTCACTCCATATCCAAAGATTAATTTGAGAGAGATGGGCAAAATCTGTAG 183
Qy 215 AlaIleHisAsnAlaIleAsnGlyAlaLeuProIleYsProIleuValAspAlaYs 234
Db 184 GCATTCACAAATCGCAAGATGGGCTTTAACCAACCACTTGAGCTAGTGATGCCAA 243
Qy 235 GlyThrIyTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuYs 254
Db 244 GTTACCAAGGTATATCTTCAAGATGATGAATCAATCGTATGTGCACTCTTAAG 303
Qy 255 TyrValAsnGlyYrCysGlnThrThr 263
Db 304 TACGTTAATGAACTGTGCAGACACT 330

RESULT 10
US-09-978-274A-32
; Sequence 32, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A


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/ PRIOR APPLICATION NUMBER: 0025225.4
/ PRIOR FILING DATE: 2000-10-14
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
US-09-978-274A-32

Alignment Scores:
Pred. No.: 4.14e-47 Length: 934
Score: 453.00 Matches: 112
Percent Similarity: 56.0% Conservative: 41
Best Local Similarity: 41.0% Mismatches: 94
Query Match: 33.4% Indels: 26
DB: Gaps: 11

US-09-978-274A-4 (1-263) x US-09-978-274A-32 (1-934)

QY 3 AsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGlu 22
DB 73 TCACACATAGTGTGTTGACGTGAGATGCCACACCAAACTACTTAATTCTTGACT 132
QY 23 SerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
DB 133 AGTTGGAGAGAGCGTGAAGACAGAAATTGACATGCCATGGATGATATATGCCACA 192
QY 43 AspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThr 62
DB 193 ACCCTCACTGAACCAACCAAGTATGTGTGGTGCCTCAATTCGGATCT---GGAACA 249
QY 63 IleThrMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsn 82
DB 250 TTCCATTAGCAATCAAGAGGGAATCTTATTTGAGGCTATTCGACATTTACAT 309
QY 83 GlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
DB 310 GGA---AATGTGCTTATTCGATCTTCAAGAT-----TCGAAATCCGATGCC 354
QY 103 GluAsnThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
DB 355 CAAAGAGCCGTTGCCCCCGGAGACAAAGCAAGCTGCGACTCAAAATATATCCCTAT 414
QY 121 AsnSerLeuTyrProThrMetGluLysLysValGluValAsnSerArgAsnGlnValGln 140
DB 415 GAAAGAGTTTACAAAGGATGAATCAAAAGGT-----GGGGCTAGAACTAAATTAGGG 468
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro 160
DB 469 TTAGGAAAGATTAACATCAAGATCGAATGGTTAAATCTACGGCAGAGATCGAACGAT 528
QY 161 -----ValLysThrGluAlaPheLeuLeuValAlaIleGlnMetValSer 176
DB 529 CAGAAAGCATATCAAAAAATGAGGCTGAATTTCTTCTTATAGCGCTTCAATGCTTACT 588
QY 177 GluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAla--- 195
DB 589 GAGGCATCAAGGTTCAATATACATTGAGAAACAAAGGCTAAATTTGATGATGCCAAT 648
QY 196 ---PheTyrProAspProLysValIleAsnLeuGlnGlyLysTyrGlyLysIleSerGlu 214
DB 649 GGGATATGACGCAATCTTAAGCTATTTCTTACAGAAAAATTTGGACAGCTTTCTTAC 708
QY 215 AlaIleHisAsnAlaLysAsnGly-----AlaLeuProLysProLeuGln 229
DB 709 GTCAAT-----GCAAAAGTGGCACTCCGGTATAGTACTGTACTTACTCTGAGAC 762
QY 230 LeuValAspAlaLysGlyThrLysThrIleValLeuArgValAspGlnIleAsnArgAsp 249
DB 763 CTAAAGATGAGATTAATAAATCTTGACTAGCGCCACCAATTAATATCCCTAT 414
QY 250 Val---AlaLeuLeuLysTyrValAsnGlyThrCysGln 261
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DB 823 ATTATGGACTCTTACCCACGTT-----ACTTGCAG 855
RESULT 11
US-11-106-187-3
/ Sequence 3, Application US/11106187
/ Publication No. US20050183162A1
/ GENERAL INFORMATION:
/ APPLICANT: TUMER, NILGUN E.
/ APPLICANT: MANG, FINGER
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106.187
/ CURRENT FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721.047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 3
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (1)..(75)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (76)..(930)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(930)
US-11-106-187-3

Alignment Scores:
Pred. No.: 4.14e-47 Length: 934
Score: 453.00 Matches: 112
Percent Similarity: 56.0% Conservative: 41
Best Local Similarity: 41.0% Mismatches: 94
Query Match: 33.4% Indels: 26
DB: Gaps: 11

US-09-978-274A-4 (1-263) x US-11-106-187-3 (1-934)

QY 3 AsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGlu 22
DB 73 TCACACATAGTGTGTTGACGTGAGATGCCACACCAAACTACTTAATTCTTGACT 132
QY 23 SerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
DB 133 AGTTGGAGAGAGCGTGAAGACAGAAATTGACATGCCATGGATGATATATGCCACA 192
QY 43 AspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThr 62
DB 193 ACCCTCACTGAACCAACCAAGTATGTGTGGTGCCTCAATTCGGATCT---GGAACA 249
QY 63 IleThrMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsn 82
DB 250 TTCCATTAGCAATCAAGAGGGAATCTTATTTGAGGCTATTCGACATTTACAT 309
QY 83 GlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
DB 310 GGA---AATGTGCTTATTCGATCTTCAAGAT-----TCGAAATCCGATGCC 354
QY 103 GluAsnThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
DB 355 CAAAGAGCCGTTGCCCCCGGAGACAAAGCAAGCTGCGACTCAAAATATATCCCTAT 414
QY 121 AsnSerLeuTyrProThrMetGluLysLysValGluValAsnSerArgAsnGlnValGln 140
```

Db 415 GAAAGAGTTACAAAGGATGATCAAGGCT-----GGGGCTAGAACTAAATTAGG 468
Qy 141 LeuGlyIleGlnIleuSerSerApIleGlyValIleSerGlyValAspSerPhePro 160
Db 469 TTGAGAAAGATACACCTCAAGAGTCGAATGGTTAAATCTACGCAAGATGCAAGGAT 528
Qy 161 -----ValIlyThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSer 176
Db 529 CAGAGCAGTATCAAAAAATGAGGCTGAATTTCTCTTATAGCGTTCAAAATGTTACT 588
Qy 177 GluAlaAlaIlePheIlySerIleGlnValIleGlnValIleThrAsnPheAsnArgAla--- 195
Db 589 GAGCAGTCAAGGTTCAATACATTCATGAGAACAAAGCTAAATTTGATGATGCAAT 648
Qy 196 ---PheIlyProAspProIlyValIleAsnLeuGlnIlyIlySerIlyIleSerGlu 214
Db 649 GGGTATACGCCAGATCTTAAGCTATTTCCCTAGAGAAAAATGGGACAGTGTTCCTAG 708
Qy 215 AlaIleHisAsnAlaIlyAsnGly-----AlaLeuProIlySerProLeuGlu 229
Db 709 GTCATT-----GCAAAAGTTGGCAGCTCCGGTGATAGTACTTACTTACCTTAGAGAC 762
Qy 230 LeuValAspAlaIlySerGlyThrIlySerIleValLeuArgValAspGluIleAsnArgAsp 249
Db 763 CTAAAGATGAGATATAATAAACCCTTGACCTAGCCGCAACGATGAACGACTTAAGAACGAC 822
Qy 250 Val---AlaLeuLeuIlySerIlyValAsnGlyThrCysGln 261
Db 823 ATTAGGCACTCTTAACCCACGTT-----ACTTGCAAG 855

RESULT 12

US-11-106-187-20
/ Sequence 20, Application US/11106187
/ Publication No. US20050183162A1
/ GENERAL INFORMATION:
/ APPLICANT: TOWER, NUGUN E.
/ APPLICANT: WANG, PINGER
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106,187
/ CURRENT FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721,047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 20
/ LENGTH: 855
/ TYPE: DNA
/ ORGANISM: *Phytolacca americana*
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(855)
US-11-106-187-20

Alignment Scores:

Pred. No.: 4.81e-47 Length: 855
Score: 452.00 Matches: 112
Percent Similarity: 56.1% Conservative: 90
Best Local Similarity: 41.3% Mismatches: 43
Query Match: 33.3% Indels: 26
DB: 10 Gaps: 11

US-09-978-274a-4 (1-263) x US-11-106-187-20 (1-855)

Qy 5 ILeThrPheAspAlaGlyAsnAlaThrIleAsnIlySerAlaThrPheMetGluSerLeu 24
Db 4 ATAGCTTTTGAACCTTGAGAAATGCCACACGAAACCTACTCTAATTTTCTGACTAGTTTG 63
Qy 25 ArgAsnGlnAlaIlyAspProIlyLeuIlyCysIlyGlyIleProMetLeuProAspThr 44

Db 64 CGAAGAGCTGTGAAGAACAAGAAATGACATGGCAGATGATGATTAATGGCACACCTTC 123
Qy 45 AsnSerThrProIlySerIlyLeuLeuValIlyIleGlnGlyAlaAsnLeuIlyThrIleThr 64
Db 124 ACTGAACACCCCAAGATATGTTGGTTGACCTCAAAATTCGAACT---GGAACTATTCACA 180
Qy 65 LeuMetLeuArgArgAsnAsnLeuIlyValIleMetGlyTyrSerAspProPheAsnGlyAsn 84
Db 181 TTAGCAATCAAGAGGGAACCTTATTTTGAGAGGCTATTTCTGACATTTCAATGGA--- 237
Qy 85 IlyCysArgGlyThrHisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsn 104
Db 238 AAATGTCTTATCGATCTTCAAGAT-----TCGAATCCGATGCCCAAGAG 285
Qy 105 ThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnIlyAsnSer 122
Db 286 ACCGTTGGCCCCGGGACAAAGCAAGCCTGGCACTCAGAAATATATCCCTATGAAAG 345
Qy 123 LeuIlyProThrMetGluIlyIlyValAlaIleAsnSerArgAsnGlnValGlnLeuGly 142
Db 346 AGTTACAAAGGATGCAATCAAGGCT-----GGGGCTAGAACTAAATTAGGTTAGGA 399
Qy 143 IleGlnIleuSerSerApIleGlyIlyIleSerGlyValAspSerPhePro----- 160
Db 400 AAGATTAACACTCAAGAGTGAATGGGTAAATCTACGGCAAGATGCAACGATCAGAG 459
Qy 161 -----ValIlyThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 178
Db 460 CAGTATCAAAAAATGAGGTGAATTTCTTATAGCCGTTCAAAATGGTTACTAGGCA 519
Qy 179 AlaArgPheIlySerIleGlnValAsnGlnValIlyThrAsnPheAsnArgAla-----Phe 196
Db 520 TCAAGGTTCAAAATCAATTCAGAACAAAGTCAGAACTTAATTTGATGATGCAATGGGTAT 579
Qy 197 TyrProAspProIlySerValIleAsnLeuGlnIlyIlySerIlyIlySerGluAlaIle 216
Db 580 CAGCCAGATCTTAACCTATTTCCCTAGAGAAAAATGGACAGTGTTCCTAGATGTCATT 639
Qy 217 HisAsnAlaIlyAsnGly-----AlaLeuProIlySerProLeuGlnLeuVal 231
Db 640 -----GCAAAAGTTGACACCTCCGGTGATAGTACTTACTTACCTGAGACCTTAAGA 693
Qy 232 AspAlaIlySerGlyThrIlySerIleValIleuArgValAspGluIleAsnArgAspVal--- 250
Db 694 GATGAGATATAATAAACCCTTGACATGAGCCACACATAGACGACTTAAGAACGATTAAG 753
Qy 251 AlaLeuLeuIlySerIlyValAsnGlyThrCysGln 261
Db 754 GCACTCTTAACCCACGTT-----ACTTGCAAG 780

RESULT 13

US-09-792-793a-66
/ Sequence 66, Application US/09792793A
/ Patent No. US20020168370A1
/ GENERAL INFORMATION:
/ APPLICANT: McDonald, John R.
/ APPLICANT: Cogline, Philip
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
/ FILE REFERENCE: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
/ CURRENT APPLICATION NUMBER: US/09/792,793A
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 66
/ LENGTH: 765
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
/ OTHER INFORMATION: Methionine-Saporin fusion protein
/ NAME/KEY: CDS

LOCATION: (1)..(765)
US-09-978-274a-66

Alignment Scores:

Pred. No.:	6.39e-34	Length:	765
Score:	349.00	Matches:	94
Percent Similarity:	56.1%	Conservative:	48
Best Local Similarity:	37.2%	Mismatches:	90
Query Match:	25.7%	Indels:	21
DB:	3	Gaps:	9

US-09-978-274a-4 (1-263) x US-09-978-274a-66 (1-765)

```
QY 1 MetlleantThrllethPheaspAlaGlyAsnAlaThrIleAsnlyTyraIaThrPhe 20
    |||:::|||||
D 1 ATGGTTACTGATATTACCTCGACCTGGTCAATCCGACCGCCGCAATATAGCAGCTTC 60
QY 21 MetGluSerleuArgAsnGlnAlaIleAspProlyseuIysCybTyrglyIlePromet 40
    |||:::|||||
D 61 GTGGATTAAGATTCTTAACAAAGTAAAGATCCGAATCGAATACGGGTACTGATATT 120
QY 41 ---LeuProAspThrAsnSerThrProlyseTyreuleuValIysleuGlnGlyAlaAsn 59
    |||:::|||||
D 121 GCGGTCAATCGGTCCGCGGAGCAAGAAAGTTCTCGCGCATTAATTCAAGCTCCGCT 180
QY 60 LeuIysThrIleThrleuMetleuArgAsnAsnleuTyraIleMetGlyTyf----- 77
    |||:::|||||
D 181 ---GCACTGTTCTCTGGGCTGAGCGCATTAACCTGATTTGTTGCTTACTGCGC 237
QY 78 SerAspProPheAsnGlyAsnIysCybArgTyrllePheAsnAspIleThrSerThr 97
    |||:::|||||
D 238 ATGATATATACGAACGTAACCGCGCC---TACTACTTTCGTAGCAGATATACGAGCGCG 294
QY 98 GluArgThrAspValGluAsnThrleuCyseSerSerSerSerSerArgValAlaMetSer 117
    |||:::|||||
D 295 GAATCCACT-----GCTCTGTTCCCGAGGCGACACTGCAAAACCAAAAGCA 342
QY 118 IleAsnTyraAsnSerleuTyfProThMetGluIysIysValGluVal----- 133
    |||:::|||||
D 343 CTGGAATATACGAAGATTACCACTCCATCGAAGAAAGACGCGCATATACCCAGGCGAT 402
QY 134 AsnSerArgAsnGlnValGlnleuGlyIleGlnIleleuSerSerAspIleGlyIysIle 153
    |||:::|||||
D 403 CAATCCCGCAAAAGACTCGGTCTGGGTATGATCTGCTGACGACGACGATGAAGCGGCTC 462
QY 154 SerGlyValAspSerPheProValIysThrGluAlaPhePheleuIleValAlaIleGln 173
    |||:::|||||
D 463 AAC---AAAAAGCTCCGCGGTGTTAAAGACGAAAGCCGCTTCGCTGATGCGCAATTCAG 519
QY 174 MetValSerGluAlaIleArgPheIysTyrlleGluAsnGlnValIysThrAsnPheAsn 193
    |||:::|||||
D 520 ATGACGCGCAAGACCGCCGCTTCGCTACATTCAGAACTCGTCATCAAAATCTCCG 579
QY 194 ArgAlaPheTyfProAspProlyseValIleAsnleuGlnIysTyfGlyIysIleSer 213
    |||:::|||||
D 580 AACAAAGTTCAATTCGGAATTAAGTCAATTCAGTTCAAGTTAATGGAATAAATATTC 639
QY 214 GluAlaIleHis---AsnAlaIysAsnGlyAlaIleuProlyseProleuGlu---LeuValAs 232
    |||:::|||||
D 640 ACCGCCATTTATGGTACGCGAAGACGCGTTCATTAATAAAGTTAATGTTGGTTTC 699
QY 232 Ala-----LysGlyThrIysTyfIle 239
    |||:::|||||
D 700 GGTAAGTACGTCAGTGAAGACCTCAATTCGCTC 736
```

RESULT 14

US-10-375-209A-66
Sequence 66, Application US/10375209A
Publication No. US20030215421A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.
CO-INVENTOR: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-6018
CURRENT APPLICATION NUMBER: US/10/375, 209A

CURRENT FILING DATE: 2003-02-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 66

LENGTH: 765

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Description of Artificial Sequence: Construct encoding

NAME/KEY: CDS

LOCATION: (1)..(765)

US-10-375-209A-66

Alignment Scores:

Pred. No.:	6.39e-34	Length:	765
Score:	349.00	Matches:	94
Percent Similarity:	56.1%	Conservative:	48
Best Local Similarity:	37.2%	Mismatches:	90
Query Match:	25.7%	Indels:	21
DB:	6	Gaps:	9

US-09-978-274a-4 (1-263) x US-10-375-209A-66 (1-765)

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QY 1 MetlleantThrllethPheaspAlaGlyAsnAlaThrIleAsnlyTyraIaThrPhe 20
    |||:::|||||
D 1 ATGGTTACTGATATTACCTCGACCTGGTCAATCCGACCGCCGCAATATAGCAGCTTC 60
QY 21 MetGluSerleuArgAsnGlnAlaIleAspProlyseuIysCybTyrglyIlePromet 40
    |||:::|||||
D 61 GTGGATTAAGATTCTTAACAAAGTAAAGATCCGAATCGAATACGGGTACTGATATT 120
QY 41 ---LeuProAspThrAsnSerThrProlyseTyreuleuValIysleuGlnGlyAlaAsn 59
    |||:::|||||
D 121 GCGGTCAATCGGTCCGCGGAGCAAGAAAGTTCTCGCGCATTAATTCAAGCTCCGCT 180
QY 60 LeuIysThrIleThrleuMetleuArgAsnAsnleuTyraIleMetGlyTyf----- 77
    |||:::|||||
D 181 ---GCACTGTTCTCTGGGCTGAGCGCATTAACCTGATTTGTTGCTTACTGCGC 237
QY 78 SerAspProPheAsnGlyAsnIysCybArgTyrllePheAsnAspIleThrSerThr 97
    |||:::|||||
D 238 ATGATATATACGAACGTAACCGCGCC---TACTACTTTCGTAGCAGATATACGAGCGCG 294
QY 98 GluArgThrAspValGluAsnThrleuCyseSerSerSerSerSerArgValAlaMetSer 117
    |||:::|||||
D 295 GAATCCACT-----GCTCTGTTCCCGAGGCGACACTGCAAAACCAAAAGCA 342
QY 118 IleAsnTyraAsnSerleuTyfProThMetGluIysIysValGluVal----- 133
    |||:::|||||
D 343 CTGGAATATACGAAGATTACCACTCCATCGAAGAAAGACGCGCATATACCCAGGCGAT 402
QY 134 AsnSerArgAsnGlnValGlnleuGlyIleGlnIleleuSerSerAspIleGlyIysIle 153
    |||:::|||||
D 403 CAATCCCGCAAAAGACTCGGTCTGGGTATGATCTGCTGACGACGACGATGAAGCGGCTC 462
QY 154 SerGlyValAspSerPheProValIysThrGluAlaPhePheleuIleValAlaIleGln 173
    |||:::|||||
D 463 AAC---AAAAAGCTCCGCGGTGTTAAAGACGAAAGCCGCTTCGCTGATGCGCAATTCAG 519
QY 174 MetValSerGluAlaIleArgPheIysTyrlleGluAsnGlnValIysThrAsnPheAsn 193
    |||:::|||||
D 520 ATGACGCGCAAGACCGCCGCTTCGCTACATTCAGAACTCGTCATCAAAATCTCCG 579
QY 194 ArgAlaPheTyfProAspProlyseValIleAsnleuGlnIysTyfGlyIysIleSer 213
    |||:::|||||
D 580 AACAAAGTTCAATTCGGAATTAAGTCAATTCAGTTCAAGTTAATGGAATAAATATTC 639
QY 214 GluAlaIleHis---AsnAlaIysAsnGlyAlaIleuProlyseProleuGlu---LeuValAs 232
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Db      640 ACCGCCATTATGTCGACGCGAAGACCGGTTTTCATTAAGATTAGATTGTTTC 699
QY      232 pAla-----LysGlyThrIleSTPile 239
Db      700 GGTAAAGTACGTACGCTGAAGACCTGCATAATGGGTC 736

RESULT 15
US-09-792-793A-60
; Sequence 60, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogswins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; NUMBER OF FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-792-793A-60

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Alignment Scores:
Pred. No.:      9.64e-34      Length:      984
Score:          349.00      Matches:      94
Percent Similarity: 56.1%      Conservative: 48
Best Local Similarity: 37.2%      Mismatches: 90
Query Match:     25.7%      Indels:      21
DB:              3          Gaps:          9

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US-09-978-274a-4 (1-263) x US-09-792-793A-60 (1-984)

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Db      220 ATGCTACTGATGATACCTCGGACCTGTCATCCGACCCGCGCAATATAGCAGCTTC 279
QY      21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMet 40
Db      280 GTGATTAAGATTGCTAACAACGTAAAGATCCGAATCTGAATAACGGTGTACTGATATT 339
QY      41 --LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsn 59
Db      340 GCGGTATCGGTCCGCGCAAGAAAGAAATTCCTCGGCATTAACCTTCAAGCTCCGT 399
QY      60 LeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr----- 77
Db      400 --GCACTGTTCTCTGGGCTGAAGCGCATTAACCTGATGTTGTTCCTATCTGGCG 456
QY      78 SerAspProPheAsnGlnLysAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 97
Db      457 ATGATTAATACGAACGTGAACCGGGCC--TACTACTTTCGTAGCGAGATTACGAGCGCG 513
QY      98 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 117
Db      514 GAATCCACT-----GCTCTGTTCCCGAGGCGCACTGCATAACCAAAAGCA 561
QY      118 IleAsnTyrAsnSerLeuTyrProMetMetGluLysValGluVal----- 133
Db      562 CTGGAATATATACGAAGATTACCATCATCAGAGAAGAACCGCATCATCACCCAGGGCGAT 621
QY      134 AsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIle 153
Db      622 CAATCCCGCAAGAAAGATGGGTCTGGGTATGATCTGCTGAGCAGAGCATGGAAGCGGTC 681

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QY      154 SerGlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGln 173
Db      682 AAC---AAAAAAGCTCGCGGTGTTAAAGACAAAGCCCGCTTCTGCTGATCGCCATTACG 738
QY      174 MetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsn 193
Db      739 ATGACGGCAGAAAGCCCGCTTCCGCTACATTCAAGAACTGGTCATCAAAAATTCCCG 798
QY      194 ArgAlaPheTyrProAspProLysValIleAsnLeuGlnGluLysTyrGlyLysIleSer 213
Db      799 AACAGTTCATTCCGAGATTAAGTCATTCACTCGAGGTTAATTGAAAAAAATTTCC 858
QY      214 GluAlaIleHis--AsnAlaLysAsnGlyAlaLeuProLysProLeuGln--LeuValAs 232
Db      859 ACCGCCATTATGTCGACGCGAAGACCGGTTTTCATTAAGATTATGATTTGGTTTC 918
QY      232 pAla-----LysGlyThrIleSTPile 239
Db      919 GGTAAAGTACGTACGCTGAAGACCTGCATAATGGGTC 955

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Search completed: April 9, 2006, 03:12:46
Job time : 945.609 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 689.867 Seconds
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Perfect score: 1357
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Searched: 9267905 segs, 2000278028 residues
Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.New:*
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1050	77.4	1360	US-11-010-795-19	Sequence 19, Appl 1
2	453	33.4	934	US-11-010-795-21	Sequence 21, Appl 1

	3	296.5	21.8	1855	8	US-10-893-584-35	Sequence 35, Appl 1
	4	294.5	21.7	1813	8	US-10-893-584-245	Sequence 245, App
	5	293	21.6	1810	8	US-10-893-584-168	Sequence 168, App
	6	292.5	21.6	1807	8	US-10-893-584-196	Sequence 196, App
	7	292	21.5	1855	8	US-10-893-584-3	Sequence 3, Appl 1
	8	292	21.5	1855	8	US-10-893-584-5	Sequence 5, Appl 1
	9	292	21.5	1855	8	US-10-893-584-7	Sequence 7, Appl 1
	10	292	21.5	1855	8	US-10-893-584-9	Sequence 9, Appl 1
	11	292	21.5	1855	8	US-10-893-584-13	Sequence 13, Appl 1
	12	292	21.5	1855	8	US-10-893-584-15	Sequence 15, Appl 1
	13	292	21.5	1855	8	US-10-893-584-17	Sequence 17, Appl 1
	14	292	21.5	1855	8	US-10-893-584-19	Sequence 19, Appl 1
	15	292	21.5	1855	8	US-10-893-584-21	Sequence 21, Appl 1
	16	292	21.5	1855	8	US-10-893-584-23	Sequence 23, Appl 1
	17	292	21.5	1855	8	US-10-893-584-25	Sequence 25, Appl 1
	18	292	21.5	1855	8	US-10-893-584-27	Sequence 27, Appl 1
	19	292	21.5	1855	8	US-10-893-584-29	Sequence 29, Appl 1
	20	292	21.5	1855	8	US-10-893-584-31	Sequence 31, Appl 1
	21	292	21.5	1855	8	US-10-893-584-33	Sequence 33, Appl 1
	22	292	21.5	1855	8	US-10-893-584-37	Sequence 37, Appl 1
	23	292	21.5	1855	8	US-10-893-584-39	Sequence 39, Appl 1
	24	292	21.5	1855	8	US-10-893-584-48	Sequence 48, Appl 1
	25	292	21.5	1855	8	US-10-893-584-50	Sequence 50, Appl 1
	26	292	21.5	1855	8	US-10-893-584-52	Sequence 52, Appl 1
	27	292	21.5	1855	8	US-10-893-584-54	Sequence 54, Appl 1
	28	292	21.5	1855	8	US-10-893-584-74	Sequence 74, Appl 1
	29	292	21.5	1855	8	US-10-893-584-77	Sequence 77, Appl 1
	30	292	21.5	1855	8	US-10-893-584-80	Sequence 80, Appl 1
	31	292	21.5	1855	8	US-10-893-584-83	Sequence 83, Appl 1
	32	292	21.5	1855	8	US-10-893-584-86	Sequence 86, Appl 1
	33	292	21.5	1855	8	US-10-893-584-89	Sequence 89, Appl 1
	34	292	21.5	1855	8	US-10-893-584-92	Sequence 92, Appl 1
	35	292	21.5	1855	8	US-10-893-584-95	Sequence 95, Appl 1
	36	292	21.5	1855	8	US-10-893-584-101	Sequence 98, Appl 1
	37	292	21.5	1855	8	US-10-893-584-101	Sequence 101, App
	38	292	21.5	1855	8	US-10-893-584-104	Sequence 104, App
	39	292	21.5	1855	8	US-10-893-584-110	Sequence 110, App
	40	292	21.5	1855	8	US-10-893-584-113	Sequence 113, App
	41	292	21.5	1855	8	US-10-893-584-116	Sequence 116, App
	42	292	21.5	1855	8	US-10-893-584-119	Sequence 119, App
	43	292	21.5	1855	8	US-10-893-584-122	Sequence 125, App
	44	292	21.5	1855	8	US-10-893-584-125	Sequence 125, App
	45	292	21.5	1861	8	US-10-893-584-11	Sequence 11, Appl 1

ALIGNMENTS

RESULT 1
US-11-010-795-19
: Sequence 19, Application US/11010795
: Publication No. US20060005271A1
: GENERAL INFORMATION:
: APPLICANT: TUMER, NIGUN E.
: TITLE OF INVENTION: RONG
: TITLE OR INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
: FILE REFERENCE: OCTRS 3.0-085
: CURRENT APPLICATION NUMBER: US/11/010,795
: PRIOR APPLICATION NUMBER: 2004-12-13
: PRIOR FILING DATE: 2003-12-12
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 19
: LENGTH: 1360
: TYPE: DNA
: ORGANISM: Phytolacca americana
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (207)..(1145)
US-11-010-795-19
Alignment Scores:

Pred. No.:	4.89e-113	Length:	136C
Score:	1050.00	Matches:	200
Percent Similarity:	87.0%	Conservative:	28
Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	77.4%	Indels:	0
DB:	14	Gaps:	0

US-09-978-274A-4 (1-263) X US-11-010-795-19 (1-1360)

QY 2 ILeaenThrlIethrPheaSpAlaGlyAenAlaThrlIeAenLyStryAlaThrPheMet 21
 Db 273 GTGATATCAATCATCTACATGTTGGAGTACACCATTAAGCAATACGCCACTTTCTG 332
 QY 22 GluSerLeuATgAenGlnAlaLyAspProLySLeuLyStryGlyTLeProMetLeu 41
 Db 333 AATGATCTTCTGTAATGAAGCGAAGATCCAAAGTTTAAATGCTATGAATACCAATGCTG 392
 QY 42 ProAapThrAnSerThProLyStryLeuLeuValLySLeuGlnGlyAlaAenLeuLyS 61
 Db 393 CCCAATCAAAATCAAAATCAAAAGTACGTGGTGTGAGCTCCAAAGTTCAATATAAAAA 452
 QY 62 ThrIleThrLeuMetLeuATgAenAenLeuLyStryValMetGlyTtrySerAspProPhe 81
 Db 453 ACCATCAACACTAAAGCTGAGACGAACAATTTGTATGATGATGGGTATTCGATCCCTT 512
 QY 82 AenGlyAenLyStryGlyTtryHisIlePheaAenApIleThrSerThGluArgThraP 101
 Db 513 GAACCAATTAATGTCGTATCACTATCTTATATGATATCTCAGGTACGAACGCCAAT 572
 QY 102 ValGluAenThrLeuCySerSerSerSerSerSerArgValAlaMetSerIleAapThraP 121
 Db 573 GTAGAGACTACTCTTTGGCCAAATGCCAATTCGTGTGTTAGTAAACATTAACCTTTGAT 632
 QY 122 SerLeuLyStryProThrMetGluLyStryAlaGluValAenSerArgAenGlnValGlnLeu 141
 Db 633 AGTCGATATCCAACTGACATGGAATCAAAACGGGAGTAATATCAAGAAAGTCAAGTCCACTG 692
 QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLyStryIleSerGlyValAspSerPheProVal 161
 Db 693 GGAATTCAAATCACTGCACAGTAATATTTGAAAGATTTCTGAGATGATGTCATTCATCGAG 752
 QY 162 LyStryThrgluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
 Db 753 AAAACCGAAGCGCAATTCCTATTTGGTACCATCAAAATGATATCAAGAGCGCAAGATTC 812
 QY 182 LyStryTlleGluAenGlnValLyStryThraPheaAenArgAlaPheTtryProAspProLyS 201
 Db 813 AAGTACATYAGGAATCAGGTGAAAACTAATTTTAAACAGACATTCMAACCTTAATCCAAA 872
 QY 202 ValIleAenLeuGlnGluLyStryTtryGlyIleSerGluAlaIleHisAenAlaLyAsn 221
 Db 873 GTACTTAATTTGCAAGACACATGGGGTAAAGATTTCAACAGCAATTCATGAAGCCCAAGAT 932
 QY 222 GlyAlaLeuProLyStryProLeuGlnLeuValAspAlaLyStryGlyThrLyStryIleValLeu 241
 Db 933 GGAATTTTACCCAACCTCTCGAGCTAGTGAATGTCACATGGTGCACAAATGATATGTGTG 992
 QY 242 ArgValAspGluIleAenArgAspValAlaLeuLeuLyStryValAenGlyThrCysGln 261
 Db 993 AGAATGTGATGAATCAACAGCTGATGTAGACACTTTAACTACGTTGGTGGAGAGCTGTGAG 1052
 QY 262 ThrThr 263
 Db 1053 ACAACT 1058
 RESULT 2
 US-11-010-795-21
 ; Sequence 21, Application US/11010795
 ; Publication No. US20060005271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TUMER, NILGUN E.
 ; APPLICANT: DT, KONG
 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE

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: TITLE OF INVENTION: RESISTANT TO TRICHOETHCENE FUNGAL TOXINS
:
: FILE REFERENCE: OCRS 3.0-085
:
: CURRENT APPLICATION NUMBER: US/11/010,795
:
: CURRENT FILING DATE: 2004-12-13
:
: PRIOR APPLICATION NUMBER: 60/529,348
:
: PRIOR FILING DATE: 2003-12-12
:
: NUMBER OF SEQ ID NOS: 44
:
: SOFTWARE: PatentIn Ver. 3.3
:
: SEQ ID NO 21
:
: LENGTH: 934
:
: TYPE: DNA
:
: ORGANISM: Phytolacca americana
:
: FEATURE:
:
: NAME/KEY: CDS
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: LOCATION: (1)..(930)
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: US-11-010-795-21

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Alignment Scores:	
Pred. No.:	5.1e-43
Score:	453.00
Percent Similarity:	56.0%
Best Local Similarity:	41.0%
Query Match:	33.4%
DB:	14
Gaps:	11
Length:	93
Matches:	41
Conservative:	11
Mismatches:	94
Indels:	26
Gaps:	11

US-09-978-274A-4 (1-263) x US-11-010-795-21 (1-934)

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Db 784 GCCTTGCTAGTCAATTCATTCAGCAAGAGCTAAATGGTTCACAAATTCAGTGTACGAT 843
Qy 243 ValaAspGluIleAsnArgAspValaAlaLeuLeuLySgLyTyr-----Val 256
Db 844 GTGAGTATATTAAATCCATATACCTCTCAATGCTGTATAGATGCTCCGACAGAAATT 903
Qy 257 AsnGlyThrCys 260
Db 904 GCAGGGCAGTGT 915
RESULT 6
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIORITY FILING DATE: 2004-07-19
; PRIORITY FILING DATE: 2000-04-14
; PRIORITY FILING DATE: 2000-04-14
; PRIORITY FILING DATE: 1999-10-29
; PRIORITY FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-196
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Score: 292.50 Matches: 86
Percent Similarity: 45.9% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 102
Query Match: 21.6% Indels: 51
Gaps: 11
US-09-978-274a-4 (1-263) x US-10-893-584-196 (1-1807)
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Qy 25 ArgAsnGlnAlaLySAspProLySLeuLySgLyTyrGlyIlePheMetLeuProAspThr 44
Db 196 CGCGGTGCTTAAACAACCTGAGCTGAGTGAACATGAATAACCAAGTGTCCAAACGA 255
Qy 45 AsnSerThrPro-----LySgLyThrLeuValLySLeuGlnGlyAlaAsnLeuLyS 61
Db 256 GTTGCTTGCTTAATTAACCAACGCTTATTTAGTGAACCTCAATCATGACAGAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuLySgLyTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTCATTAAGCGCTGAGATGCACCAATCATATGCTGCGCTACCGT----- 366
Qy 82 AsnGlyAsnLySgLySgLyTyr----- 88
Db 367 GCTGAATAATGCGCATATTTCTTTCATCTGACATCAAGAAATGCAGAAACATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108

Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerArgValAlaMetSerIleAsnLySgLyThrAsnSerLeuTyrProThrMetGlu 128
Db 451 -----CAATTAATCAATTCCTTGTGTGTAT-----TATGATATACCTTGA 492
Qy 129 LysLySAlaGluValaAsnSerArgAsnGlnAlaGlnLeuGlyIleGlnIleLeuSerSer 148
Db 493 CACTTGCTGTG---ATCTGAGAGAAATATCAAGTGGGAAATGTCTCACTGAGAGAG 549
Qy 149 AspIleGlyLySLe-----SerGlyValaAspSerPheProValLySgLyThrGlu 164
Db 550 GCTATCTCAGCGCTTATATTATACAGTCTGTGGCACTGACCTTCCAACTCTGCTGCT 609
Qy 165 AlaPhePheLeuValaAlaIleGlnMetValSerGluAlaIleArgPheLySgLyTyrIle 184
Db 610 TCCTTT-----ATTAATTCATCCAAATGATTTCCAGAACGACGAAAGATTCCAAATATATT 663
Qy 185 GluAsnGlnValLySgLyThr-----AsnPheAsnArgAlaPheTyrProAspProLySgVal 202
Db 664 GAGGAGAAATGCGCACAGAAATTAAGTACACCGAGATCTGCACCAAGATCTAGCGTA 723
Qy 203 ILeAsnLeuGlnGluLySgLyTyrGlyLySgLyIleSerGluAlaIleHisAsnAlaLySAsnGly 222
Db 724 ATTAACCTTGAGAAATAGTGGGGAGACTTTCACCTGCATTCAGAGCTTAACCAAGGA 783
Qy 223 AAlaLeuProLySProLeuGlueValaAspAlaLySgLyThrLySgLyThrIleValaLeuArg 242
Db 784 GCCTTGCTAGTCAATTCACCTGCAAAAGCTAAATGCTTCCAAATTCAGTGTACGAT 843
Qy 243 ValaAspGluIleAsnArgAspValaAlaLeuLeuLySgLyTyr-----ValaAsn 257
Db 844 GTGAGTATATTAAATCCATATACCTCTCATGCTGTATAGATCCACGACGAGTAGTCTC 903
Qy 258 GlyThrCys 260
Db 904 GCAGGGCAGTGT 912
RESULT 7
US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIORITY FILING DATE: 2004-07-19
; PRIORITY FILING DATE: 2000-04-14
; PRIORITY FILING DATE: 2000-04-14
; PRIORITY FILING DATE: 1999-10-29
; PRIORITY FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cathepsin B linker regions of PAP-214
US-10-893-584-3
Alignment Scores:
Pred. No.: 1.1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44


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US-09-978-274A-4 (1-263) x US-10-893-584-9 (1-1855)
QY 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
DB 136 ATAACTTTACCAACAGCGGGTGCACGTGTGAAAGCTACCAAACTTTATCAGAGCTGT 195
QY 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
DB 196 CGCGGTGCTTTAAACAACAGCTGATGTGACATGATATATACAGAGTTGCCAAACAGA 255
QY 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyIleAsnLeuLys 61
DB 256 GTTGGTTTGCCTTAAACCAACGCTTATTTAGTTAGTTCAACTTCGAAATCATGACAGCTT 315
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 316 TCGTTACATTTAGCGGTGAGTGTGACCAATGCAATATGTGTGGCTACCGT----- 366
QY 82 AsnGlyAsnLysCysArgTyr----- 88
DB 367 GCTGGAATAGCCCATATTTCTTTTCATCTGACAAATCAGAAAGATGAGAAAGCAATCACT 426
QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
DB 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
DB 451 -----CGATATACATTCGCTTGTGGTGATAT-----TATGATAGACTTGA 492
QY 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
DB 493 CAACCTGCTGCTGCT--AATCTGAGAGAAATATCAGATGGGAAATGCTCCACTAGAGAG 549
QY 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
DB 550 GCTATCTCAGCGCTTATTTATTTACAGTACGTGGTGCGCACTGCACTTCCAACTGCGCTGT 609
QY 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
DB 610 TCCTTT-----ATAATTGCAATCCAAATGATTTGCAAGACAGCAAGATTTCCATATATTT 663
QY 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
DB 664 GAGGGAATAGCGCACGAGAAATTAAGTACACCGGAGATCTGCACACAGATCTTAGCGTA 723
QY 203 IleAsnLeuGlnGluLysThrPGlyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
DB 724 ATTACCTTGAGAAATAGTTGGGGAGACTTTCCACTGCAATTCAGAGTCTTAACCAAGGA 783
QY 223 AlaLeuProLysPheLeuGlnLeuValAspAlaLysGlyThrLysThrPileValLeuArg 242
DB 784 GCTTTGCTTAGTCCCAATTCACCTGCAAGACGTAATGTTCCAAATTCACATGTGTACGAT 843
QY 243 ValAspGlnIleAsnArgAspValAlaLeuLeuLysTyr 255
DB 844 GTGAGTATATTAATCCCTATCATAGCTCATGCTGAT 882

RESULT 11
US-10-893-584-13
/ Sequence 13, Application US/10893584
/ Publication No. US2005022048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Admit
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ PRIORITY FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151

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/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 1855
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pap-224 insert
US-10-893-584-13

Alignment Scores:
Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
DB: Gaps: 10

US-09-978-274A-4 (1-263) x US-10-893-584-13 (1-1855)
QY 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
DB 136 ATAACTTTACCAACAGCGGGTGCACGTGTGAAAGCTACCAAACTTTATCAGAGCTGT 195
QY 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
DB 196 CGCGGTGCTTTAAACAACAGCTGATGTGACATGATATATACAGAGTTGCCAAACAGA 255
QY 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyIleAsnLeuLys 61
DB 256 GTTGGTTTGCCTTAAACCAACGCTTATTTAGTTAGTTCAACTTCGAAATCATGACAGCTT 315
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 316 TCGTTACATTTAGCGGTGAGTGTGACCAATGCAATATGTGTGGCTACCGT----- 366
QY 316 TCGTTACATTTAGCGGTGAGTGTGACCAATGCAATATGTGTGGCTACCGT----- 366
QY 82 AsnGlyAsnLysCysArgTyr----- 88
DB 367 GCTGGAATAGCCCATATTTCTTTTCATCTGACAAATCAGAAAGATGAGAAAGCAATCACT 426
QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
DB 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
DB 451 -----CGATATACATTCGCTTGTGGTGATAT-----TATGATAGACTTGA 492
QY 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
DB 493 CAACCTGCTGCTGCT--AATCTGAGAGAAATATCAGATGGGAAATGCTCCACTAGAGAG 549
QY 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
DB 550 GCTATCTCAGCGCTTATTTATTTACAGTACGTGGTGCGCACTGCACTTCCAACTGCGCTGT 609
QY 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
DB 610 TCCTTT-----ATAATTGCAATCCAAATGATTTGCAAGACAGCAAGATTTCCATATATTT 663
QY 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
DB 664 GAGGGAATAGCGCACGAGAAATTAAGTACACCGGAGATCTGCACACAGATCTTAGCGTA 723
QY 203 IleAsnLeuGlnGluLysThrPGlyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
DB 724 ATTACCTTGAGAAATAGTTGGGGAGACTTTCCACTGCAATTCAGAGTCTTAACCAAGGA 783

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Db 136 ATAACTTTACCAAGCGGGTCCACTGTGCAAGACTACAACTTTATCAGAGCTGTT 195
Qy 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGGTGCTTTAACTGAGAGCTGATGTGAGACATATACAGAGTGGTCCAAACAGA 255
Qy 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGCGTTATTTATTTAGTTAACTCTCAATTCATGACAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTCATTTAGCGCTGATGTTCACCAATGATGTGTGGCTACCGT----- 366
Qy 82 AsnGlyAsnLysCysArgTyr----- 88
Db 367 GCTGGAATAATGCGCATTTCTTTCATCTGCACATCAGGAAGATGAGAAAGCATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
Db 493 CAACCTTGCTGGT---AATCTGAGAGAAATATGCAAGTTGGGAATGGTCCACTAGAGAG 549
Qy 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
Db 550 GCTATCTCAGCGCTTATTTATTTACAGTACGTGCGCACTCAGCTTCCAACTCGTGGCTGT 609
Qy 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
Db 610 TCCTTT-----ATAATTGCATTCCAATATATTTACAGAACAGCAAAATTCCAATATAT 663
Qy 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
Db 664 GAGGAGAAATGCGCAGCAAGAAATTAGGTACACCGAGATCTGCACCAAGATCTCAGGTA 723
Qy 203 IleAsnLeuGlnGluLysTyrGlyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
Db 724 ATTAACCTTGAGATAGATTGGGGAGACTTCCACTGCAATTCAGAGTCTAACCAAGGA 783
Qy 223 AlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTrpIleValLeuArg 242
Db 784 GCCTTTGCTAGTCCAAATTCACGCAAAAGCCTAATGTTCCAAATTCAGTGTGTACGAT 843
Qy 243 ValAspGluLysAsnArgAspValAlaLeuLeuLysTyr 255
Db 844 GTGAGTATATTAATCCCTATCATAGCTCTCATGTGTAT 882

RESULT 14
US-10-893-584-19
Sequence 19, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058

PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 195
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pAP-230 insert
US-10-893-584-19

Alignment Scores:
Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
DB: Gaps: 10

US-09-978-274A-4 (1-263) x US-10-893-584-19 (1-1855)

Qy 5 IleThrPheAspAlaGluValAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACTTTACCAAGCGGGTCCACTGTGCAAGACTACAACTTTATCAGAGCTGTT 195
Qy 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGGTGCTTTAACTGAGAGCTGATGTGAGACATATACAGAGTGGTCCAAACAGA 255
Qy 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGCGTTATTTATTTAGTTGAATCTCAATCATGACAGACTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTCATTTAGCGCTGATGTTCACCAATGATGTGTGGCTACCGT----- 366
Qy 82 AsnGlyAsnLysCysArgTyr----- 88
Db 367 GCTGGAATAATGCGCATATTTCTTTCCTGCAATCAGGAAGATGCAAGACATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
Db 493 CAACCTTGCTGGT---AATCTGAGAGAAATATGCAAGTTGGGAATGGTCCACTAGAGAG 549
Qy 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
Db 550 GCTATCTCAGCGCTTATTTATTTACAGTACGTGCGCACTCAGCTTCCAACTCGGCTGT 609
Qy 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
Db 610 TCCTTT-----ATAATTGCATTCCAATATATTTACAGAACAGCAAAATTCCAATATAT 663
Qy 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
Db 664 GAGGAGAAATGCGCAGCAAGAAATTAGGTACACCGAGATCTGCACCAAGATCTCAGGTA 723
Qy 203 IleAsnLeuGlnGluLysTyrGlyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
Db 724 ATTAACCTTGAGATAGATTGGGGAGACTTCCACTGCAATTCAGAGTCTAACCAAGGA 783
Qy 223 AlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTrpIleValLeuArg 242
Db 784 GCCTTTGCTAGTCCAAATTCACGCAAAAGCCTAATGTTCCAAATTCAGTGTGTACGAT 843

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QY 243 ValAspGluIleAsnArgAspValAlaLeuLeuTyr 255
DB 844 GTGACTATATTAATCCCTATCATAGCTCTCATGGTGTAT 882

RESULT 15
US-10-893-584-21
: Sequence 21, Application US/10893584
: Publication No. US20050272048A1
: GENERAL INFORMATION:
: APPLICANT: Borgford, Thor
: APPLICANT: Braun, Curtis
: APPLICANT: Purac, Admink
: APPLICANT: Stoll, Dominik
: TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
: FILE REFERENCE: 10447-025
: CURRENT APPLICATION NUMBER: US/10/893,584
: PRIOR FILING DATE: 2004-07-19
: PRIOR APPLICATION NUMBER: US 09/551,151
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: US 09/403,752
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 10/089,058
: NUMBER OF SEQ ID NOS: 274
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 1855
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: pAF-232 insert
US-10-893-584-21

Alignment Scores:
Pred. No.: 1.1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
DB: 8 Gaps: 10

US-09-978-274a-4 (1-263) x US-10-893-584-21 (1-1855)
QY 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerIleu 24
DB 136 ATAACTTACCAACAGCGGGTCCACTGTGCAAGCTACACAACTTATCATGAGCTGTT 195
QY 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
DB 196 CGCGGTGCTTAAACAAGTGAAGTGAATGATATACCATGATATACCATGATATACCATGAT 255
QY 45 AsnSerThrPro-----LysTyrIleuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 256 GTTGCTTGCCTATTAACCAACGGTTATTTAGTTGAACCTCAAAATCATGACAGAGCTT 315
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 316 TCTGTACATTAGCGCTGATGTCAACCATGATATGTGTGCTACCTG----- 366
QY 82 AsnGlyAsnLysCysArgTyr----- 88
DB 367 GCTGCAATAGCGCATTTTCTTCATCTCGACATCATGCAAGATGCAAGAAATCATCACT 426
QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
DB 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
DB 451 -----CATATACATTGCGCTTGTGTGTAAT-----TATGATAGACTTGAA 492
QY 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148

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DB 493 CAACCTGCTGGT-----AATCTGAGAGAAATATTCAGTTGGGAAATGTCCTACAGAGAG 549
QY 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
DB 550 GCTATCTCAGCGCTTATTTATTAACAGTACTGTGGCACTCAGCTTCCAATCTGGCTCGT 609
QY 165 AlaPhePheLeuLeuValAlaIleGluMetValSerGluAlaIleArgPheLysTyrIle 184
DB 610 TCCTTT-----ATTAATTGCATTCMAATGATTTTCAGAGCAGCAGATTCMAATATAT 663
QY 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
DB 664 GAGGAGAAATGCGCAGCAAGAAATTAAGTACAAACCGAGATCTGCACCAATCTTACGCTA 723
QY 203 IleAsnLeuGlnGlyLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGly 222
DB 724 ATTACACTTGAGAAATAGTTGGGAGACTTCCACTGCATTAAGAGCTTAACCAAGCA 783
QY 223 AlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArg 242
DB 784 GCTTTGCTAGTCCAAATTCAATCACTGCAAGACGTAAATGCTTCAAAATTCAGTGTACAT 843
QY 243 ValAspGluIleAsnArgAspValAlaLeuLeuTyr 255
DB 844 GTGAGTATATTAATCCCATCATAGCTCTCATGGTGTAT 882

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Job time : 696.867 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:06:24 ; Search time 2734.97 Seconds
(without alignments)
9664.530 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465
Sequence: 1 atgataatcagatcacctt.....acattggaataactctctaa 465

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1:*
1: gb Da:*
2: gb In:*
3: gb Env:*
4: gb Om:*
5: gb Ov:*
6: gb Pat:*
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8: gb Pr:*
9: gb Ro:*
10: gb Sts:*
11: gb Sy:*
12: gb Un:*
13: gb Vi:*
14: gb Htg:*
15: gb Pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	465	6	AX427706 Sequence
2	462	99.4	792	6	AX427704 Sequence
3	462	99.4	1092	6	AX427720 Sequence
4	459	98.7	945	6	AX427702 Sequence
5	459	98.7	1249	15	PAPAPSRIP
6	447.8	96.3	786	15	AB071855
7	353.4	76.0	783	15	AB071854
8	314	67.5	939	15	AY327475
9	313.2	67.4	882	6	A67183
10	312.4	67.2	714	15	AY603354
11	309.2	66.5	1114	15	AF533515
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13	303.8	65.3	714	15	AY603353
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16	302.8	65.1	1164	15	PAPAP
17	302.8	65.1	1195	6	A42103
18	302.8	65.1	1195	6	I43835

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20	301.2	64.8	714	15	AY603352	AY603352 Phytolacc
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23	301.2	64.8	1379	6	AR136704	AR136704 Sequence
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26	299.6	64.4	1195	6	A36639	A36639 Sequence 1
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31	278	59.8	1052	15	AY137202	AY137202 Phytolacc
32	266.4	57.3	951	6	A67185	A67185 Sequence 3
33	266.4	57.3	2369	15	AF141331	AF141331 Phytolacc
34	255.8	55.0	1113	15	AY071928	AY071928 Phytolacc
35	238.8	51.4	918	6	A43003	A43003 Sequence 1
36	238.8	51.4	918	6	A48150	A48150 Sequence 1
37	238.8	51.4	918	6	I60482	I60482 Sequence 1
38	238.8	51.4	918	6	I89987	I89987 Sequence 1
39	145.6	31.3	1226	15	CAANTPR	X96593 C.aculeatum
40	145.6	31.3	1226	15	CAAV	X96474 C.aculeatum
41	100.6	21.6	1180	15	MCUB0072	U80072 Mesembryant
42	60.6	13.0	926	15	AY491967	AY491967 Beta vulg
43	60.6	13.0	1080	15	BVBETAVUL	X85967 B.vulgaris
44	54.6	11.7	934	6	AX427733	AX427733 Sequence
45	54.6	11.7	1187	15	PAPAPIT	X78628 P.americana

ALIGNMENTS

RESULT 1	AX427706	Sequence 5 from Patent WO0233107.	465 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427706					
DEFINITION	Sequence 5 from Patent WO0233107.					
ACCESSION	AX427706					
VERSION	AX427706.1	GI:21537817				
KEYWORDS						
SOURCE						
ORGANISM	Phytolacca americana (American pokeweed)					
	Phytolacca americana					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;					
	Caryophyllales; Phytolaccaceae; Phytolacca.					
REFERENCE	1	Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.				
AUTHORS						
TITLE	Plant cell death system					
JOURNAL	Patent: WO 0233107-A 5 25-APR-2002;					
	CAMBRIDGE ADVANCED TECH (GB)					
FEATURES						
Source	1..465	location/Qualifiers				
	/organism="Phytolacca americana"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:3527"					
misc_feature	1..3	/note="Initiation codon added via PCR primer"				
misc_feature	462..465	/note="Stop codon added via PCR primer"				
ORIGIN						
Query Match	100.0%; Score 465; DB 6; Length 465;					
Best Local Similarity	100.0%; Pred. No. 4.1e-95;					
Matches	465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGATAATACGATACCTTTGATGCTGAATGCCACATTAACAATATGCACCTTT	60			
Db	1	ATGATAATACGATACCTTTGATGCTGAATGCCACATTAACAATATGCACCTTT	60			
QY	61	ATGGAATCTTGTGATATCAAGCAAGATCCAAACTAAATAGCTATGCAATCAATG	120			
Db	61	ATGGAATCTTGTGATATCAAGCAAGATCCAAACTAAATAGCTATGCAATCAATG	120			
QY	121	CTACCTGATCTAATTCAGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAAGTGAACCTA	180			

|||||
Db 121 CTACCTGATATCTAATTGAGCCCTTAAGTATTGTTAAGCTCCAAAGGTGCAAACTTA 180
Qy 181 AAAACCATTCACCTAATAGTGGAGCGAAATTAACCTTAATACGAGGGCTATTGATGCC 240
Db 181 AAAACCATTCACCTAATAGTGGAGCGAAATTAACCTTAATACGAGGGCTATTGATGCC 240
Qy 241 TTCAATGCAATTAAGTGGCTGTTACCATTAATTAATGATTAATTAACAAGCAGCACT 300
Db 241 TTCAATGCAATTAAGTGGCTGTTACCATTAATTAATGATTAATTAACAAGCAGCACT 300
Qy 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGCTGTTGCAATGTCATTAACTAC 360
Db 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGCTGTTGCAATGTCATTAACTAC 360
Qy 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCA 420
Db 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCA 420
Qy 421 TTGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAAAATCTCTTAA 465
Db 421 TTGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAAAATCTCTTAA 465

RESULT 2
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704
VERSION AX427704.1 GI:21537816

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bakayotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
TITLES Plant cell death system
JOURNAL Patent: WO 0233107-A 3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source location/Qualifiers

misc_feature 1..792
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
misc_feature 1..29
/note="Binding site for primer PS1BP"
misc_feature 1..3
/note="Initiation codon added via PCR primer"
misc_feature complement(436..462)
/note="Binding site for primer PS1SR"
misc_feature 463..492
/note="Binding site for primer PS2BP"
variation 612
/note="Nucleotide change from published sequence"
variation 681..686
/note="Sequence replacing removed XbaI site"
misc_feature complement(765..792)
/note="Binding site for primer PS2SR"
misc_feature 790..792
/note="Stop codon added via PCR primer"

ORIGIN

Query Match 99.4%; Score 462; DB 6; Length 792;
Best Local Similarity 100.0%; Pred.No.1.7e-94;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACATTAACAATATGCACTTT 60
Db 1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACATTAACAATATGCACTTT 60
Qy 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120

|||||
Db 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120
Qy 121 CTACCTGATATCTAATTGAGCCCTTAAGTATTGTTAAGCTCCAAAGGTGCAAACTTA 180
Db 121 CTACCTGATATCTAATTGAGCCCTTAAGTATTGTTAAGCTCCAAAGGTGCAAACTTA 180
Qy 181 AAAACCATTCACCTAATAGTGGAGCGAAATTAACCTTAATACGAGGGCTATTGATGCC 240
Db 181 AAAACCATTCACCTAATAGTGGAGCGAAATTAACCTTAATACGAGGGCTATTGATGCC 240
Qy 241 TTCAATGCAATTAAGTGGCTGTTACCATTAATTAATGATTAATTAACAAGCAGCACT 300
Db 241 TTCAATGCAATTAAGTGGCTGTTACCATTAATTAATGATTAATTAACAAGCAGCACT 300
Qy 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGCTGTTGCAATGTCATTAACTAC 360
Db 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGCTGTTGCAATGTCATTAACTAC 360
Qy 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCA 420
Db 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCA 420
Qy 421 TTGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAAAATCTCT 462
Db 421 TTGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAAAATCTCT 462

RESULT 3
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829

SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
TITLES Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source location/Qualifiers

misc_feature 1..1092
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"
misc_feature 1..29
/note="Binding site for primer PS1BP"
variation 681..686
/note="Modified XbaI site"
misc_feature complement(742..786)
/note="Binding site for primer PCS-PAPSR"
misc_feature 766..806
/note="Binding site for primer PCS-Delta86P"
misc_feature 766..786
/note="REV NIA protease cleavage site"
misc_feature complement(1066..1092)
/note="Binding site for primer SYNPOTDelta86SR"

ORIGIN

Query Match 99.4%; Score 462; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred.No.1.5e-94;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACATTAACAATATGCACTTT 60
Db 1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACATTAACAATATGCACTTT 60
Qy 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120

Db 61 ATGAAATCTCTTGGTATCAAGCGAAGATCCAAATAAATGCTATGCAATACCAATG 120
Qy 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATTTGTTAGTCCAGGTGCAAACTTA 180
Db 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATTTGTTAGTCCAGGTGCAAACTTA 180
Qy 181 AAAACCATTAACATTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTTGATCC 240
Db 181 AAAACCATTAACATTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTTGATCC 240
Qy 241 TTCAATGCAATAGTGTCTGCTTACCATTAATTAATGATTAATTAACAGACCGAAGCACT 300
Db 241 TTCAATGCAATAGTGTCTGCTTACCATTAATTAATGATTAATTAACAGACCGAAGCACT 300
Qy 301 GATGAGCAATACCTTTGCTCAAGTCTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 GATGAGCAATACCTTTGCTCAAGTCTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 361 AATAGCTTAATTCGACCGACGAGAAAGCAAGAGTAACTCAAGAAATCAAGTCCAA 420
Db 361 AATAGCTTAATTCGACCGACGAGAAAGCAAGAGTAACTCAAGAAATCAAGTCCAA 420
Qy 421 TTGGGAATTCGAAATATCTCAAGAGTGAATTTGGAATTAATCTCT 462
Db 421 TTGGGAATTCGAAATATCTCAAGAGTGAATTTGGAATTAATCTCT 462

RESULT 4
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS AX427702
DEFINITION Sequence 1 from Patent WO0233107.
ACCESSION AX427702
VERSION AX427702.1 GI:21537815
KEYWORDS

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
Plant cell death system
Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES
source
location/Qualifiers

1. .945
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
1. .24
/note="Binding site for primer P818P"
misc_feature
complement(735..776)
/note="Binding site for primer PSXDR"
736..777
misc_feature
/note="Binding site for primer PSXDP"
750..759
variation
/note="Sequence replacing removed XbaI site"
complement(922..945)
misc_feature
/note="Binding site for primer P8S2SR"

ORIGIN

Query Match 98.7%; Score 459; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 7.7e-94;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ATAAATGATCACTTGTATGCTGAATGCAATTAACAATATGCACTTTATG 63
Db 73 ATAAATGATCACTTGTATGCTGAATGCAATTAACAATATGCACTTTATG 132
Qy 64 GAATCTCTTGTATCAAGCAAGATCCAAATTAATTAATGCTATGCAATCAATGCTA 123
Db 133 GAATCTCTTGTATCAAGCAAGATCCAAATTAATTAATGCTATGCAATCAATGCTA 192

Qy 124 CCGATACCTAATTCGACCCCTTAAGTACTTATTTGTTAGTCCAGGTGCAAACTTAA 183
Db 193 CCGATACCTAATTCGACCCCTTAAGTACTTATTTGTTAGTCCAGGTGCAAACTTAA 252
Qy 184 ACCATTAACATTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTTGATCCCTTC 243
Db 253 ACCATTAACATTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTTGATCCCTTC 312
Qy 244 AATGCAATAGTGTCTGCTTACCATTAATTAATGATTAATTAACAGACCGAAGCACTGAT 303
Db 313 AATGCAATAGTGTCTGCTTACCATTAATTAATGATTAATTAACAGACCGAAGCACTGAT 372
Qy 304 GTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
Db 373 GTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Qy 364 AGCTTAATTCGACCGACGAGAAAGCAAGAGTAACTCAAGAAATCAAGTCCAAATG 423
Db 433 AGCTTAATTCGACCGACGAGAAAGCAAGAGTAACTCAAGAAATCAAGTCCAAATG 492
Qy 424 GGAATTCGAAATATCTCAAGAGTGAATTTGGAATTAATCTCT 462
Db 493 GGAATTCGAAATATCTCAAGAGTGAATTTGGAATTAATCTCT 531

RESULT 5
PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS PAPASRIP
DEFINITION P.americana mRNA for pokeweed antiviral protein.
ACCESSION X98079
VERSION X98079.1 GI:1707648
KEYWORDS
PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Poyet, J.L. and Hoeveler, A.
cDNA cloning and expression of pokeweed antiviral protein from
cells in *Bescherichia coli* and its inhibition of protein synthesis
in vitro
FRBS Lett. 406 (1-2), 97-100 (1997)
9109394

REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 1249)
Poyet, J.L.
Direct Submission
Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Molculaire, UPR Sciences et Techniques, 16
route de Gray, 25030 Besancon Cedex, FRANCE
Revised by author 20-SEP-1996

REMARK
FEATURES
source
location/Qualifiers
1. .1249
/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"
/tissue_type="seeds"
1. .1249
/gene="PAP-S"
106..1050
/gene="PAP-S"
/note="ribosome-inactivating protein type I"
/codon_start=1
/product="pokeweed antiviral protein"
/protein_id="CAA6702.1"
/db_xref="GI:1707649"
/db_xref="NCBI:P33444"
/db_xref="InterPro:IPR001574"
/db_xref="UniProt/TrEMBL:P33444"
/translation="MRVLMVVVTLTAMIAPTSTCAINTITPDAGNATINKYATFM
ESLRNADKPKLKYGI PMLPDNTPSKYLVLDGAGNLTITLMLRNRLVYMGYS
PFGNRCYHIFNDITSTERTIVENTLCSSSSRVAMSINYNLSVPTMEKAEVNSN

gene
CDS

QVQLGQIISDGIKSGVDSFVKTAEFLVAIQMVSSEAPFKYIENQKTNENKA
FYDPKQVILNEKMGKISDAIHAKNGALPKPELVDAKGTWIVLRVDEINRDVALL
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sig_peptide
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106..177
mat_peptide
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178..1047
polya_signal
/product="unnamed"
1212..1217
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1235
polya_site
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1235

ORIGIN

Query Match 98.7%; Score 459; DB 15; Length 1249;
Best Local Similarity 100.0%; Pred. No. 7.1e-94;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ATAAATACGATCACCTTGAATGCTGGAATGCCACCTTAACAATAATGCCACTTTATG 63
DB 178 ATAAATACGATCACCTTGAATGCTGGAATGCCACCTTAACAATAATGCCACTTTATG 237
QY 64 GAATCTCTTGATATCAAGGAAGAAATCAAACTAATAGCTATGGCATACCAATGCTA 123
DB 238 GAATCTCTTGATATCAAGGAAGAAATCAAACTAATAGCTATGGCATACCAATGCTA 297
QY 124 CCGATATCTAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACCTTAAA 183
DB 298 CCGATATCTAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACCTTAAA 357
QY 184 ACCATTCACATAATGCTGGAAGCAAAATTAATGATGAGCTATTTCTGATCCCTTC 243
DB 358 ACCATTCACATAATGCTGGAAGCAAAATTAATGATGAGCTATTTCTGATCCCTTC 417
QY 244 AATGCAATAAGTGTGCTACATATTTAATGATTTTCAAGACCGAAGCAGCTGAT 303
DB 418 AATGCAATAAGTGTGCTACATATTTAATGATTTTCAAGACCGAAGCAGCTGAT 477
QY 304 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGAAATGTCATTAACTACAT 363
DB 478 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGAAATGTCATTAACTACAT 537
QY 364 AGCTTATATCCGACCATGAGAAAGCAAGATAATCTCAAGAAATCAAGTCCAAATG 423
DB 538 AGCTTATATCCGACCATGAGAAAGCAAGATAATCTCAAGAAATCAAGTCCAAATG 597
QY 424 GGAATTCAAATACCTCAGCAGTGACATTTGAAAAATCTCT 462
DB 598 GGAATTCAAATACCTCAGCAGTGACATTTGAAAAATCTCT 636

RESULT 6
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS
DEFINITION
Phytolacca americana pap2 gene for PAP-S2, partial cds.
AB071855
AB071855.1 GI:19570839
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Honjo, E. and Watanabe, K.
Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 786)
Watanabe, K. and Honjo, E.
Direct Submission
Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,

Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watanake@saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)
Location/Qualifiers

FEATURES

source
1..786
/organism="Phytolacca americana"
/mol_type="genomic DNA"
/db_xref="taxon:3527"
1..786
/gene="pap82"
1..786
/gene="pap82"
/note="mature pokeweed antiviral protein-S2"
/codon_start=1
/product="PAP-S2"
/protein_id="BAB86350.1"
/db_xref="GI:19570840"

gene

CDS

ORIGIN
Query Match 96.3%; Score 447.8; DB 15; Length 786;
Best Local Similarity 98.5%; Pred. No. 2.8e-91;
Matches 452; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 ATAAATACGATCACCTTGAATGCTGGAATGCCACCTTAACAATAATGCCACTTTATG 63
DB 1 ATCAATACCTTCACTTTGATGCTGGAATTCACCACTTAACAATAATGCCACTTTATG 60
QY 64 GAATCTCTTGATATCAAGGAAGAAATCAAACTAATAGCTATGGCATACCAATGCTA 123
DB 61 GAATCTCTTGATATCAAGGAAGAAATCAAACTAATAGCTATGGCATACCAATGCTA 120
QY 124 CCGATATCTAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACCTTAAA 183
DB 121 CCGATATCTAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACCTTAAA 180
QY 184 ACCATTCACATAATGCTGGAAGCAAAATTAATGATGAGCTATTTCTGATCCCTTC 243
DB 181 ACCATTCACATAATGCTGGAAGCAAAATTAATGATGAGCTATTTCTGATCCCTTC 240
QY 244 AATGCAATAAGTGTGCTACATATTTAATGATTTTCAAGACCGAAGCAGCTGAT 303
DB 241 AATGCAATAAGTGTGCTACATATTTAATGATTTTCAAGACCGAAGCAGCTGAT 300
QY 304 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGAAATGTCATTAACTACAT 363
DB 301 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGAAATGTCATTAACTACAT 360
QY 364 AGCTTATATCCGACCATGAGAAAGCAAGATAATCTCAAGAAATCAAGTCCAAATG 423
DB 361 AGCTTATATCCGACCATGAGAAAGCAAGATAATCTCAAGAAATCAAGTCCAAATG 420
QY 424 GGAATTCAAATACCTCAGCAGTGACATTTGAAAAATCTCT 462
DB 421 GGAATTCAAATACCTCAGCAGTGACATTTGAAAAATCTCT 459

RESULT 7
AB071854 783 bp DNA linear PLN 19-MAR-2002
LOCUS
DEFINITION
Phytolacca americana pap1 gene for PAP-S1, partial cds.
AB071854
AB071854.1 GI:19570837
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
gene
CDS

1
Honjo, E. and Watanabe, K.
Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 783)
Watanabe, K. and Honjo, E.
Direct Submission
Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan [E-mail:watakei@saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774]
Location/Qualifiers
1. .783
/organism="Phytolacca americana"
/mol_type="genomic DNA"
/db_xref="taxon:3527"
1. .783
/gene="papel"
/note="papel"
/note="mature pokeweed antiviral protein-S1"
/product="PAP-S1"
/codon_start=1
/protein_id="PAB86349.1"
/db_xref="GI:19570838"
/translation="INITITPDAGNAITINKATPMSLRNKAQBSLKCYGIPMLPNTN
STIKTLVKQASLKTITTLNRNNUYVMSYSDPYDKCKYHIFNDIKGYSVDN
SLCPSSNRYAKPQINNGLYPTLEKAGVSRNVLQGLIQLSDIDIKSGQSFTEK
IEAKFLVLAQWSEARFKIENQKTNFRDPSPDNDKVDLENNKGIKSTAIHNSK
NGALPKELERKNADGKVIYLRVDEIKPDVGLNLYNGTCOAT"

ORIGIN
Query Match 76.0%; Score 353.4; DB 15; Length 783;
Best Local Similarity 87.1%; Pred. No. 7.2e-70;
Matches 400; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

4 ATAAATACGATCACCTTGTGATGCTGGAATGCCACCTTAACTAATAGCACCTTATG 63
Db 1 ATCAATACGATACGATGCTGAGCTGGAATGCCACCTTAACTAATAGCTTATG 60
Qy 64 GAATCTCTTGCTAATCAAGCGAAGATCCAAATTAATAGCTATGCTATCAATGCTA 123
Db 61 GAATCTCTTGCTAATCAAGCGAAGATCCAAATTAATAGCTATGCTATCAATGCTA 120
Qy 124 CTGATATCTAATGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAACCTTAAA 183
Db 121 CCCAATATCTAATCAACCATCAAGTACTTATGTTAAGCTCAAGGTGCAAGCTTAAA 180
Qy 184 ACCATTACCTAATGCTGAGCGAAGATTAATAGCTATGCTATGCTATGCTATGCTATG 243
Db 181 ACCATTACCTAATGCTGAGCGAAGATTAATAGCTATGCTATGCTATGCTATGCTATG 238
Qy 244 AATGCAATTAAGTCTGCTAATCATATATTAATGATATTAACAACGACGACGATGAT 303
Db 239 -AGAGCAATTAAGTCTGCTAATCATATCTTATATGATTAAGCACTGATTAAGATGAT 297
Qy 304 GTGAGCAATTAAGTCTGCTAATCATATCTTATATGATTAAGCACTGATTAAGATGAT 363
Db 298 GTGAGCAATTAAGTCTGCTAATCATATCTTATATGATTAAGCACTGATTAAGATGAT 357
Qy 364 AGCTTATATCGACCATGAGAAAGCAAGCAATTAATCAAAATCAAGTCCAAATG 423
Db 358 GGCTTATATCGACCATGAGAAAGCAAGCAATTAATCAAAATCAAGTCCAAATG 417
Qy 424 GGAATTCAAATACACAGTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 462
Db 418 GGAATTCAAATACACAGTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 456

RESULT 8
AY327475

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
gene
CDS

AY327475 939 bp mRNA linear PLN 01-JUL-2004
Phytolacca heterotepala anti-viral protein PAP (RIP1) mRNA,
complete cde.
AY327475
AY327475.1 GI:37625511
Phytolacca heterotepala
Phytolacca heterotepala
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 939)
Delli Bovi, P. and Corrado, G.
Direct Submission
Submitted (23-JUN-2003) Department of Soil, Plants and
Environmental Sciences, University of Naples 'Federico II', via
Universita' 100, Portici, Naples 80055, Italy
Location/Qualifiers
1. .939
/organism="Phytolacca heterotepala"
/mol_type="mRNA"
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1. .939
/gene="RIP1"
1. .939
/note="RIP1, ribosome inactivating protein"
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/db_xref="GI:37625512"
/translation="MKSMLVVTITVSWLILAPSTWAVNTIIVVGSITTSKVAFTLDD
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QLSILQILSDIDIKISGVSFSEKTEARFLVLAQISAAARFKIENQKTNFRDPS
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ORIGIN
Query Match 67.5%; Score 314; DB 15; Length 939;
Best Local Similarity 80.3%; Pred. No. 5.9e-61;
Matches 368; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

5 TAAATACGATCACCTTGTGATGCTGGAATGCCACCTTAACTAATAGCACCTTATG 64
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Qy 65 AATCTCTCTGTAATCAAGCGAAGATCCAAATTAATAGCTATGCTATCAATGCTATC 124
Db 128 ATGATCTCTGTAATCAAGCGAAGATCCAAATTAATAGCTATGCTATCAATGCTATC 187
Qy 125 CTGATATCTAATGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAACCTTAAA 184
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Qy 244 CCAATTAATTAAGTCTGCTAATCATATATTAATGATATTAACAACGACGACGATGAT 303
Db 248 CCAATTAATTAAGTCTGCTAATCATATATTAATGATATTAACAACGACGACGATGAT 307
Qy 304 AATGCAATTAAGTCTGCTAATCATATATTAATGATATTAACAACGACGACGATGAT 363
Db 308 AATGCAATTAAGTCTGCTAATCATATATTAATGATATTAACAACGACGACGATGAT 357
Qy 364 TGAAGCAATTAAGTCTGCTAATCATATCTTATATGATTAAGCACTGATTAAGATGAT 423
Db 368 TGAAGCAATTAAGTCTGCTAATCATATCTTATATGATTAAGCACTGATTAAGATGAT 417
Qy 424 GGAATTCAAATACACAGTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 462
Db 428 GGAATTCAAATACACAGTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 456

RESULT 8
AY327475

Db	GAATTCAAACTACTCGACAGTGACATTGGAAAAGATTCT	525
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LOCUS	A67183	882 bp DNA linear PAT 05-MAY-1998
DEFINITION	Sequence 1 from Patent EP0808902.	
ACCESSION	A67183	
VERSION	A67183.1	GI:4756167
KEYWORDS		
SOURCE		
ORGANISM	Phyolacca insularis	
	Phyolacca insularis	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
	Caryophyllales; Phycolaccaceae; Phycolacca.	
REFERENCE	1 (bases 1 to 882)	
AUTHORS	Moon,Y., Choi,J., Yun,Y., Jin,J., Hong,E., Lee,J., Choi,K., Lee,J.,	
	Song,S., Choi,Y., Kim,C. and Kim,M.	
	Novel genes encoding antiviral proteins of Phyolacca insularis	
	Nakai and recombinant microorganisms expressing the same proteins	
	Patent: EP 0808902-A 1 26-NOV-1997;	
JOURNAL	JINRO LTD (KR)	
	Other publication JP 9308489 19971202	
	Other publication CA 2186303 19971123	
	Other publication AU 6570696 19971127.	
FEATURES	location/Qualifiers	
source	1..882	
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	/clone_11b="GENOMIC LIBRARY FROM PHYLOLACCA"	
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Query Match	67.4%; Score 313.2; DB 6; Length 882;	
Best Local Similarity	79.9%; Pred. No.9,1e-61;	
Matches	369; Conservative 0; Mismatches 99; Indels 0; Gaps 0;	
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DB	1 ATGGGAATACCATCATCTATCTACCAATGTTGAAGTACACACATTAGCAATATAGCCACTTTT	60
QY	61 ATGGAATCTCTGTAATCAAGCGAAAGATCCAAACGTAATAGTATGAGTATCCAAATG	120
DB	61 CTGGTAATCTTCGTAAGAGCAAAAGATCCAAAGTTTAAATGCTATGAGAAATCCAAATG	120
QY	121 CTACCTGATCTAATTCGACCCCTTAAGTACTTATGTTAAAGCTCCAAAGTCAAACTTA	180
DB	121 TTGCCAATCAAAATCCAAATCCAAAGTACGTTGTTAGTTCGTTCAAGTTCAAATGAA	180
QY	181 AAAACATTACATTAATGCTGAGAGCAAAATTAATTATAGTATGAGTGGCTATTTGATCCC	240
DB	181 AAAACATTACATTAATGCTGAGAGCAAAATTAATTATAGTATGAGTGGCTATTTGATCCC	240
QY	241 TTCAATGCGAATTAATGCTGATCCATATATTTAATGATATTTACAAGACCGAAGCACT	300
DB	241 TTGATTAACCAATTAATGCTGATCCATATATTTAATGATATTTACAAGACCGAAGCACT	300
QY	301 GATGTGAGAAATACCTTTGCTCAAGTCTTGAATTCGATGTTGCAATGCTTAATTAATAC	360
DB	301 GATGTGAGAAATACCTTTGCTCAAGTCTTGAATTCGATGTTGCAATGCTTAATTAATAC	360
QY	361 AATAGCTTATATTCGACATGAGAAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA	420
DB	361 GATAGTCATATTCCAACATTTGAATCAAAAGGAGGAGTAAATCAAGAAATCAAGTCCA	420
QY	421 TTGGGAATTCAAATCTCAGCAGAGGACATTGGAAAAATCTCT	462
DB	421 CTGGGAATTCAAATCTCAGCAGAGGACATTGGAAAAATCTCT	462
RESULT 10		
LOCUS	AY603354	714 bp DNA linear PLN 17-MAY-2004

DEFINITION	Phytolactase acinosa antiviral protein PAPA2 (papa2) gene, papa2-s allele, partial cds.
ACCESSION	AY603354.1 GI:47175558
VERSION	AY603354.1
KEYWORDS	
SOURCE	Phytolactase acinosa (food pokeweed)
ORGANISM	Phytolactase acinosa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
AUTHORS	Chen,G., Lei,J., Zeng,G. and Cao,B.
JOURNAL	1 (bases 1 to 714)
REFERENCE	2 (bases 1 to 714)
AUTHORS	Chen,G., Lei,J., Zeng,G. and Cao,B.
TITLE	Direct Submission
JOURNAL	Submitted (20-APR-2004) Horticultural College, South China Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR China
FEATURES	
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mRNA	
gene	
CDS	
ORIGIN	
Query Match	67.2%; Score 312.4; DB 15; Length 714;
Best Local Similarity	80.1%; Pred. No. 1,5e-60;
Matches 367; Conservative 0; Mismatches 91; Indels 0; Gaps 0;	
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Dd	2 TGAATACATCATCTCAATATGTTGGAAGTCACCACTTACCAAAATACGCCACTTTCTCG 61
Dy	65 AATCTCTGTAATCAGCAGAAAGATCCAAAATCTAAATGCTATGCGATCCCATGCTAC 124
Dd	62 ATAATCTTCGTAATGAAAGCAAAGATCAAGTTAAATGCTATGGAATACCAATGTTC 121
Dy	125 CTGATACTAAATGCACCCCTTAAGTACTATTTGGTTAAGTCCCAAGTGCAAACCTTAATA 184
Dd	122 CCATTAACAATCCAAATCCAAAGTAGCTGTGGTTAAGTCCCAAGTTCAAAATGAAAAA 181
Dy	185 CCATTACCTTAATGCTGAGAAGAAATACCTTAATACGTAATGAGGCGTATTCTGATCCCTTCA 244
Dd	182 CCAACACACAAATGCTGAGACGAAACAAATTTGATGTAATGAGGCGCTATTCTGATCCCTTG 241
Dy	245 ATGGCAATAGTGCCTTACCATATATTTATGATATTAACAAGACCGAAGCACTGATG 304
Dd	242 ATTACCAATAGTGCCTTACCATATCTTTATGATATCTAGGATCTGAACGCGAAGATG 301
Dy	305 TGGAGAACTACTTTGCTCAAGTTCTAAGTTCTCGTGTGCAATGTCCATTACTACATA 364

Db	302	AAGACACTACTCTTTGGCCCAATGCCAATTCCTCGTTAGTATATAAACAATACTATGATA	361
Qy	365	GCTTATATCCGACATGGAAAAAGAGCAAGTAACTCAAGAAATCAAGTCAATTGG	424
Db	362	GTGCAATATCCAAATGGAAATCAAAAGCGGGAGTAAATCAAGAAGTCAAGTTCAACTGG	421
Qy	425	GAATTCAAATACTGACGAGTGCATTTGGAAAAAATCTCT	462
Db	422	GAATTCAAATACTCGACAGTGCATTTGGAAAAAATTTCT	459
RESULT 11			
LOCUS	AF533515	1114 bp	mRNA linear PLN 01-AUG-2005
DEFINITION	Phytolacca octandra anti-viral protein (pap) mRNA, partial cds.		
VERSION	AF533515		
KEYWORDS	AF533515.1 GI:3329822		
SOURCE			
ORGANISM	Phytolacca octandra		
Phytolacca octandra			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.			
1 (bases 1 to 1114)			
Lin, J.S. and McNulty, K.P.			
Direct Submission			
Submitted (29-JUL-2002) Reproductive Technologies, AgResearch			
Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand			
FEATURES			
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ORIGIN			
Query Match	66.5%; Score 309.2; DB 15; Length 1114;		
Best Local Similarity	79.7%; Pred. No. 6.9e-60;		
Matches	365; Conservative 0; Mismatches 93; Indels 0; Gaps 0;		
Qy	5	TAAATGAGTACCTCTTGATGCTGGAAATGCGACCATTAACAATAATGCACTTTATGG	64
Db	46	TGAATATCAATCATCTTCAATGTTGGAGTACCAACATTAGCAAAATACACCACTTCTCGG	105
Qy	65	AATCGTTTCGTAATCAAGCGGAAAGATCCAAACATTAATGCTATGCAATCAATGCTAC	124
Db	106	ATGATCTTCGTAATGAAGCGGAAAGATCCAAATTTAAATGCTATGGAATVCAATATGCTGC	165
Qy	125	CTGATACTAATATGACCCCTTAAGTACTATATGTTAAGCTCCAAGTGCAAACTATAAAA	184
Db	166	CCAAATCAAAATCCAGATCCAAAGTACGCTGTTGAGCTCCAGAGTTCCAAATATAAAAAA	225
Qy	185	CCATTACACTAATGCTGACGAAATVATCTTATACGTATGAGGCTATTTCTGATCCTTCA	244
Db	226	CCATTCACACTATGCTGAGACGAAACAATTTGATGATGAGGCTATTTCTGATCCTTTG	285
Qy	245	ATGGCAATAAATGTCCTTACCAATATATTTATGATATTAACAAGACGGAAGCACTGATG	304
Db	286	ATACCAATAAATGTCCTTACCAATATATTTATGATATTAACAAGACGGAAGCACTGATG	345

QY	305	TGAGAAATACCTTTGCTCAAGTTCAGTTCCTCGGTGGCAATGTCATTAACTACATA	364
DB	346	TAGACACTACTCTTGGCCCAATCCCAATTCCTGCTATTATTTAAAAACATAAATATGATA	405
QY	365	GCTTATATCCGACCATGGAAAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCAAATTGG	424
DB	406	GTGCATATCCAACTTGGATATCAAAAGGGGAGTAAATCAAGAAAGTCAAGTCCAACTGG	465
QY	425	GAATTCAAATTACTAGCAGGTGACATTGGAAAAATCTCT	462
DB	466	GAATTCAAATTACTGACAGTACATGGAAAAATTTCT	503
RESULT 12			
LOCUS	AY049785	1164 bp	mRNA
DEFINITION	Phytolacca acinosa anti-viral protein PAP (PAP) mRNA, complete cds.		
ACCESSION	AY049785		
VERSION	AY049785.1	GI:16356654	
KEYWORDS	Phytolacca acinosa (food pokeweed)		
ORGANISM	Phytolacca acinosa		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.		
AUTHORS	1 (bases 1 to 1164)		
TITLE	Peng,X., Yuan,J. and Qiang,B.		
JOURNAL	Direct Submission		
FEATURES	Submitted (27-JUL-2001) Department of Biochemistry, Institute of Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, P.R. China		
source	location/Qualifiers		
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	2..943		
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	/db_xref="GI:16356655"		
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ORIGIN			
Query Match	65.8%;	Score 306;	DB 15; Length 1164;
Best Local Similarity	79.3%;	Pred. No. 3.6e-59;	
Matches 363;	Conservative 0;	Mismatches 95;	Indels 0; Gaps 0;
QY	5	TAATAGATACCTTGTGATGCTGGAAATGCGACCATTAACAATAATGCGACCTTTATGG	64
DB	69	TGAATACAACTATTTACAAATGTGGAAATGCACCATTAACAATAATGCGACCTTTCTGG	128
QY	65	AATCTTCTGTAATCAAGCGAAAGATCCAAAACTAAATGCTATGCGATACCAATGCTAC	124
DB	129	ATAATCTTCTGTAATGGAAGCGAAAGATCAAGATTTAAATGCTATGGAATACCAATGTTGC	188
QY	125	CTGATTAATTCGACCCCTAAGTACTTATTTGTTAAGTCCAAAGTGCAAACCTAAAA	184
DB	189	CCAATACAAATCCAAATCCAAAGTACGTGTGGTGAAGTCCAAAGTTCAAATAAAAAA	248
QY	185	CCATTAACATTAATGCTGAGCGAAATTAATTAACGTGAATGGGTATTTGATCCCTTCA	244
DB	249	CCATCAACATTAATGCTGAGCGAAACAAATTTGATGATGGGCTATTTGATCCCTTTG	308

QY	245	ATGCGAAATGAAGTGTGTTACCATATATATTTAAATGATTAACAAGCACCAGACCTGATG	304
Db	309	ATACCAATGAAGTGTGTTACCATATCTTTAGTATATCTCAAGTCTGAAAGCCCAAGT	368
QY	305	TGAGAAATCTCTTGTCTCAAGTTCTAGTTCGTGTTCGATATGTCATTAATCAATA	364
Db	369	TAGAGACTACTCTTGTGCCCAATGCCAATTCCTGTGTAGTATGAAAAATTAATCATATGATA	428
QY	365	GCTTATATCCGACCATGGAAAAAGAACGAAGTAACTCAAGAAATCAAGTCCATTTGG	424
Db	429	GTGATATCCCAATGGAAATCCAAAGCGGGATAAATCAAGAAATCAAGTTCAACTGG	488
QY	425	GAATTCAAATACTCAGACGTGACATTTGGAAAAATCTCT	462
Db	489	GAATTCAAATACTCAGACGATATATTTGGAAAGATTCT	526
RESULT 13			
LOCUS	AY603353	714 bp	DNA
DEFINITION	Phytolacca actinosa antiviral protein PAPA1 (papa1) gene, papa1-s	linear	PLN 17-MAY-2004
ACCESSION	AY603353		
VERSION	AY603353.1	GI:47175556	
KEYWORDS			
SOURCE			
ORGANISM	Phytolacca actinosa (food pokeweed)		
REFERENCE	Phytolacca actinosa		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.		
JOURNAL	1 (bases 1 to 714)		
REFERENCE	Chen, G., Lei, J., Cao, B. and Zeng, G.		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 714)		
AUTHORS	Chen, G., Lei, J., Cao, B. and Zeng, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-2004) Horticultural College, South China Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR China		
FEATURES			
source	Location/Qualifiers		
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	/allele="g"		
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	KNGLPRLBELVDASGAKW"		
ORIGIN			
Query Match	65.3%	Score 303.8	DB 15; Length 714;
Best Local Similarity	78.9%	Pred. No. 1.3e-58;	
Matches 362;	Conservative 9%;	Mismatches 97;	Indels 0; Gaps 0;
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Db 1 ATGATATACATCTCTACAAATGTTGGAAAGTACACCAATTACCAAAATACGCCACTTTTCTG 60

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Db 61 AATGATCTCTGTAATGAAAGCAAAAGATCCAAAGTTTAAATGCTATGAAATCCAAATGCTG 120

QY 124 CCTGATCTAATTTGGAACCCCTTAAGTACTTATTTGGTAAAGCTCCAAAGGTGCAAACTTAA 183

Db 121 CCCAATACAAATACAAATCCAAAGTACGCTGTGGTGGTAGCTCCAAAGGTCCAAATTAATA 180

QY 184 ACCATTACATTAATGCTGAGACGAATTACTTAATCGATGGGCTATTTGATCCCTTC 243

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QY 244 AATGGCAATAAAGTCTGTTACCATATATTTAATGATATTACAGACCGAAGCGACTGAT 303

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QY 304 GTGGAGATACTCTTGTCTCAAGTTCTAGTTCTGTGTGCAATGTCATTAACTACAAT 363

Db 301 GTAGAGACTACTCTTGTGCCCAAATGCCAATTTCTGTGTGATAGAAAATTAATCTTTGAT 360

QY 364 AGCTTATATCCGACCAATGAAAAGAAAAGACAGAACTAAATCTCAAGAAATCAAGTCCAA 423

Db 361 AGTGATATCCAAATGGAATCAAAAAGCGGAGATAAATCAAGAAAGTCAAGTCCAACTG 420

QY 424 GGAATTCAAATTAATCAGACGATGACATTTGGAATAATCTCT 462

Db 421 GGAATTCAAATTAATCAGACGATTAATTTGGAATAAGATTTCT 459

FEATURES	source
LOCUS	AF338910
DEFINITION	711 bp mRNA linear
ACCESSION	AF338910
VERSION	AF338910.1
KEYWORDS	GI:13398616
ORGANISM	Phytolacca americana (American pokeweed)
REFERENCE	Phytolacca americana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Gnaphylliales; Phytolaccaceae; Phytolacca.
AUTHORS	1 (bases 1 to 711) Chen, D., Wang, X. and Zhou, G.
TITLE	Pokeweed antiviral protein gene, partial cds
AUTHORS	Unpublished
TITLE	2 (bases 1 to 711) Wang, X., Chen, D. and Zhou, G.
AUTHORS	Direct Submission
TITLE	Submitted (20-JAN-2001) Plant Pathology, Institute of Plant Protection, Chinese Academy of Agriculture Sciences, Yuanmingyuanxilin No.2, Beijing 100094, China
LOCATION/Qualifiers	1..711 /organism="Phytolacca americana" /mol_type="mRNA" /db_xref="taxon:3527" <1..>711 /gene="mpap" <1..>711 /gene="mpap" /note="AYP" /codon_start=1 /product="antiviral protein" /protein_id="AAK21951.1" /db_xref="GI:13398617" /translation="VMTIIYVGSTISKYATFLINDLRNKAQPSLKYGVIPMLPMTN TNKRYVLEQGSNKRTITLMLRNRLNYGSGDPPRANKCRHIFINDISGRDVE TTICPNRNSVSKNINPDSRYPTLSSGAGVKSQVQLGIQIDSNTGKISGWSFTE KTEAEFLVALIQWSEARPKYLEINQVKNFPAFNPVKVNLQETWGIKSTAIHGA KNQVLPDELVLVDSAGAKW"

Query Match 65.1%; Score 302.8; DB 15; Length 711;
Best Local Similarity 78.8%; Pred. No. 2,2e-58;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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QY 5 TAAATACGATCACTTTGATGCTGGAATGCGACCATTAACAATATGACCTTTATGG 64
Db 2 TGAATACATCATCTACATGTTGAGATGACCATTAAGCAATATGCGACCTTTTCTGA 61
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Db 62 ATGATCTTGTATGATGAGGAAAGATCCAAAGTTTAAATGCTATGAGATACCAATGCTGC 121
QY 125 CTGATCTAATTTGCAACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTCCAACTTAAAA 184
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QY 185 CCATTTACCTAATGCTGAGAGCAAAATTAATATGCTATGAGGCTATTTCTGATCCCTTCA 244
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QY 245 ATGCAATTAAGTCTGATGAGGAAATTAATTAATGATTAACAAGCCGAAAGCACTGATG 304
Db 242 AAGCAATTAATGCTGATGAGGAAATTAATTAATGATTAACAAGCTGAAAGCCAAAGATG 301
QY 305 TGGAGAACTACTCTTTGCTCAAGTTCTAGTCTCGTGTGCAATGCTCAATTACTACATA 364
Db 302 TAGAGACTACTCTTTGCCCAATGCGCAATTTCTCGTGTGCAATTAATTAATTTGATTA 361
QY 365 GCTTATATCCGACCATGGAAGAAAGCAAGTAATCAAGAAATCAAGTCCAAATGG 424
Db 362 GTCATATCCCAATGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 421
QY 425 GAATTCAAATCTGAGGAGTCAATGGAATTAATCTCT 462
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RESULT 15
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
DEFINITION AY572976
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (american pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolacaceae; Phytolacca.
REFERENCE
AUTHORS Xiao,Z.A. and Jiang,Y.
TITLE A gene encoding the pokeweed antiviral protein in the leaf of
Phytolacca americana
JOURNAL Unpublished
REFERENCE
AUTHORS Xiao,Z.A.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
100875, China

FEATURES
source
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/mol_type="mRNA"
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/gene="PAP"
/codon_start=1
/product="antiviral protein"
/protein_id="AA577872.1"

/db_xref="GI:45826467"
translation="MKVWLVTYISIMLLAPSTSWAVNTIIYNVGSSTISKYATPLND
LRNAXDPSLKVCIGIPMLPNTNTPKVVIVELQSNKKTITLMLRNMLYMGVSDP
ETNCRHIFPDIDIGTERDQVETTLCSNARSVRKINPDRRYTTLBSKAVKRSQV
QUGIYIDSNIGKISGWSFTEKTEFLVAIDQVBSAARFKITENQVKNRFAFN
PNPVLNMQETWGI STAIHDARKGVLPKLELDVAGAKKI VLRVDEIKPDVALNY
VGSCQTTYNONAMPQLIMSTYVNVNIGDLDEGP"

Query Match 65.1%; Score 302.8; DB 15; Length 942;
Best Local Similarity 78.8%; Pred. No. 2e-58;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Db 68 TGAATACATCATCTACATGTTGAGATGACCATTAAGCAATATGCGACCTTTTCTGA 127
QY 65 AATCTCTGTAATGATGAGGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
Db 128 ATGATCTTGTATGATGAGGAAAGATCCAAAGTTTAAATGCTATGAGATACCAATGCTGC 187
QY 125 CTGATCTAATTTGCAACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTCCAACTTAAAA 184
Db 188 CCAATACAAATACAAATGCAAGTACGTTGTTGTTAGCTCCAAAGTCCAAATTAATAAAA 247
QY 185 CCATTTACCTAATGCTGAGAGCAAAATTAATATGCTATGAGGCTATTTCTGATCCCTTCA 244
Db 248 CCATTCACCTAATGCTGAGAGCAAAATTAATGATGAGGCTATTTCTGATCCCTTGG 307
QY 245 ATGCAATTAAGTCTGATGAGGAAATTAATTAATGATTAACAAGCCGAAAGCACTGATG 304
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QY 305 TGGAGAACTACTCTTTGCTCAAGTTCTAGTCTCGTGTGCAATGCTCAATTACTACATA 364
Db 368 TAGAGACTACTCTTTGCCCAATGCGCAATTTCTCGTGTGCAATTAATTAATTTGATTA 427
QY 365 GCTTATATCCGACCATGGAAGAAAGCAAGTAATCAAGAAATCAAGTCCAAATGG 424
Db 428 GTCATATCCCAATGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 487
QY 425 GAATTCAAATCTGAGGAGTCAATGGAATTAATCTCT 462
Db 488 GAATTCAAATCTGAGGAGTCAATGGAATTAATGGAATTTCT 525
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Job time : 2736.97 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 23:57:17 ; Search time 280.284 Seconds
(without alignments)
11056.934 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465
Sequence: 1 atgataatacagcaccctt.....acattgaaaatactctcttaa 465

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*
14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	465	6	AAD42717 Pokeweed
2	462	99.4	792	6	AAD42716 Pokeweed
3	462	99.4	1092	6	AAD42729 Pokeweed
4	459	98.7	945	6	AAD42715 Pokeweed
5	313.2	67.4	882	2	AAT99556 Pokeweed
6	306	65.8	1164	11	ADMT4765 HIV-1 inh
7	304.4	65.5	1164	11	ADMT4765 HIV-1 inh
8	301.2	64.8	1378	12	ADG76061 Pokeweed
9	301.2	64.8	1379	3	AAD45197 Wild-type
10	301.2	64.8	1379	3	AAD45197 Wild-type
11	301.2	64.8	1379	4	AAC87929 P. amercic
12	301.2	64.8	1379	6	AAD42738 Pokeweed
13	301.2	64.8	1379	10	AD105787 DNA encod
14	299.6	64.4	1195	2	AAD081457 Sequence
15	298	64.1	1195	2	AAD081457 Sequence
16	298	64.1	1378	6	AAD42739 Pokeweed
17	298	64.1	1379	6	AAD42739 Pokeweed
18	282.8	60.8	2472	2	AAD43967 Variant P
19	266.4	57.3	2369	2	AAT99557 Phycolacc

20	266.4	57.3	2369	2	ABA96543	ABA96543 Phycolacc
21	238.8	51.4	918	2	AAQ64893	AAQ64893 Antiviral
22	238.8	51.4	918	2	AAT04782	AAT04782 DNA pWc2
23	97.8	21.0	600	2	ABA96716	ABA96716 Cloning v
24	97.8	21.0	603	2	ABA96547	ABA96547 Cloning v
25	54.6	11.7	934	3	AAD45198	AAD45198 Wild-type
26	54.6	11.7	934	6	AAD42740	AAD42740 Pokeweed
27	46.6	10.0	765	3	AAZ61131	AAZ61131 DNA encod
28	46.6	10.0	984	3	AAZ61125	AAZ61125 DNA encod
29	46.6	10.0	993	3	AAZ61128	AAZ61128 DNA encod
30	46.6	10.0	999	3	AAZ61122	AAZ61122 DNA encod
31	46.6	10.0	999	3	AAZ61119	AAZ61119 DNA encod
32	44	9.5	96	3	AAZ59222	AAZ59222 Putative
33	43.2	9.3	1233	2	AAT43997	AAT43997 E. coli C
34	43.2	9.3	1233	3	AAI2896	AAI2896 Escherich
35	43.2	9.3	1233	9	ACD27613	ACD27613 Bacteri
36	43.2	9.3	1233	10	ADC34646	ADC34646 E. coli C
37	43.2	9.3	1233	10	ADH92070	ADH92070 Fibroblas
38	41.6	8.9	2000	11	ACL35363	ACL35363 Rice stre
39	41.6	8.9	9723	6	ABL34380	ABL34380 Human imm
40	39.8	8.6	2000	11	ACL37108	ACL37108 Rice stre
41	39.6	8.5	783	2	AAT18231	AAT18231 Amplified
42	39.6	8.5	1002	2	AAT17959	AAT17959 HBGR Val
43	39.6	8.5	1002	2	AAT18219	AAT18219 Linker am
44	39.6	8.5	1004	2	AAT18232	AAT18232 Sapotin-H
45	39.6	8.5	1154	2	AAT35743	AAT35743 SAP-Alame

ALIGNMENTS

RESULT 1	
AAAD42717	
ID	AAAD42717 standard; DNA; 465 BP.
XX	
AC	AAAD42717;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed PAP-Salpa protein encoding DNA.
XX	
KW	Necrotic effect; transgenic plant; antiviral protein; pokeweed; gene;
XX	PAP-Salpa; ds.
XX	
OS	Phycolacca americana.
XX	
PH	Key
FT	Location/Qualifiers
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FT	/*tag= a
FT	/product= "PAP-Salpa protein"
XX	
PN	WO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PR	15-OCT-2001; 2001WO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.
XX	
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX	
PI	Thomas CDR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX	
DR	WPI; 2002-489891/52.
XX	
XX	P-PSDB; AAE25920.
PT	Inducing necrotic effect in specific cells of plant by transforming plant
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT	which acts in response to application of specific stimulus to plant.
XX	
PS	Claim 3; Page 77; 87pp; English.
XX	
XX	The invention relates to a method of inducing a necrotic effect in

Db 361 AATAGCTTATATCCGACCATGAGAAAAGAGAGAGAACTAACTCAGAAATCAAGTCCAA 420
Oy 421 TTGGGAATTCAAATATCTCAGACGATGACATTTGGAAAATCTCT 462
Db 421 TTGGGAATTCAAATATCTCAGACGATGACATTTGGAAAATCTCT 462

RESULT 3
AAD42729
ID AAD42729 standard; DNA; 1092 BP.
XX
AC AAD42729;
XX 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW chimeric; rice; cystatin delta D86; NIA protease cleavage site; PCS; ds.
XX
OS Phytoacca americana.
OS Oryza sativa.
OS Tobacco; Etch virus.
OS Chimeric.
XX
FH Key
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FT misc_feature 681..686
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FT /*tag= c
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XX W0200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Disclosure; Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect

CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
CC and Tobacco Etch virus (TEV) NIA protease cleavage site (PCS). (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Query Match 99.4%; Score 462; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred. No. 4.5e-123; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGATTAATATGATACCTTTGATGCTGGAATGCCACATTAACAAATATGCCACTTT 60
Db 1 ATGATTAATATGATACCTTTGATGCTGGAATGCCACATTAACAAATATGCCACTTT 60
Oy 61 ATGGAATCTCTTGTAATCAAGCAAGAACATCAAAATCTAAATGCTATGCAATCAATG 120
Db 61 ATGGAATCTCTTGTAATCAAGCAAGAACATCAAAATCTAAATGCTATGCAATCAATG 120
Oy 121 CTACCTGATTAATGACCCCTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
Db 121 CTACCTGATTAATGACCCCTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
Oy 181 AAAACATTAACATAAGCTGAGACGAAGAAATTAATTATACGATAGGCTATTGATCCC 240
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Db 301 GATGTGAGAAATATCTTTTGTCAAGTTCTAGTTCTGCTGTGCAAGTGCATTAATC 360
Oy 361 AATAGCTTATATCCGACCATGAGAAAAGAGAGAGAACTAACTCAAGAAATCAAGTCCAA 420
Db 361 AATAGCTTATATCCGACCATGAGAAAAGAGAGAGAACTAACTCAAGAAATCAAGTCCAA 420
Oy 421 TTGGGAATTCAAATATCTCAGACGATGACATTTGGAAAATCTCT 462
Db 421 TTGGGAATTCAAATATCTCAGACGATGACATTTGGAAAATCTCT 462

RESULT 4
AAD42715
ID AAD42715 standard; DNA; 945 BP.
XX
XX AAD42715;
XX
XX 15-NOV-2002 (first entry)
XX
XX pokeweed pro-PAP-S protein encoding DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX gene; ds.
XX
XX Phytoacca americana.
XX
XX
XX Key
XX CDS 1..945 location/Qualifiers
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XX primer_bind 1..24 /*tag= b
XX /bound_molecy= "Primer PPS1BP"
XX primer_bind complement(735..776) /*tag= c
XX /bound_molecy= "Primer PSXDR"
XX primer_bind 736..777 /*tag= d
XX /bound_molecy= "Primer PSXDF"
XX misc_feature 750..759

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FT      /note= "Sequence replacing removed XbaI site"
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FT      /cag= f
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XX      NO200233107-A2.
XX      25-APR-2002.
XX      15-OCT-2001; 2001WO-GB004593.
XX      14-OCT-2000; 2000GB-00025217.
XX      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX      Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX      WPI; 2002-489891/52.
XX      P-PSDB; AAE25918.
XX      Inducing necrotic effect in specific cells of plant by transforming plant
PT      with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT      which acts in response to application of specific stimulus to plant.
XX      Claim 24; Page 73-74; 87bp; English.
XX      The invention relates to a method of inducing a necrotic effect in
XX      specific cells of a plant. The method involves transforming the plant
XX      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX      in response to the application of a specific stimulus to the plant so as
XX      to facilitate expression of the pokeweed antiviral protein in specific
XX      cells of the plant. The method is useful for inducing a necrotic effect
XX      in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
XX      protein encoding DNA
SQ      Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
Query Match      98.7%; Score 459; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 3.2e-122; Indels 0; Gaps 0;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      73 ATAAATACGATCACTTTGATGCTGGAATGCGACCATTAACAATATGCGACCTTATG 122
QY      64 GAATCTTCTGTAATCAAGGAAAGATCCAAACTAAATATGCTATGCGATACCAATGCTA 123
DB      133 GAATCTTCTGTAATCAAGGAAAGATCCAAACTAAATATGCTATGCGATACCAATGCTA 192
QY      124 CCTGATACATAATCGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAAACTTAAA 183
DB      193 CCTGATACATAATCGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAAACTTAAA 252
QY      184 ACCATTAACATAATGCTGAGACGAAATTAATTAACGTAATGCGCTATTTGATCCCTTC 243
DB      253 ACCATTAACATAATGCTGAGACGAAATTAATTAACGTAATGCGCTATTTGATCCCTTC 312
QY      244 AATGGCAATTAAGTGTGTTACCATATATTAAATGATTTTCAAGCACCAGCACTGAT 303
DB      313 AATGGCAATTAAGTGTGTTACCATATATTAAATGATTTTCAAGCACCAGCACTGAT 372
QY      304 GTGGAATTAATCTTTTCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTTACAAT 363
DB      373 GTGGAATTAATCTTTTCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTTACAAT 432
QY      364 AGCTTATATCCGACCATGAAAAAGAAAGCAAGATTAACCAAGAAATCAAGTCCATTTG 423
DB      433 AGCTTATATCCGACCATGAAAAAGAAAGCAAGATTAACCAAGAAATCAAGTCCATTTG 492
QY      424 GGAATTCAAATATCTACGACGATGACCTTGGAAAAATCTCT 462
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DB      493 GGAATTCAAATATCTACGACGATGACATTTGAAAAATCTCT 531
RESULT 5
ID      AAT99556 standard; DNA; 882 BP.
XX      AAT99556;
XX      17-OCT-2003 (revised)
DT      08-JUN-1998 (first entry)
XX      Phytoacca insularis antiviral protein gPIP2 gene.
XX      Antiviral protein; gPIP2 gene; viroicide; transgenic plant;
XX      virus resistance; immunocjugate; AIDS; cancer; therapy; ss.
XX      Phytoacca insularis; Nakai.
XX      OS
XX      FH      Location/Qualifiers
XX      FT      1..882
XX      FT      CDS
XX      FT      /cag= a
XX      FT      /transl_except= (pos:715..717, aa:Ile)
XX      EPB08902-A2.
XX      26-NOV-1997.
XX      30-SEP-1996; 96EP-00307159.
XX      22-MAY-1996; 96KR-00017404.
XX      (JINR-) JIN RO LTD.
XX      Moon Y, Choi J, Yun Y, Jin J, Hong B, Lee J, Choi K, Lee J;
XX      PI      Song S, Choi Y, Kim C, Kim M;
XX      WPI; 1998-001788/01.
XX      P-PSDB; AAW26773.
XX      Antiviral proteins of Phytoacca insularis Nakai and their genes - useful
PT      in plant antiviral agents and immunocjugates for the treatment of AIDS
PT      and cancer.
XX      Claim 2; Page 10-12; 26pp; English.
XX      This polynucleotide comprises the coding region of the Phytoacca
XX      insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
XX      designated gPIP2 (see AAW26773). The gPIP2 gene was isolated from leaf
XX      genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
XX      CC      AAT99557), encoding a 35.7 kDa protein (see AAW26774) designated gPIP50,
XX      has also been isolated from P. insularis Nakai. Also claimed are vectors
XX      encoding these antiviral proteins and host cells transformed or
XX      transfected with these vectors. E. coli XL1-Blue MRP. gPIP2 (RCM-10080)
XX      host cells are claimed, as is a process for preparing antiviral protein
XX      by cultivating these cells and purifying the protein from inclusion
XX      bodies. The antiviral proteins and recombinant proteins inhibit protein
XX      synthesis. They can be used as active ingredients of antiviral agents of
XX      plant viruses, and employed in the manufacture of immunocjugates for
XX      the treatment of AIDS and cancer. The isolated genes can be used in the
XX      breeding of transgenic plants having viral resistance. (Updated on 17-OCT
XX      -2003 to standardise OS field)
SQ      Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;
Query Match      67.4%; Score 313.2; DB 2; Length 882;
Best Local Similarity 79.9%; Pred. No. 4.1e-80;
Matches 369; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY      1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACCATTAACAATATGCGACCTTT 60
DB      1 ATGATTAATACGATCACTTTGATGCTGGAATGCGACCATTAACAATATGCGACCTTT 60
|||||
```


PR 02-AUG-2001; 2001CN-00123911.
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX Peng X, Bai L, Yan B;
XX WPI; 2003-469263/45.
DR P-PSDB; ADM74752.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT its expression, separation and purification method in protokaryon.
XX
XX Example 8; Page 9-10; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
CC human immunodeficiency virus (HIV-1) activity, including separation clone
CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC and application of the cDNA in preparation of preparation for curing the
CC virus and tumours. One of the described cDNAs is obtained by separation
CC and cloned from a plant Chinese phytolacca leaf, and one from the trans-
CC acting activation factor (Tat) mutant coded by human immunodeficiency
CC virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
CC the HIV-1 inhibition activity of the invention.
XX

Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;

Query Match 65.5%; Score 304.4; DB 11; Length 1164;
Best Local Similarity 79.0%; Pred. No. 1.5e-77;

Matches 362; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 5 TAAATACGATCAGCTTGTGCTGGAATGCCACATTAAACAATATGCACTTATG 64
DB 290 TGAATACATCATCTCAATGTTGGAATGACACCATACCAATACGCACTTTCTGG 349
QY 65 AATCTCTGTATCAAGGAAAGATCCAAATGCTATGCGATCAATGCTAC 124
DB 350 ATATCTCTGTATGAGGCAAGATCCAGTTTAAATGCTATGGAATACCAATGTC 409
QY 125 CTGATATCTATGAGCCCTTAACTTATGTTAGTTCAGTCAAGTGCAACCTAATA 184
DB 410 CCAATCAATCCAAATCCAAAGTACGTTGGTGGTCCAGGTTCAATTAATAAAAA 469
QY 185 CCATTACATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 244
DB 470 CCAATCACTTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 244
QY 245 ATGCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 304
DB 530 ATACCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 304
QY 305 TGAAGATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 364
DB 590 TAGAGCTACTGTTGCTCCCAATCCCAATCTGCTGTTAGTAAATTAATTAAGTAT 649
QY 365 GCTTATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 424
DB 650 GTCGATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 424
QY 425 GAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 462
DB 710 GAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 462

RESULT 8
ADG76061
ID ADG76061 standard; DNA; 1378 BP.

XX ADG76061;

XX 11-MAR-2004 (first entry)

XX American pokeweed antiviral protein (PAP) DNA Segid 1.

KM gene; de; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX american pokeweed; retroviral.

XX Phytolacca americana.

XX WO2003106479-A2.

XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019141.

XX 17-JUN-2002; 2002US-0389649P.

XX (PARK-) PARKER HUGHES INST.

XX Uckun FM;

XX WPI; 2004-082156/08.

XX P-PSDB; ADG76064.

XX Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

XX This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC depurinating viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX

Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 64.8%; Score 301.2; DB 12; Length 1378;

Best Local Similarity 78.6%; Pred. No. 1.4e-76;

Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCAGCTTGTGCTGGAATGCCACATTAAACAATATGCACTTATG 64
DB 291 TGAATACATCATCTCAATGTTGGAATGACACCATTAACAATACGCACTTTCTGA 350
QY 65 AATCTCTGTATCAAGGAAAGATCCAAATGCTATGCGATCAATGCTAC 124
DB 351 ATGATCTCTGTATGAGGCAAGATCCAGTTTAAATGCTATGGAATACCAATGTC 410
QY 125 CTGATATCTATGAGCCCTTAACTTATGTTAGTTCAGTCAAGTGCAACCTAATA 184
DB 411 CCAATCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 470
QY 411 CCAATCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 470
DB 185 CCATTACATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 244
DB 471 CCAATCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 244
QY 245 ATGCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 304
DB 531 ATACCAATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 304
QY 305 TGAAGATTAAGTCGAGCGAAATTAATTAAGTATGAGGCTATTCGATCCCTCA 364
DB 591 TAGAGCTACTGTTGCTCCCAATCCCAATCTGCTGTTAGTAAATTAATTAAGTAT 649

OY 365 GCTTATATCCGACCATGGAAGAAAGAGAACTCAAGAAATCAAGTCCATTGG 424
 DB 651 GTGATATCCCAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAAGTCAAGTCCAACTGG 710
 OY 425 GAATTCAAATATCTGACGAGTGCATTTGAAAAATCTCT 462
 DB 711 GAATTCAAATATCTGACGAGTAAATTTGAAAAAGATTCT 748

RESULT 9
 AAZ45197
 ID AAZ45197 standard; DNA, 1379 BP.
 AC AAZ45197;
 XX
 DT 29-FEB-2000 (first entry)
 DB
 XX Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
 KM Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
 KM ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
 KM potato virus X; cucumber mosaic virus; CMV; ss;
 KM tomato yellow leaf curl virus.
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "PAP"
 FT /note= "Pokeweed antiviral protein"
 FT
 XX
 PN MO9960843-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011301.
 XX
 PR 22-MAY-1998; 98US-0086374P.
 XX
 PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Turner NE, Wang P;
 XX
 DR WPI; 2000-062555/05.
 DR P-PSDB; AAY58025.
 XX
 PT New antiviral DNA useful for generating transgenic plants resistant to
 PT viruses and/or fungi.
 XX
 PS Example; Page 4-5; 43pp; English.
 XX
 CC This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
 CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
 CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
 CC catalytically removes a specific adenine residue from a highly conserved
 CC stem-loop structure in the 26S rRNA of eukaryotic ribosomes. The pokeweed
 CC antiviral protein II (PAP II) protein confers antiviral and or antifungal
 CC activities to plants. A DNA molecule encoding a PAP II protein with an
 CC intact catalytic active site amino acid residue (S172) is useful for
 CC generating transgenic plants. PAP II DNA is useful for generating a
 CC transgenic plants (especially cereal crops) through transforming a
 CC protoplast or introducing the DNA directly into a plant part prior to
 CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
 CC activity thus have increased resistance to viruses and/or fungi. Viruses
 CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
 CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
 CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
 CC other plants pests including insects, bacteria and nematodes. PAP II DNA
 CC is also useful for identifying a PAP II protein having reduced
 CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
 CC unlike PAP transgenic plants which are stunted and sterile, PAP II
 CC transgenic plants have a normal and fertile phenotype

XX
 SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 Query Match 64.8%; Score 301.2; DB 3; Length 1379;
 Best Local Similarity 78.6%; Pred. No. 1.4e-76;
 Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

OY 5 TAAATACGATCACCTTGATGCTGGAAATGCGACCATTAACAAATATGACCTTTATG 64
 DB 292 TGAATACAAATCTTACAAATGTTGAAATGACACCATTAAGCAATATGCGCACTTTCTGA 351
 OY 65 AATCTCTGTAATCAACGGAAGATCCAAAACATAAAATGCTATGACATACCAATGCTAC 124
 DB 352 ATGATCTTGTATGAAAGCGAAAGTCCAAAGTTTAAATGCTATGGAATACCAATGCTGC 411
 OY 125 CTGATACATAATTCGACCCCTTAAGTACTTATGTTAGCTCCAGAGTGCAAACCTAATA 184
 DB 412 CCAATACAAATACAAATTCCAAAGTACGTTGTTGAGCTCCAAAGTTCAATATAAAAA 471
 OY 185 CCATTACACTAATGCTGAGAGCAATATACCTATACGTAAGGGCTATTCTGATCCCTCA 244
 DB 472 CCAATCACTAATGCTGAGAGCAATATGTAATGATGAGGTTATTTCTGATCCCTTGG 531
 OY 245 ATGCAATATAGTGTGTTACCATATATTTAATGATATTAACAAGACCGAAGCACTGATG 304
 DB 532 AAACCAATTAATGTGTTACCATATCTTTAATGATATCTGAGTATGAAAGCGCAAGATG 591
 OY 305 TGGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTTGCAATGCTCAATTAACATAA 364
 DB 592 TAGAGACTACTCTTTGCCCCAAATCCAAATCTCTGTTAGTAAACATAAATCTTGATA 651
 OY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAACTCAAGAAATCAAGTCCAAATGG 424
 DB 652 GTGATATCCCAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAAGTCAAGTCCAACTGG 711
 OY 425 GAATTCAAATATCTGACGAGTGCATTTGAAAAATCTCT 462
 DB 712 GAATTCAAATATCTGACGAGTAAATTTGAAAAAGATTCT 749

RESULT 10
 AAZ59220
 ID AAZ59220 standard; cDNA, 1379 BP.
 XX
 AC AAZ59220;
 XX
 DT 20-APR-2000 (first entry)
 DB
 XX Pokeweed antiviral protein coding sequence spring leaf form.
 XX
 KM Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 KM resistance; potato virus X; potato virus Y; potato leaf roll virus;
 KM tuber; ss.
 XX
 OS Phytolacca americana.
 XX
 PN US6015940-A.
 XX
 PD 18-JAN-2000.
 XX
 PF 07-APR-1992; 92US-00865169.
 XX
 PR 07-APR-1992; 92US-00865169.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Kaniewski WK, Turner NE, Lodge JK;
 XX
 DR WPI; 2000-126326/11.
 XX
 PT Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX

PS Claim 6; Fig 4; 30pp; English.

CC This is the coding sequence for the spring leaf form of the pokeweed
CC antiviral protein (PAP) which is used to generate transgenic potato
CC plants. PAP is able to confer resistance to infection by potato virus X
CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC potato plant or tuber expressing PAP

SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match	64.8%	Score	301.2	DB	3	Length	1379
Best Local Similarity	78.6%	Pred. No.	1.4e-76				
Matches 360, Conservative	0	Mismatches	98	Indels	0	Gaps	0

Qy	5	TAAATACGATCACTTGGATGCTGGAAATGGCCACATTAACAATATAGCAACCTTATGG	64
Db	292	TGAATACCAATCAATCTACAAATGTTGGAAAGTACCAACATTAGCAATATGCGCACTTTCTGA	357
Qy	65	AATCTCTTGTAATCAAGCGAAAGATCCAAACTAAATAGCTATGGCATACCAATGCTAC	124
Db	352	ATGATCTTGTAATGAAGCGAAAGATCCAAAGTTTAAATGCTATGGAAATCCAAATGCTGC	411
Qy	125	CTGATATCTAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAAGGTGCAACTATAAA	185
Db	412	CCAAATCAAAATCAAAATCCAAAGTACGTGTTGGTGGCTCCAAAGTTCAAAATATAAAAAA	471
Qy	185	CCATTACACTAATGCTGACGACGAAATAACTTATACGATAGGGCTATTGATCCCTTCA	244
Db	472	CCATCAACTAATGCTGACGACGAAACAAATTTGATATGATAGGGTATATTGATCCCTTGG	531
Qy	245	ATGGCAATPAGTGTGCTTACCATATATTTATATGATATTCACAGCACCGAAGCGACGTGATG	304
Db	532	AAACCAATPAAAGTGTGCTTACCATATCTTTAATGATATTCAGGTACTGAAAGCGCAAGATG	591
Qy	305	TGGAGAATATCTTTTGCTCAAGTTCAGTTCGTGCTGTCGTAAGTCCATTAACTTACATATA	364
Db	592	TAGAGCTATCTTTTGCCCAATGCGCAATTTCTGCTTAGTATAAAAACATPAACTTTGATA	651
Qy	365	GCTTATATCCGACCAATGAAAAAGAAAGACAGATTAACATGAAATCAAGTCCAAATTGG	424
Db	652	GTGCAATATCCAACTTTGGAAATCAAAAGCGGAGTAAATATCAAAAGTCAGGTCCAACTGG	711
Qy	425	GAATTCAAATATCTCAGACGATGACATTTGAAAAATCTCT	462
Db	712	GAATTCAAATATCTCAGACGATTAATTTGAAAGATTTCT	749

RESULT 11

ID	standard; DNA; 1379 BP
AAC87929	

AC AAC87929 ;

DT 06-MAR-2001 (first entry)

DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.

KM Phytoecacia americana; pokeweed, pokeweed antiviral protein, PAP; cancer
KM biotherapeutic; fusion protein; immunoconjugate; mutant; cytostatic;
KM anti-IV; human immunodeficiency virus; AIDS; leukemia, lymphoma;
KM brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.

Phytolacca americana.

FH	Key	Location/Qualifiers
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2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
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100	100	100

FT	CDS	225. .1166
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/product= "pokeweed antiviral protein (PAP)"

PN US6146628-A.

PD 14-NOV-2000.

PF 11-JUL-1995; 95US-00501253.

PR 11-JUL-1995; 95US-00501253.

PA (MINU) UNIV MINNESOTA & RUTGERS.

2000

2000

DR P-PSDB; AAB36500.

PT	Immun conjugates used
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PT moiety that binds a cell surface receptor.

PS Disclosure; Col 47-50; 32pp; English

CC The present invention describes a fun

acid substitution at residue 75, 97

CC anti-FLT activities, and is an inhibitor of cellular RNA or protein
CC synthesis. (I) is useful for treating AIDS and cancers including
CC leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
CC tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
CC colon cancer. Immunconjugates prepared using PAP mutants exhibit an
CC improved therapeutic index over immunconjugates containing either wild-
CC type PAP or variant PAP. The present sequence encodes the wild-type PAP,
CC which is given in the exemplification of the present invention

SQ Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match	64.8%	Score 301.2	DB 4	Length 1379
Best Local Similarly	78.6%	Pred. No. 1.4e-76		
Matches 360; Conservative	0	Mismatches 98	Indels 0	Gaps 0

Qy	5	TAATACGATCACTTTGATGCTGGAAATGCAACATTTACAAATATGCCACTTATGG	64
Db	292	TGATTCATCATCTACAAATGTTGGAGATCACCATTTAGCAATAGCCACTTTCTGA	351
Qy	65	AATCTCTGTGATCAAGGAAAGATCCAAAAGTAAATGCTATGGATACCAATGCTAC	124
Db	352	ATGATCTTGTATGAAGGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTGC	411
Qy	125	CTGATCTGATTCGACCCCTAGTACTTATGTTAGTCCAGAGTGCACAACTTAAA	184
Db	412	CCAAATCAAAATCAAAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCCAAATAAAAA	471
Qy	185	CCATTCACTAATGCTGAGACGAAATTAATTATACGATGGCTATTCGATCCCTCA	244
Db	472	CCATCACTAATGCTGAGAGGAAACATTTGTATGATGATGGTTATTCGATCCCTTG	531
Qy	245	ATGGCAATAGTGTGTTTCCATATATTTAATGATATTACAGACCGAAGCGACTGATG	304
Db	532	AAACCAATAAATGTGGTATCCATATCTTTAATGATATCTCAGGTACTGAAAGCGCAAGATG	591
Qy	305	TGGAGAACTCTTTTGGCTCAAGTTCTACTTCCGTTTGAATGTCATTAATCAACATA	364
Db	592	TAGAGCTACTCTTTGGCCCAATGCAATTCCTGGTATGTAATAAACATTAACCTTGATA	651
Qy	365	GCTTATATTCGACATGNAAGAAAGACGAGTAACTCAAGAAATCAAGTCCAAATGG	424
Db	652	GTCGATATCCAACTTGGATCAAAAGGGGAGTAAATCAAGAAAGTCAAGTCCAACTGG	711
Qy	425	GAATTCAAATCTCAGCAGTGCATTTGGAAAAATCTCT	462
Db	712	GAATTCAAATCTCAGCAGTATATATTTGAAAGATTTCT	749

RESULT 12

ID AAD42738 standard; DNA; 1379 BP

ID AAD42738 standard; DNA; 1379 BP.

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XX AC AAD42738;
XX DT 15-NOV-2002 (first entry)
XX DE Pokeweed PAP' DNA #1.
XX KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; de.
XX OS Phytolacca americana.
XX FH Key Location/Qualifiers
XX FT misc_feature 290..1076
XX FT /*tag= a
XX FT /note= "Mature PAP' sequence"
XX PN WO20023107-A2.
XX PD 25-APR-2002.
XX PP 15-OCT-2001; 2001WO-GB004593.
XX PR 14-OCT-2000; 2000GB-00025217.
XX PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX PI Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX DR WPI; 2002-489891/52.
XX PT Inducing necrotic effect in specific cells of plant by transforming plant
XX PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX PS Claim 5; Page 86; 87pp; English.
XX CC The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 64.8%; Score 301.2; DB 6; Length 1379;
Best Local Similarity 78.6%; Pred. No. 1.4e-76;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCACTTGTATGCTGGAATGCGACCATTAACAATATGCCACTTTATGG 64
DB 292 TGAATACATCATCTACAAATGTGGAGTACACACATTAAGAAATACGCCACTTTCTGA 351
QY 65 AATCTTCTGATCAAGCGAAGATCGAATAAATAATGCTATGCGATACCAATGCTAC 124
DB 352 ATGATCTTGTAAAGAGCGAAGATCGAAGTTTAAATGCTATGAAATACCAATGCTGC 411
QY 125 CTGATCTAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAAGTCAAACTTAAAA 184
DB 412 CCAATACAAATACAAATCAAGTACGTTGGTTGAGCTCCAAAGTTCAAATTAABAAAA 471
QY 185 CCATTACCTAATGCTGAGAGGAATTAATTAATGATGAGGCTATTTGATCCCTTCA 244
DB 472 CCATTCACCTAATGCTGAGAGGAATTAATTAATGATGAGGCTATTTGATCCCTTCA 531
QY 245 ATGCAATTAAGTCTGATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCAATTAATGCTGATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAAGAAATCTCTTGTCTCAAGTTCTAGTCTCGTGTGCAATGTCATTAATTAATTA 364

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DB 592 TAGAGACTACTCTTGTCCCAATGCAATTCGTTGATGAATAAAACATAAAGCTTGATA 651
QY 365 GCTTATATCCGACCATGGAAGAAAGAGATTAATCAAGAAATCAAGTCCCAATTGG 424
DB 652 GTGATATCCCAAGATTGGAATCAAAAGCGGAGTAAATCAAGATGAGTCCAACTGG 711
QY 425 GAATTCAAATAGTACGACGATGAGATTTGGAATAAATCTCT 462
DB 712 GAATTCAAATAGTACGACGATTAATTAATTAATTAATTAATTAATTAATTAATTA 749

RESULT 13
AD105787
ID AD105787 standard; DNA; 1379 BP.
XX AC AD105787;
XX DT 15-APR-2004 (first entry)
XX DE DNA encoding the wild-type pokeweed antiviral protein.
XX KW ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
XX KW cytosolic; immunosuppressive; agricultural biotechnology; pharmaceuticals;
XX KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX KW ds.
XX OS Phytolacca americana.
XX FH Key Location/Qualifiers
XX FT CDS 225..1166
XX FT /*tag= a
XX FT /product= "wild-type pokeweed antiviral protein"
XX PN WO200262952-A2.
XX PD 15-AUG-2002.
XX PP 01-FEB-2002; 2002WO-US002792.
XX PR 02-FEB-2001; 2001US-0266396P.
XX PA (RUTP ) UNIV Rutgers STATE NEW JERSEY.
XX PI Turner NE, Hudak KA, Parikh B;
XX DR WPI; 2003-156656/15.
XX DR P-PSDB; AD105788.
XX PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
XX PT type PAP, useful in agricultural biotechnology or in the fields of
XX PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
XX PT or autoimmune disease.
XX PS Disclosure; SEQ ID NO 1; 51pp; English.
XX CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
XX CC that is less toxic than wild-type PAP and exhibits ribosome depurination
XX CC activity, where the mutant is a central domain mutant or N-terminal
XX CC domain mutant. The PAP mutants have the following activities: antifungal,
XX CC antiviral, virucide, anti-HIV, cytosolic and immunosuppressive. The PAP
XX CC mutants are useful in agricultural biotechnology as well as in the fields
XX CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
XX CC treating mammals with cancer, AIDS, viral infection or autoimmune
XX CC diseases associated with proliferations of unwanted T-cells or B-cells.
XX CC The transgenic plants are useful in exhibiting resistance to a broad
XX CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
XX CC sequence represents the DNA encoding the wild-type pokeweed antiviral
XX CC protein of the invention.
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 64.8%; Score 301.2; DB 10; Length 1379;

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Best Local Similarity 78.6%; Pred. No. 1.4e-76;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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OY 5 TAAATACGACCTTGTGATGCTGAAATGCGACCATTAACAATATGCCCTTTATG 64
D 292 TGAATACACATCTTACAAAGTGGAGTACACCATTAAGCAATAGCCCTTTTGA 351
OY 65 AATCTCTGTATCAAGCGAAGATCCAAATTAATGCTATGCAATACCAATGCTAC 124
D 352 ATGATCTTGTATGAAGCGAAGATCCAAAGTTTAAATGCTATGCAATACCAATGCTGC 411
OY 125 CTGATACTAATGACCCCTTAAGTCTTATGTTAAGTCCAAAGGTCGAACCTTAAAA 184
D 412 CCAATACAAATACAAATCCAAAGTACGTGTGAGCTCCAAAGTTCAAATTAATAAAA 471
OY 185 CCAATACAAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
D 472 CCAATACAAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 531
OY 245 ATGCAATTAAGTGTGCTTACCATTAATTAATGATTAATCAAGCAGCACTGATG 304
D 532 AAACCAATTAATGCTGCTTACCATTAATTAATGATTAATCAAGCAGCACTGATG 591
OY 305 TGAAGATTAATCTTTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 364
D 592 TAGAGACTACTCTTTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 651
OY 365 GCTTATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 424
D 652 GTGATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 711
OY 425 GAAATCAATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 462
D 712 GAAATCAATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 749
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RESULT 14

AA056672
ID AA056672 standard; cDNA; 1195 BP.

AC AA056672;

DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)

DE Sequence of Phytolecta antiviral protein (PAP) cDNA.

KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.

OS Phytolecta americana; L.

FH Key location/Qualifiers
FT CDS 33..974
FT /*tag= a

PN EP58554-A1.

PD 09-MAR-1994.

PF 30-JUN-1993; 93EP-00110445.

PR 16-AUG-1992; 92KR-00014895.

PA (JINR-) JIN RO LTD.

PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;

DR WPI; 1994-076002/10.

DR P-PSDB; AAR48548.

PT Expression vector for phytolecta antiviral protein - used for producing transgenic virus-resistant plants and for producing the antiviral agent.

XX Disclosure; Fig 1; 15pp; English.

PS To isolate PAP gene, total cellular mRNA was purified from leaves of
CC Phytolecta americana L. obtd. in Korea. A cDNA library was constructed.
CC The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC sequence of the PAP gene was determined. (Updated on 25-MAR-2003 to
CC correct FN field.) (Updated on 16-OCT-2003 to standardise OS field)

SO Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match 64.4%; Score 299.6; DB 2; Length 1195;

Best Local Similarity 78.4%; Pred. No. 3.8e-76;
Matches 359; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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OY 5 TAAATACGACCTTGTGATGCTGAAATGCGACCATTAACAATATGCCCTTTATG 64
D 100 TGAATACAAATCAATCTAATGTTGAAATGCAACCATTAACAATAGCCCACTTTCTGA 159
OY 65 AATCTCTGTATCAAGCGAAGATCCAAATTAATGCTATGCAATGCTAC 124
D 160 ATGATCTTGTATGAAGCGAAGATCCAAATGCTATGAATACCAATGCTGC 219
OY 125 CTGATACTAATGACCCCTTAAGTCTTATGTTAAGTCCAAAGTCCAAATTAATA 184
D 220 CCAATACAAATTAATGCTGCTTACCATTAATTAATGATTAATCAAGCAGCACTGATG 279
OY 185 CCAATACAAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
D 280 CCAATACAAATGCTGAGACGAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 339
OY 245 ATGCAATTAAGTGTGCTTACCATTAATTAATGATTAATCAAGCAGCACTGATG 304
D 340 AAACCAATTAATGCTGCTTACCATTAATTAATGATTAATCAAGCAGCACTGATG 399
OY 305 TGAAGATTAATCTTTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 364
D 400 TAGAGACTACTCTTTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 459
OY 365 GCTTATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 424
D 460 GTGATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 519
OY 425 GAAATCAATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 462
D 520 GAAATCAATTAATGCTGCTGCTCAAGTTCTAGTTCTGCTGTTCAATGCTCAATTAACAATA 557
```

RESULT 15

AA081457
ID AA081457 standard; cDNA; 1195 BP.

AC AA081457;

DT 16-OCT-2003 (revised)
DT 25-AUG-1995 (first entry)

DE Phytolecta antiviral protein (PAP) cDNA.

KW Antiviral protein; vector pm12; KCCM 10037; PAP; ss.

OS Phytolecta americana; L.

PN AU9350642-A.

PD 19-JAN-1995.

PF 11-NOV-1993; 93AU-00050642.

PR 02-JUL-1993; 93KR-00012360.

PA (JINR-) JIN RO LTD.

XX Lee K, Choi K, Jeon H, Kim M, Moon Y;
XX
XX
DR WPI, 1995-067518/10.
XX

PT Recombinant vector for producing Phytolacca anti-viral protein - and
PT transformed E. coli useful for making immunoconjugates for treatment of
PT AIDS.
XX

PS Claim 1; Fig 1; 27pp; English.
XX

CC Total cellular mRNA from leaves of P. americana was used to produce a
CC cDNA library and this screened with anti-PAP antibody raised in rabbits
CC against purified PAP. Inserts were isolated from 2 clones and sequenced
CC to identify a 1195 ORF (AA081457) that encodes a 313 AA PAP including a
CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
CC amplification using primers AA081458 and AA081459. The amplification
CC product was cut with Hind III and inserted into the commercial FLAG (RTM)
CC vector cut with the same enzyme to form pMJ2. pMJ2 is deposited with
CC the Korean Collection of Culture and Microorganism (KCCM), an
CC International Depository Authority, on June 30 1993, ad deposition No.
CC KCCM 10037, and claimed. (updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Query Match 64.1%; Score 298; DB 2; Length 1195;
Best Local Similarity 78.2%; Pred. No. 1,1e-75;

Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 5 TAAATACGATCACTTGTGATGCGAATGCGACCATTAACAATATGCGACCTTTATG 64
Db 100 TGAATACATCATCTACATGATGAGAGACACCATTAAGCAATACCGCACTTTCTGA 159
QY 65 AATCTCTGATATGACGGAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
Db 160 ATGATCTTCGTAATGGAAGCAAGATCCAAAGTTTAAATCTATGAAATACCAATGCTGC 219
QY 125 CTGATACTAATTCGACCCCTAAGTACTTATGTTAAGCTCCAAAGTGCAAACTAAAA 184
Db 220 CCAATACAAATACAAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATAAAAA 279
QY 185 CCATTACATTAATGCTGAGAGAAATTAATACGATGAGGCTATTCGATCCCTCA 244
Db 280 CCATCAGCTAATGCTGAGAGAAATTAATGATGATGAGGTTATTCGATCCCTCA 339
QY 245 ATGCAATTAATGCTGATACATTAATTAATGATTAACAAGCAGCAAGCACTGATG 304
Db 340 AAACCACTAAATGCTGATACATTAATTAATGATTAATCAAGTACTGAACGCCAAGATG 399
QY 305 TGAGAAATACCTTGTGCTCAAGTCTAGTCTCGGTGCAATGCTCAATTAATACATA 364
Db 400 TAGAGACTACTCTTTGCCAAATGCCAATTCCTCGTGAATTAATAAATTAATTTGATA 459
QY 365 GCTTATATCCGACCATGAGAAAGAGAGAAATTAATCAAGAAATCAAGTCCAAATGG 424
Db 460 GTGATATCCCAATGAGATGAGAAAGAGAGAAATTAATCAAGTCCAAATGG 519
QY 425 GAATTCAAATTAATGACGATGATGATGATGATGATGATGATGATGATGATGATG 462
Db 520 GAATTCAAATTAATGACGATGATGATGATGATGATGATGATGATGATGATGATG 557

Search completed: April 9, 2006, 00:50:28
Job time : 282.284 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 2202.83 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465

Sequence: 1 atgataaacgacacaccc.....acattgaaaaatccttca 465

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_g881:*
10: gb_g882:*
11: gb_g883:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62.2	13.4	498	5	BQ588134 E012337-0
2	47.8	10.3	829	7	CN782289 EST00385
3	46.6	10.0	489	2	BE130330 L48-484T3
4	44	9.5	701	9	BZ031330 cej24f09.
5	42.4	9.1	561	9	AO156306
6	41.8	9.0	658	10	CZ857242
7	41	8.8	788	10	CG690741
8	40.4	8.7	563	9	AO670952
9	40.4	8.7	528	7	CO102355
10	40	8.6	530	10	AG960279
11	39.6	8.5	878	10	CNS01878
12	39.6	8.5	913	10	CNS00C20
13	39.6	8.5	1204	10	CNS01682
14	39.4	8.5	880	10	CL848175
15	39.2	8.4	473	7	CN466064
16	39.2	8.4	853	10	BN147963
17	39	8.4	1019	10	CNS006FW
18	38.6	8.3	707	5	BQ545338
19	38.4	8.3	879	10	CZ945561
20	38.2	8.2	456	2	BG555640
21	38.2	8.2	739	8	DR166187
22	38	8.2	586	7	CK768171

23	37.8	8.1	946	4	AK015929
24	37.8	8.1	959	5	BY116082
25	37.8	8.1	964	5	BY115491
26	37.8	8.1	1382	4	AK016430
27	37.4	8.0	492	3	BM967727
28	37.4	8.0	613	7	CK133860
29	37.2	8.0	472	3	BO133949
30	37.2	8.0	543	3	BO134091
31	37.2	8.0	580	6	CD408931
32	37.2	8.0	715	9	CC004347
33	37.2	8.0	1146	10	CNS021G2
34	37	8.0	343	7	CV500814
35	37	8.0	410	7	CV292656
36	37	8.0	937	7	CK282629
37	36.8	7.9	317	7	CK632351
38	36.8	7.9	947	10	CZ944913
39	36.6	7.9	315	7	CK632387
40	36.6	7.9	410	7	CK495303
41	36.6	7.9	512	1	AW199192
42	36.6	7.9	664	9	BZ003153
43	36.6	7.9	670	10	AG073512
44	36.6	7.9	680	3	BQ78909
45	36.6	7.9	854	10	DU089625

ALIGNMENTS

RESULT 1
BQ588134
LOCUS
DEFINITION
E012337-024-009-G14-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-G14 5-PRIME, mRNA sequence.
ACCESSION
BQ588134
VERSION
BQ588134.1 GI:26117717
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnach, H.
and Kadetloff, U.
1 (bases 1 to 498)
Construction of a 'uniGene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTGCTGACACTTAG.
Location/Qualifiers
1. 498
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/note="Vector: PCMVSPORT6; Site 1: SalI; site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:

TITLE
JOURNAL
PUBMED
COMMENT
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTGCTGACACTTAG.
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/cultiVar="KWS2320 (double haploid, monogerm breeding
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/clone="024-009-G14"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_id="MP1Z-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: SalI; site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:

FEATURES
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1. 498
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultiVar="KWS2320 (double haploid, monogerm breeding
line)"
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/note="Vector: PCMVSPORT6; Site 1: SalI; site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NciI, primer sites and orientation:
SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NciI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Query Match 13.4%; Score 62.2; DB 5; Length 498;
Best Local Similarity 56.7%; Pred. No. 4e-06;
Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;

QY 14 TCACCTTGATGCGGAAATGCGACCAATTACAAATATGCGACCTTATGGAATCTCTC 73
DB 169 TAACTTTGACCTTGAACAGCTTCAAGACAAATATGCGACTTTCTTAAGCAATCTAC 228
QY 74 GTAATCAAGCGAAAGATCCAAACTAAATGCTATGCGATCAATGCTACTGATACTA 133
DB 229 GCAACATGTGAAGATTCAAAGCTATGATAGAGAAATTCATGCTCCCTGCACCAT 288
QY 134 ATTGACCCCTTAAGTACTTATGTTAGTCAAGTGCAA-----CCTAAAA 184
DB 289 CAAACACGCAAAATACCTTTTACCGGCTAAAGCTAAAGCCCGTACTGACATTA 348
QY 185 CCATTACACTAATGCTGACGAAATACCTATACGTATGAGGCTATTCTGATCCCTCA 244
DB 349 CCATCACTCTGCTTTAGCAAAATGACTTATATGTATGTGCTTTTACTATCAAGTAG 408
QY 245 ATGGCAA 251
DB 409 CAGGTAA 415

RESULT 2 829 bp mRNA linear EST 21-MAY-2004
CN782289
LOCUS
DEFINITION
EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
antiviral ribosome-inactivating protein CAP30B (Chenopodium album),
mRNA sequence.

ACCESSION
CN782289
VERSION
CN782289.1 GI:47561753
KEYWORDS
EST.

SOURCE
ORGANISM
Chenopodium quinoa (quinoa)

REFERENCE
AUTHORS
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)

REFERENCE
AUTHORS
Coles, N.D., Coleman, C.E., Christensen, S.A., Jellen, B.N.,
Stevens, M.R., Bonifacio, A., Rojas-Beltran, J.A., Fairbanks, D.J. and
Maughan, P.J.

TITLE
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms

JOURNAL
COMMENT
Plant Sci. 168 (2), 439-447 (2005)
Brigham Young University
Department of Plant and Animal Sciences
Contact: Coleman, Craig E.
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.

FEATURES
source
1. .829
Location/Qualifiers

/organism="Chenopodium quinoa"
/mol_type="mRNA"
/culturvar="Real"
/db_xref="taxon:63459"
/clone="S02J22"

/tissue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_lib="cgsed"
/note="Vector: pTrilBx2; Site_1: SfiI; Site_2: SfiI;
Developing Seed cDNA Library from Chenopodium quinoa"

ORIGIN

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Best Local Similarity 51.7%; Pred. No. 0.041;
Matches 140; Conservative 0; Mismatches 122; Indels 9; Gaps 1;

QY 30 AATGCCACATTAACAATATGCGACCTTATGGAATCTCTGTAATGAGGAAAGA 89
DB 115 AAAACCTACACAGAACTTATTAACACTTTGCAAGATAGCGACCAACTAAGA 174
QY 90 TCCAAATCTAAATGCTATGCAATACCAATGCTATGCTATGCAATGCAATGCTA 149
DB 175 TCCAAAGCTTATGATAGAGAAATCCCAATGATCCGACCAACCAACCAATGATA 234
QY 150 CTTATGTTAAGCTCCAGGTGCAAACTTAAAC-----CATTAACATATGCT 200
DB 235 TCTTTGCTTGAACCTTGAATCTTAAAGATAGATAGATATTCATTACCTTGCCTT 294
QY 201 GAGACGAATTAATTAATGATATGATGAGGCTATTTGATCCTTCAATGCAATTAAGTGC 260
DB 295 AAGTAGAAAGACTTGTATGATAGTGCCCTTGTGATTAATTTGAGGCAAAAGTTCGCG 354
QY 261 TTACCATATTAATTAATGATATTAACAAGCAC 291
DB 355 CCATTCTTTCCACTTAAACATTAAGACACC 385

RESULT 3 489 bp mRNA linear EST 20-FEB-2001
BE130330
LOCUS
DEFINITION
L48-484T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-484 5',
mRNA sequence.

ACCESSION
BE130330
VERSION
BE130330.1 GI:8577693
KEYWORDS
EST.

SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)

REFERENCE
AUTHORS
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)

JOURNAL
COMMENT
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR primers
FORWARD: T7
BACKWARD: T3
Plate: L48-5 row: G column: 12
Seq primer: T3
High quality sequence stop: 350
POLYA=no.

FEATURES
source
1. .489
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-484"
/tissue_type="Leaf", 48 h 0.4M NaCl"
/dev_stage="Six week old"

ORIGIN

/clone_11b="Ice plant lambda Uni-Zap XR expression library, 48 hours NaCl treatment"
 /note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site_1: EcoRI, Site_2: XhoI"

Query Match 10.0%; Score 46.6; DB 2; Length 489;
 Best Local Similarity 54.7%; Pred. No. 0.08;
 Matches 122; Conservative 0; Mismatches 89; Indels 12; Gaps 1;

QY 44 ACAATATGCCACCTTATGAGATCTCTGATATCAGCGAAAGATCCAAACTTAAT 103
 DB 196 ATACATACCAATCATCTCCGATCTCTACGCAATGAATGAGATCCCAATGAGAAAC 255
 QY 104 GGTATGACATACCAATGATCTACCTGATCTACTATTCGACCC-----TAACTACT 151
 DB 256 CCCATAGATATATCATGATGATGCGAAACCTTACGATCTTCAAGATGACAAAGATTAATC 315
 QY 152 TATTGTTAAGCTCCAGAGTGCAAACTTAACCACTTAAGTCTGAGACGAAATA 211
 DB 316 TGTATGATAGAGCTGACGAGGACACCAAGTCCATCATATATCTCTAGACAGAGCA 375
 QY 212 ACTTATAGCTGATGGCTATTTGATCCCTTGAATGGCAATA 254
 DB 376 ATTATATTTCAATGGCTTACAGTGAATTTGTTAAATA 418

RESULT 4

LOCUS BZ031330 701 bp DNA linear GSS 09-OCT-2002
 DEFINITION oej24t09.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 sequence.

ACCESSION BZ031330
 VERSION BZ031330
 KEYWORDS GSS: GI:23604775

SOURCE

ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

Dejeanunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 Whole genome shotgun reads from Brassica oleracea
 Unpublished (2002)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Plate: oej24 row: f column: 09
 Seq primer: -21UPOT forward
 Class: shotgun
 High quality sequence start: 47
 High quality sequence stop: 551.
 Location/Qualifiers

FEATURES

COMMENT

source

1..701
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 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_11b="B.oleracea002"
 /note="Vector: POTW13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea T01000DH3 buds provided by
 Thomas Osborn at the University of Wisconsin. Genomic
 DNA was provided by Fabio Rabinowicz (CSHL) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

ORIGIN

Query Match 9.5%; Score 44; DB 9; Length 701;
 Best Local Similarity 53.5%; Pred. No. 0.44;
 Matches 92; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 112 ATACCAATGCTACTGATACCTAATTCGACCCCTAGTACTTATGTTAGCTCAAGT 171
 DB 322 ATACCAATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 263
 QY 172 GCAAACTTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 231
 DB 262 CCAAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 203
 QY 232 TCTGATCCCTCAATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 283
 DB 202 TTATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 151

RESULT 5

LOCUS AQ156306 561 bp DNA linear GSS 12-SEP-1998
 DEFINITION nbxb000707f CUGI Rice BAC library Oryza sativa (japonica
 cultivar-group) genomic clone nbxb000707f, genomic survey
 sequence.

ACCESSION AQ156306
 VERSION AQ156306
 KEYWORDS GSS: GI:3553331

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae;
 Eriatridae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Wing,R.A. and Dean,R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu

COMMENT

Seq primer: TTAATACACTACTACTATGAGG
 Class: BAC ends
 High quality sequence stop: 262.
 Location/Qualifiers

FEATURES

source

1..561
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="japonica"
 /cultivar="Nipponbare"
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 /clone="nbxb000707f"
 /issue_type="leaf"
 /lab_host="B. coli DH10B"
 /clone_11b="CUGI Rice BAC library"
 /note="Vector: pBelBAC11; Site 1: HindIII, Site 2:
 HindIII; Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp
 (Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9%. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."

ORIGIN

Query Match	9.1%; Score 42.4; DB 9; Length 561;
Best Local Similarity	51.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 100; Conservative	0; Mismatches 96; Indels 0; Gaps 0;
Qy	76 AATCAACGGAAGATCCAAAACCTAAATGCTATGCGATACCAATGCTACTGATACATAT 135
Db	392 AATTATATAAATTTATCAAAAATAAATACAAAGATGAATTAATAATTAATTAATGAT 333
Qy	136 TCGACCCCTTAAGTACTTATGTTAGCTCCAGAGTGCAACCTTAAAAACATTAAGCTA 195
Db	332 TCCAAACGACCGCAATTAATCTACCAAAAACAATGGTAACTACCTATGACACCCAAATC 273
Qy	196 ATGCTGAGAGCAATTAATCTTAAGCTATGGGCTATTCGATCCCTCAATGGCAATAG 255
Db	272 ATCCGCAATTAATCAATATATTTCTTTTTCAAAACCTCCTCCCTTTTTCATGAT 213
Qy	256 TGTGCTTACCATATAT 271
Db	212 TTTGTTTTTCTTAAT 197
RESULT 6	
LOCUS	CZ857242.c 658 bp DNA linear GSS 27-JUN-2005
DEFINITION	OC__Ba0248N02.r OC__Ba Oryza coarctata genomic clone OC__Ba0248N02
ACCESSION	CZ857242
VERSION	CZ857242.1 GI:71330002
KEYWORDS	GSS.
SOURCE	Oryza coarctata (Porteresia coarctata)
ORGANISM	Oryza coarctata
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	Kim, H., Collura, K., Misosaki, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and Wing, R.
TITLE	OMP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL	Unpublished (2005)
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu PCR primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0248 row: N column: 02 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
FEATURES	
source	location/Qualifiers
	1..658
	/organism="Oryza coarctata"
	/mol_type="genomic DNA"
	/db_xref="taxon:77588"
	/clone="OC_Ba0248N02"
	/rfeature_type="leaves"
	/dev_stage="mature"
	/lab_host="PH10B"
	/clone_1fb="OC_Ba"
	/note="Vector: pAGHBAC1; site_1: HindIII; site_2: HindIII"
ORIGIN	
Query Match	9.0%; Score 41.8; DB 10; Length 658;
Best Local Similarity	52.6%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 91; Conservative	0; Mismatches 82; Indels 0; Gaps 0;
Qy	247 GGCAATTAAGTGTCTTACCATATATTTATGTATTTACAGACGACGAGCAAGCATGATGG 306
Db	478 GGACCAAAAGTGTGGGCAAAAATCTGACGATGACCTTTATGTGACACGATGACCTG 419

Qy	307	GAGAAATCTCTTTGCTCAAGTTCTAGTCTCGGTGCGATTGCAATGCCATTAACCTCAATAGC	366
Db	418	GGAGATCTGCTTAACCTCAAGTGAAGTGGTCTTAGCTTTGTCCTTAGAGGCTATGACAGTTAA	359
Qy	367	TTATATCCGACATGTGMAAAGAAAGAGAGTAAGTCAAGAAATCAAGTCCA	419
Db	358	TTTGATCTCTAATTTGACAGAAACATVAGCAAAAGTAAGGACCTTGAGCCAA	306
RESULT 7			
LOCUS	CG690741/c	788 bp	DNA linear
DEFINITION	ZMMBc0135P02r ZMMBc (EcORI)	Zea mays genomic clone ZMMBc0135P02	
ACCESSION	CG690741		
VERSION	CG690741.1	GI:37588131	
KEYWORDS	3', genomic survey sequence.		
SOURCE	GS.		
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 788)		
AUTHORS	Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zolovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.		
TITLE	Sequencing of the maize genome at PCR (2003c)		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Bharti,A.K. Dr. Joseph Messing's lab The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08854, USA Tel: 732 445 3801 Fax: 732 445 5735 Email: bharti@waksman.rutgers.edu Seq primer: SP6 Class: BAC ends High quality sequence start: 88. Location/Qualifiers		
FEATURES			
source	1..788		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/culivar="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMMBc0135P02"		
	/lab_host="E. coli DH10B"		
	/clone_1lb="ZMMBc (EcORI)"		
	/note="vector: pTARAC2.1; Site_1: EcORI; Site_2: EcORI"		
ORIGIN			
Query Match	8.8%; Score 41; DB 10; Length 788;		
Best Local Similarity	55.2%; Pred. No. 3;		
Matches	80; Conservative 0; Mismatches 65; Indels 0; Gaps 0;		
Qy	317	TTTGCTCAAGTTCAGTTCCTCGTGTGCATGTCCATTACTACAAATGCTTAATTCGA	376
Db	470	TGTTTCAACTTAATGCTGTTTGGCATGTGTGCAATTAATCTCCGTAAATATTTT	411
Qy	377	CCATGGAAAAGAAAGCAAGTAATCAACAAATCAAGTCCATTGGGAATTCAAATAC	436
Db	410	CCATGGATAAAGAAATTAATTAATCTATTTTCATTAACCAATGCCAAAGATGAATCATGTTT	351
Qy	437	TCAGCAATGACATTCGAAAAATCTC	461
Db	350	CTTACTTGGAATCTGAACAACAC	326
RESULT 8			
LOCUS	A0670952	563 bp	DNA linear
DEFINITION	HS_5429 B2 B06 TRA RPC1-11 Human Male BAC library Homo sapiens genomic clone Plate=1005 Col=12 Row=J, genomic survey sequence.		

ACCESSION A0670952 GI:5203698
 VERSION A0670952.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 563)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 CONTACT: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm) or from Research Genetics (info@resgen.com). BAC end web Server: http://www.htsc.washington.edu
 plates: 1005 row: J column: 12
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 563.
 Location/Qualifiers
 1..563
 /organism="Homo sapiens"
 /mol_type="Genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=1005 Col=12 Row=J"
 /sex="male"
 /clone.lib="RPCI-11 Human Male BAC Library"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
 ORIGIN
 Query Match 8.7%; Score 40.4; DB 9; Length 563;
 Best Local Similarity 52.4%; Pred. No. 4.2;
 Matches 89; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
 QY TCTCTTGGTATCAAGCAAGATCAAACTAAATGCTATGCGATACCAATGCTACT 126
 DB TCTTCAAGATTATCTTGGCAAGATATTAATTTCTTGTGATTTGATCTTGTATG 445
 QY 127 GATACATAATGAGCCCTAGTACTTATGTTAGTCCCAAGGCAAACTAAAAAC 186
 DB 446 CATATATTAATTAACCTATGTTGGCTGTGGCTTTAAATGATCAAGGTGTAAC 505
 QY 187 ATTACATAATGCTAGACGAATTAATTAATGAGTGGCTATTCTGA 236
 DB 506 ATTACAAAGTGTGATACATATCTCTAATAGTGTGCTCTACTATTA 555
 RESULT 9
 COI02355/c 630 bp mRNA linear EST 16-JUN-2004
 LOCUS GR_EB0029M03.f GR_Eb Gossypium raimondii cDNA clone GR_EB0029M03
 DEFINITION 5'__mRNA sequence.
 ACCESSION COI02355
 VERSION COI02355.1 GI:48801041
 KEYWORDS EST.

SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 REFERENCE 1 (bases 1 to 630)
 Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
 Global assembly of Cotton ESTs
 Unpublished (2004)
 CONTACT: Rod A. Wing
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 0029 row: M column: 03.
 Location/Qualifiers
 1..630
 /organism="Gossypium raimondii"
 /mol_type="mRNA"
 /db_xref="taxon:29730"
 /clone="GR_EB0029M03"
 /issue_type="floral"
 /dev_stage="3 to +3 DPA"
 /lab_host="DHL0B"
 /clone.lib="GR_EB"
 /note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Clones plated/picked by Agt. More glycerol clones held in -80."
 ORIGIN
 Query Match 8.7%; Score 40.4; DB 7; Length 630;
 Best Local Similarity 53.9%; Pred. No. 4.3;
 Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
 QY 147 GTACTTATGTTAGTCCCAAGGTGCAAACTTAAACCTTACATATGCTGAGACG 206
 DB GTTGTCAATTTATAGAGCAAAAGTAAAGATTAGCTTAAAGCTGAGATGAGCA 361
 QY 207 AAATTAATTAATGATGAGTATTTGATTCCTTCAATGCAATTAATGTTTACCA 266
 DB 360 AAAAAGCAGCATATGATGATCACTGAGACTTGAATGATGATGTTCTGGGAC 301
 QY 267 TATATTAATGATTAATCAAGCAGCAGCAGCAGT 300
 DB 300 TATCTTGATTAACATTCATGCTTTGATGTTAAT 267
 RESULT 10
 AG960279 528 bp DNA linear GSS 01-FEB-2005
 LOCUS AG960279
 DEFINITION Drosophila sechellia DNA, clone: DSEI-018H10.R.1a, genomic survey
 sequence.
 ACCESSION AG960279
 VERSION AG960279.1 GI:58493439
 KEYWORDS GSS.
 ORGANISM Drosophila sechellia
 Drosophila sechellia
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1
 Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A., Toshio,T.K. and Sakaki,Y.
 BAC end sequences of library DNE1
 Unpublished
 REFERENCE 2 (bases 1 to 528)
 Hattori,M.
 TITLE Direct Submission

Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A., Toshio,T.K. and Sakaki,Y.
 BAC end sequences of library DNE1
 Unpublished
 REFERENCE 2 (bases 1 to 528)
 Hattori,M.
 TITLE Direct Submission

JOURNAL

Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gscc.riken.jp, URL: http://hnp.gscc.riken.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the BAC library D581
For BAC library availability, please contact Masa-Toshi Yamamoto (Yamamoto@kit.jp).
Submitted (30-11-2004) by Masahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gscc.riken.jp, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT

This work was done in collaboration with Yamamoto, M-T. Drosophila Genetic Resource Center
Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
Tel: 81-75-873-2660 FAX: 81-75-861-0881
PRIMERS

Sequencing : R

LIBRARY

Vector : pKS150
R.Site 1 : SacI
R.Site 2 : SacI

Location/Qualifiers

1..528
/organism="Drosophila sechellii"
/mol_type="genomic DNA"
/db_xref="taxon:7238"
/clone="DSE1-018H10.R.fa"
/clone_lib="DSE1 Drosophila BAC library"

ORIGIN

Query Match 8.6%; Score 40; DB 10; Length 528;
Best Local Similarity 51.7%; Pred. NO. 5.3;
Matches 91; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

172 GCAACCTGAAACCATCTACCTAATGCTGAGACGAATTAATCTTATGATGGGCTAT 231
117 GCAAGATTATATCATCTATTATTAAGTGAAGTATTGGAATTAATCTGATATTTAT 176
232 TCTGATCCCTCAATGCAATAGAGTGTACCATATATTTAATGATATTACAAGCACC 291
177 GCGAGTTTGTGCTTTATTTAGAGTTCGTTTAAATTTGGGAGCTGATATTAG 236
292 GAAGCAGCTGATGTGAGAAATCTTGTCTCAAGTTCTAGTTCGTTGTCGAAT 347
237 ACACATATGATTAGGCGAATAGACATTCACAAAGTAATTCGTTTATATTTTAA 292

RESULT 11

CNS0187R 878 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN04804 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL108993
VERSION AL108993.1 GI:5629297
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 878)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr
determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre

FEATURES

source

1..878
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN04804"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : SP6"

ORIGIN

Query Match 8.5%; Score 39.6; DB 10; Length 878;
Best Local Similarity 23.1%; Pred. No. 7.5;
Matches 48; Conservative 73; Mismatches 87; Indels 0; Gaps 0;

250 AATAAGTGTGTTACATATATTTAATGATATTACAAGACCGAAGCAGTATGAG 309
92 WAAAAAAMWMAAAAAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAA 151
310 AATACCTTTGCTCAAGTCTAGTCTGTTGCAATGTCATTAACTACATAGCTTA 369
152 AAAAAAATCTTGCTGCTGATGATGTTGTTTAAATTTTAAATTTTAAATTTTAA 211
370 TATCCGACATGAGAAAAAGCAAGTAAATCAAGAAATCAAGTCAATGGAAAT 429
212 WAAAAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMA 271
430 CAATACCTGACAGTGAATGAGAAAA 457
272 WMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMAAAMWMA 299

RESULT 12

CNS00C20 913 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TERT end of BAC #
DEFINITION BACR26P05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL059715
VERSION AL059715.1 GI:4947359
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 913)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr
determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..913
Location/Qualifiers

ORIGIN

/clone.lib="OR_CBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
dir created 36 hrs before harvest"

Query Match 8.5%; Score 39.4; DB 10; Length 880;
Best Local Similarity 48.8%; Pred. No. 8.6;
Matches 106; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 75 TAATCAAGCGAAGATCCAAACTAAATGCTATGCGATACCAATGCTACTACTACTAA 134
DB 246 TAATAGATGAATGAATATCCCGGCTTGACTCAGAAAGACTACAGCAATTATTACAAAG 305
QY 135 TTGACCCCTTAAGTACTTATTGTTAAGCTCCAGGTGCAAACTTAAACCATTTACACT 194
DB 306 AAGCACACTTAAAGTGTGCTAAATTAACAGCACCAACCAAAATPAAACA 365
QY 195 AATGCTGAGACGAATTAATTAATGATGATGGGCTATCTGATCCCTTCATATGCAATPA 254
DB 366 AGACCTAACATGACAGAAACATTTATTCAGTGAATCTCATTCATGATTGGCAAAA 425
QY 255 GTGTGTTACCATATATTATTATGATTTACAGCAC 291
DB 426 GTTGCAATACCGTTGACTCAAGGTTATGACATGCAAC 462

RESULT 15

CN466064 473 bp mRNA linear EST 21-APR-2004
LOCUS CN466064/C
DEFINITION LCB003C12c Leymus chinensis root cDNA library Leymus chinensis cDNA
clone LCB003C12, mRNA sequence.

ACCESSION CN466064
VERSION CN466064.1 GI:46471790
KEYWORDS EST.

SOURCE

ORGANISM Leymus chinensis
Leymus chinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Leymus.
1 (bases 1 to 473)
Jin, H., Plaha, P., Hong, C.P., Yang, Z.H., Lee, I.S., Liu, S.K. and
Lim, Y.P.

REFERENCE

AUTHORS
TITLE
Expressed sequence tags from a root cDNA library of Leymus
chinensis

JOURNAL

COMMENT
Unpublished (2004)
Contact: Yong Pyo Lim
Department of Horticulture, Genome Research Center
Chungnam National University
220, Kung-Dong, Yuseong-Gu, Daejeon, 305-764, Korea
Tel: +82-42-861-5739
Fax: +82-42-823-1382
Email: yplim@cnu.ac.kr

FEATURES

SOURCE
Seq primer: T3.

Location/Qualifiers
1..473
/organism="Leymus chinensis"
/mol_type="mRNA"
/db_xref="taxon:52714"
/clone="LCB003C12"
/issue_type="Root"
/dev_stage="2 months old plant"
/clone.lib="Leymus chinensis root cDNA library"
/note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds of Leymus chinensis were germinated at 40C under
dark conditions and seedlings were grown under greenhouse
conditions (maximum light intensity of 1200 umol s-1 m-2
and temperature ranges from 210C night to 320C day).
Two-month-old plants were treated with 100 mM Na2CO3, pH
11.4 for 48 hours, and roots were harvested and stored at
-700C until RNA extraction for cDNA construction. The mRNA
was selected with PolyAtract mRNA Isolation System III
(Promega). The cDNA was ligated unidirectionally into the
Bc0RI and XhoI site of the lambda-ZAP vector

ORIGIN

(Stratagene). "

Query Match 8.4%; Score 39.2; DB 7; Length 473;
Best Local Similarity 57.3%; Pred. No. 8.6;
Matches 71; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 173 CAACCTAAACCATTAACATAATGCTGAGACGAATTAATTAATACGATGCGCTATT 232
DB 358 CAATAGTACAAAATATTTCAATCTGAGCAAACTATCTGACAGAGATTGCTGAT 299
QY 233 CTGATCCCTTCATATGCAATTAAGTGTGTTACCATATATTATGATTTACAAACCG 292
DB 298 CTTCTCTTTGCAATAGCAAGTTTCTCATTTCCCTATATATATATATACATACCGCTCT 239
QY 293 AACG 296
DB 238 GATG 235

Search completed: April 9, 2006, 04:10:52
Job time : 2207.83 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 8, 2006, 09:19:56 / Search time 161.42 Seconds
(without alignments)
5120.590 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465
Sequence: 1 atgataaatacgcacaccc.....acattgaaaacatctcttaa 465

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/R.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfill1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	302.8	65.1	1195	2	US-08-373-858-1
2	302.8	65.1	1195	2	US-08-342-786B-1
3	301.2	64.8	1379	2	US-08-500-611-1
4	301.2	64.8	1379	2	US-08-500-694-1
5	301.2	64.8	1379	3	US-07-865-169-1
6	301.2	64.8	1379	3	US-09-005-273-1
7	301.2	64.8	1379	3	US-08-501-253A-1
8	301.2	64.8	1379	6	PCT-US96-11546-1
9	298	64.1	1379	3	US-07-865-169-2
10	298	64.1	1379	3	US-09-005-273-3
11	238.8	51.4	918	2	US-08-138-636-1
12	238.8	51.4	918	2	US-08-319-622A-1
13	238.8	51.4	918	2	US-08-471-564-1
14	43.2	9.3	1233	3	US-08-718-904-80
15	43.2	9.3	1233	3	US-09-449-249-80
16	39.6	8.5	1167	6	PCT-US95-10973A-57
17	39.6	8.5	1230	2	US-08-356-161-12
18	39.6	8.5	1230	3	US-08-356-161-13
19	39.6	8.5	1230	3	US-08-718-904-53
20	39.6	8.5	1230	3	US-09-449-249-53
21	39.6	8.5	1230	6	PCT-US93-05702-12
22	39.6	8.5	1230	6	PCT-US93-05702-13
23	39.6	8.5	1230	6	PCT-US95-10973A-12
24	39.6	8.5	1230	6	PCT-US95-10973A-13

25	39.6	8.5	1251	3	US-08-718-904-74	Sequence 74, Appl
26	39.6	8.5	1251	3	US-09-449-249-74	Sequence 74, Appl
27	39.6	8.5	1260	3	US-08-718-904-72	Sequence 72, Appl
28	39.6	8.5	1260	3	US-09-449-249-72	Sequence 72, Appl
29	39.6	8.5	1266	3	US-08-718-904-75	Sequence 75, Appl
30	39.6	8.5	1266	3	US-09-449-249-75	Sequence 75, Appl
31	39.6	8.5	1269	3	US-08-718-904-78	Sequence 78, Appl
32	39.6	8.5	1269	3	US-09-449-249-78	Sequence 78, Appl
33	39.6	8.5	1275	3	US-08-718-904-73	Sequence 73, Appl
34	39.6	8.5	1275	3	US-09-449-249-73	Sequence 73, Appl
35	39.6	8.5	1299	3	US-08-718-904-77	Sequence 77, Appl
36	39.6	8.5	1299	3	US-09-449-249-77	Sequence 77, Appl
37	39.6	8.5	1299	6	PCT-US95-10973A-58	Sequence 58, Appl
38	39.6	8.5	1320	3	US-08-718-904-76	Sequence 76, Appl
39	39.6	8.5	1320	3	US-09-449-249-76	Sequence 76, Appl
40	39.6	8.5	1557	6	PCT-US95-10973A-78	Sequence 78, Appl
41	39.6	8.5	1809	6	PCT-US95-10973A-79	Sequence 79, Appl
42	38.2	8.2	832	3	US-09-621-976-2813	Sequence 2813, Ap
43	38	8.2	765	3	US-08-718-904-79	Sequence 79, Appl
44	38	8.2	765	3	US-09-449-249-79	Sequence 79, Appl
45	37.6	8.1	771	6	PCT-US95-10973A-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytoacta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 65.1%; Score 302.8; DB 2; Length 1195;
Best Local Similarity 78.8%; Pred. No. 1.3e-78;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 5 TAAATAGATCATTGATGCTGGAATGCGACCATTAACAATATGCGCCTTTATG 64
DB 100 TGAATACAAATCATCTACAAATGTTGAAATGACACCATTAGCAAAATACGCCCTTTCTGA 159
QY 65 AATCTCTGTAATCAAGCGAAGATCCAAATCTAAATGCTATGAGCATTAATGCTAC 124
DB 160 ATGATCTTCTGTAAGAGCGAAGATCCAAATGCTATGAAATGCTATGAAATGCTGC 219
QY 125 CTGATCTAAATGACCCCTTAAGTATGTTATGTTAAGCTCAAGTCAAACTTAA 184
DB 220 CCAATACAAATATCAAAATCAAAATGATGTTGTTGTTAGCTCAAGTCAAAATTA 279
QY 185 CCATTAACATTAATGCTGAGCAAAATTAATTAATGCTGATGCTATGCTATGCTCA 244
DB 280 CCAATCACTAAATGCTGAGCAAAATTAATTAATGCTGATGCTATGCTATGCTATG 339
QY 245 ATGCAATTAAGTGTGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 340 AAACCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 399
QY 305 TGAGAAATCTCTTGTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 400 TAGAGACTACTCTTGTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
QY 365 GCTTATTCGACCATGGAAGAAAGCAAGCAAGTCAAGTCAAGTCAAGTCAAGT 424
DB 460 GTCGATTCGAATGGAATCAAAAGCGGAGTGAATCAAGTCAAGTCAAGTCAAGT 519
QY 425 GAATTCAAATCTGAGCATGATGGAATTAATCTCT 462
DB 520 GAATTCAAATCTGAGCATGATGGAATTAATCTCT 557

RESULT 2

US-08-342-786B-1

Sequence 1, Application US/08342786B

Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Whan

APPLICANT: Lee, Kwan-Ho

APPLICANT: Kim, Man-Keun

TITLE OF INVENTION: A No. 5648234e1 Expression Vector for Phytolacca

TITLE OF INVENTION: Antiviral Protein

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,786B

FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/147,024

FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Phytolacca americana L.

IMMEDIATE SOURCE:

CLONE: PAP

US-08-342-786B-1

Query Match 65.1%; Score 302.8; DB 2; Length 1195;
Best Local Similarity 78.8%; Pred. No. 1.3e-78;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 5 TAAATAGATCACCCTTGTGATGCTGAAATGCGACCATTAACAATATGCGCCTTTATG 64
DB 100 TGAATACAAATCATCTACAAATGTTGAAATGACACCATTAGCAAAATACGCCCTTTCTGA 159
QY 65 AATCTCTGTAATCAAGCGAAGATCCAAATCTAAATGCTATGAGCATTAATGCTAC 124
DB 160 ATGATCTTCTGTAAGAGCGAAGATCCAAATGCTATGAAATGCTATGAAATGCTGC 219
QY 125 CTGATCTAAATGACCCCTTAAGTATGTTATGTTAAGCTCAAGTCAAACTTAA 184
DB 220 CCAATACAAATATCAAAATCAAAATGATGTTGTTGTTAGCTCAAGTCAAAATTA 279
QY 305 TGAGAAATCTCTTGTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 400 TAGAGACTACTCTTGTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
QY 365 GCTTATTCGACCATGGAAGAAAGCAAGCAAGTCAAGTCAAGTCAAGTCAAGT 424
DB 460 GTCGATTCGAATGGAATCAAAAGCGGAGTGAATCAAGTCAAGTCAAGTCAAGT 519
QY 425 GAATTCAAATCTGAGCATGATGGAATTAATCTCT 462
DB 520 GAATTCAAATCTGAGCATGATGGAATTAATCTCT 557

RESULT 3

US-08-500-611-1

Sequence 1, Application US/08500611

Patent No. 5756322

GENERAL INFORMATION:

APPLICANT: Turner, Nijun E.

TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leiner, David, Litzenberg, Krumholz & Mentlik

STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Query Match 64.8%; Score 301.2; DB 2; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Db 5 TAAATACGATACCTTGTGATGCTGAATGCGACCATTAACAATAATGCGACCTTTATG 64
292 TGAATACATCATCTACCAATGTTGGAAGTACCACTTAGCAAAATACGCCACTTTCTGA 351
Qy 65 AATCTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGCGATCAATGCTAC 124
Db 352 ATGATCTTCTGTAATGAGCGAAAGATCCAACTTTAAATGCTATGAGATACCAATGCTGC 411
Qy 125 CTGATTAATTCGACCCCTTAAGTACTTATTGTTAGCTCCAAAGTGCATAAATA 184
Db 412 CCAATACAAATACAAATCCAAAGTACGTTGTTAGCTCCAAAGTTCATAATATAAAAA 471
Qy 185 CCATTACCTAATGCTGAGAGAAATACTTATAGGTATGGGCTATTCTGATCCCTTCA 244
Db 472 CCATCACACTAATCTGAGAGAAATACTTATAGGTATGGGCTATTCTGATCCCTTGG 531
Qy 245 ATGCAATTAAGTGCCTTGAACATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Db 532 AAACCAATTAATGCTGTTACATCTTTAATGATATCTCGATGTAAGCGCAAGT 591
Qy 305 TGAAGAACTCTTGTGCTCAAGTTCTAGTCTCGTTGCAATGTCATTAATTAATTA 364
Db 592 TAGAGACTACTCTTGGCCCAATGCAATTCCTCGTTAGTAAATTAATTAATTAATTA 651
Qy 365 GCTTATATCCGACCATGGAAGAAAGAGAGAAATCAAGAAATCAATGCTCAATG 424
Db 652 GTGATATCCAACTTGAATCAAAAGGAGGAGTAAATCAAGAGTCAAGTCCAAAGT 711

Qy 425 GAATTCAAATACGAGGAGTACGATGGAATAATCTCT 462
Db 712 GAATTCAAATACGAGGAGTACGATGGAATAATCTCT 749
RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 580329
GENERAL INFORMATION:
APPLICANT: Tumei, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1
Query Match 64.8%; Score 301.2; DB 2; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Db 5 TAAATACGATACCTTGTGATGCTGAATGCGACCATTAACAATAATGCGACCTTTATG 64
292 TGAATACATCATCTACCAATGTTGGAAGTACCACTTAGCAAAATACGCCACTTTCTGA 351
Qy 65 AATCTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGCGATCAATGCTAC 124
Db 352 ATGATCTTCTGTAATGAGCGAAAGATCCAACTTTAAATGCTATGAGATACCAATGCTGC 411
Qy 125 CTGATTAATTCGACCCCTTAAGTACTTATTGTTAGCTCCAAAGTGCATAAATA 184
Db 412 CCAATACAAATACAAATCCAAAGTACGTTGTTAGCTCCAAAGTTCATAATATAAAAA 471

QY 185 CCATTACCTAATGCTGAGAGCAAAATACCTTATACGTGATGGCTATTCTGATCCCTTCA 244
 DB 472 CCATCACACATATCTGAGAGCAAAATATGTATGTATGATGGGTATCTGATCCCTTGG 531
 QY 245 ATGGCAATTAAGTGTGCTGATCAATATATTTATATATTAACAAGACCGAAGCCTGATG 304
 DB 532 AAACCAATTAATATGCTGATCAATATATTTATATATTAACAAGACCGAAGCCTGATG 591
 QY 305 TGAGAAATCTCTTGTGCTCAAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 364
 DB 592 TAGAGACTACTCTTGTGCTCAAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 651
 QY 365 GCTTATATCCGACATGGAAGAAAGCAAGATTAATCAAGAAATCAAGTCAATGCTGATG 424
 DB 652 GTCATATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAAATCAAGTCAATGCTGATG 711
 QY 425 GAATTCAAATATCTGACAGTGAATGGAATAATCTCT 462
 DB 712 GAATTCAAATATCTGACAGTGAATATGGAATAATCTCT 749

RESULT 5

US-07-865-169-1
 ; Sequence 1, Application US/07865169
 ; Patent No. 6015940
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, Nilgun E.
 ; APPLICANT: Lodge, Jennifer K.
 ; APPLICANT: Kaniewski, Wojciech K.
 ; TITLE OF INVENTION: Virus Resistant Potato Plants
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
 ; STREET: 700 Chesterfield Parkway No. 6015940th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/865,169
 ; FILING DATE: 19920407
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoerner Jr., Dennis R.
 ; REGISTRATION NUMBER: 30,914
 ; REFERENCE/DOCKET NUMBER: 38-21(10547)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314)537-6099
 ; TELEFAX: (314)537-6047
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1379 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-07-865-169-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
 Best Local Similarity 78.6%; Pred. No. 4,1e-78;
 Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATAGATCACTTTGATGCTGGAATGCAACATTAAATATGCACTTTATG 64
 DB 292 TGAATACATCATCTCAATATGTTGGAATGACCACTTAGCAATATGCGCACTTTGTA 351
 QY 65 AATCTCTTGAATCAAGCGAAATATCCAAATTAATGTATGATGATGCTGATC 124

DB 352 ATGATCTTGTAAATGAGCGAAAGATCCAGTTTAAATCTATGAAATCAATGCTGAC 411
 QY 125 CTGATTAATATGAGACCCCTAAGTACTTATGTTAAGTCCAAAGTCAACCTAATAA 184
 DB 412 CCAATACAAATATCAATATCCAAAGTACTGTTGGTTGAGCTCCAAAGTTCAATTAATAA 471
 QY 185 CCATTACCTAATGCTGAGAGCAAAATTAATTAACGTATGAGGCTATTCTGATCCCTTCA 244
 DB 472 CCATCACACATATCTGAGAGCAAAATATGTATGTATGATGGGTATCTGATCCCTTGG 531
 QY 245 ATGGCAATTAAGTGTGCTGATCAATATATTTATATATTAACAAGACCGAAGCCTGATG 304
 DB 532 AAACCAATTAATATGCTGATCAATATATTTATATATTAACAAGACCGAAGCCTGATG 591
 QY 305 TGAGAAATCTCTTGTGCTCAAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 364
 DB 592 TAGAGACTACTCTTGTGCTCAAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 651
 QY 365 GCTTATATCCGACATGGAAGAAAGCAAGATTAATCAAGAAATCAAGTCAATGCTGATG 424
 DB 652 GTCATATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAAATCAAGTCAATGCTGATG 711
 QY 425 GAATTCAAATATCTGACAGTGAATGGAATAATCTCT 462
 DB 712 GAATTCAAATATCTGACAGTGAATATGGAATAATCTCT 749

RESULT 6

US-09-005-273-1
 ; Sequence 1, Application US/09005273
 ; Patent No. 6137030
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, Nilgun E.
 ; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
 ; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLTZ &
 ; ADDRESS: MENTILIK
 ; STREET: 600 South, Avenue West
 ; CITY: Westfield
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07090
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/005,273
 ; FILING DATE: 09-JAN-1998
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/500,611
 ; FILING DATE: 11-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/500,694
 ; FILING DATE: 11-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/11546
 ; FILING DATE: 11-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foley, Shawn P.
 ; REGISTRATION NUMBER: 33,071
 ; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-654-7866
 ; TELEFAX: 908-654-5000
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1379 base pairs
 ; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FRAMES:
NAME/KEY: sig_peptide
LOCATION: 225..230
US-09-005-273-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATAGATCACTTGAATGCTGAATGCAACATTAACAAATATGCACTTATAG 64
DB 292 TGAATACATCATCTACATATGTAAGTACACCATTAAGCAACCTTTCTGA 351
QY 65 AATCTCTGTAATCAAGCGAAGATCCAAACTAAATGCTATGCAATGCTAC 124
DB 352 ATGATCTTGTGAATGAAGCGAAGATCCAACTTAAATGCTATGCAATGCTAC 411
QY 125 CTGATCTAATTCAGCCCTTAAGTATTGTTAGCTCCAAAGTCAAACTTAA 184
DB 412 CCATTAACAATACAAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAA 471
QY 185 CCATTAACAATGCTGAGAGAAATTAATTAAGTATGCTATGCTATGCTTCA 244
DB 472 CCATTAACAATGCTGAGAGAAATTAATTAAGTATGCTATGCTATGCTTCA 531
QY 245 ATGCAATTAAGTGTGTTACATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCAATTAATGCTGTTACATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAAGATCTCTTGTCTCAAGTTCTGTTGCTCAATGCTCAATTAATTAATTA 364
DB 592 TAGAGCTACTCTTGTGCTCAAGTTCTGTTGCTCAATGCTCAATTAATTAATTA 651
QY 365 GCTTAATTCGACCATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 424
DB 652 GTGATATTCGAATGGAATCAAAAGGGAAGAAAGAAAGAAAGAAAGAAAGAAAG 711
QY 425 GAATTCAAATCTGACGATGATGGAATTAATCTCT 462
DB 712 GAATTCAAATCTGACGATGATGGAATTAATCTCT 749

RESULT 7
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628

GENERAL INFORMATION:
APPLICANT: Uckun, Patih
APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.253A
FILING DATE: 11-JUL-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATAGATCACTTGAATGCTGAATGCAACATTAACAAATATGCACTTATAG 64
DB 292 TGAATACATCATCTACATATGTAAGTACACCATTAAGCAACCTTTCTGA 351
QY 65 AATCTCTGTAATCAAGCGAAGATCCAAACTAAATGCTATGCAATGCTAC 124
DB 352 ATGATCTTGTGAATGAAGCGAAGATCCAACTTAAATGCTATGCAATGCTAC 411
QY 125 CTGATCTAATTCAGCCCTTAAGTATTGTTAGCTCCAAAGTCAAACTTAA 184
DB 412 CCATTAACAATACAAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAA 471
QY 185 CCATTAACAATGCTGAGAGAAATTAATTAAGTATGCTATGCTATGCTTCA 244
DB 472 CCATTAACAATGCTGAGAGAAATTAATTAAGTATGCTATGCTATGCTTCA 531
QY 245 ATGCAATTAAGTGTGTTACATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCAATTAATGCTGTTACATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAAGATCTCTTGTCTCAAGTTCTGTTGCTCAATGCTCAATTAATTAATTA 364
DB 592 TAGAGCTACTCTTGTGCTCAAGTTCTGTTGCTCAATGCTCAATTAATTAATTA 651
QY 365 GCTTAATTCGACCATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 424
DB 652 GTGATATTCGAATGGAATCAAAAGGGAAGAAAGAAAGAAAGAAAGAAAGAAAG 711
QY 425 GAATTCAAATCTGACGATGATGGAATTAATCTCT 462
DB 712 GAATTCAAATCTGACGATGATGGAATTAATCTCT 749

RESULT 8
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546

GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Query Match          64.8%; Score 301.2; DB 6; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4,1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCCTTGTGATGCTGGAATGCGCACCATTTAACTAATATGCGACCTTTATGG 64
DB 292 TGAATACAAATCATCTACATGTTGGAAGTACACCATTAGCAATAGCGCACTTTCTGGA 351
QY 65 AATCTCTTGGTAATCGAAGCGAAAGATCCAAATGCTAATGCTATGCGATCCCATGCTAC 124
DB 352 ATGATCTTGGTAATGGAAGCGAAAGATCCAAATGCTAATGCTATGCGATCCCATGCTAC 411
QY 125 CTGATACTAATTCGACCCCTTAAGTACTTATGTTAGTTCGAAGTCAAGTCAAACTTAATA 184
DB 412 CCAATCAAAATTAACAATCCAAAGTACGTGTGAGTCCAAAGTTCAAATTAATAA 471
QY 185 CCAATTACATTAAGCTGAGAGCAAAATTAATTATGCTATGAGTGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACAATTAAGCTGAGAGCAAAATTAATTATGAGTGGCTATTCGATCCCTTCA 531
QY 245 ATGGCAATTAAGTGGCTGATCAATATTTAATGATATTAACAAGCAGGACGCACTGATG 304
DB 532 AAACCAATTAATGCTGTTACCAATATCTTAAATGATATCTCAGGATGAAAGCGCAAGATG 591
QY 305 TGGAGAAATCTCTTGGCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTATACATA 364
DB 592 TAGAGACTACTCTTTGGCCAAATGCGCAATCTCGTGTAGTAAATAAATTAACCTTTGATA 651
QY 365 GCTTATATCCGACATGGAAGAAAGCAAGTAACTCAAGAAATCAAGTCCATTTGG 424
DB 652 GTGCAATATCCAAATGGAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCCATTTGG 711
QY 425 GAATTCAAATTAATCAAGATGATGATTTGAAATAATCTCT 462
DB 712 GAATTCAAATTAATCAAGATGATGATTTGAAATAATCTCT 749
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```

RESULT 9
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kandlewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. BB4P
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match          64.1%; Score 298; DB 3; Length 1379;
Best Local Similarity 78.2%; Pred. No. 3,5e-77;
Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCCTTGTGATGCTGGAATGCGCACCATTTAACTAATATGCGACCTTTATGG 64
DB 292 TGAATACAAATCATCTACATGTTGGAAGTACACCATTAGCAATATGCGCACTTTCTGGA 351
QY 65 AATCTCTTGGTAATCGAAGCGAAAGATCCAAATGCTAATGCTATGCGATCCCATGCTAC 124
DB 352 ATGATCTTGGTAATGGAAGCGAAAGATCCAAATGCTAATGCTATGCGATCCCATGCTAC 411
QY 125 CTGATACTAATTCGACCCCTTAAGTACTTATGTTAGTTCGAAGTCAAGTCAAACTTAATA 184
DB 412 CCAATCAAAATTAACAATCCAAAGTACGTGTGAGTCCAAAGTTCAAATTAATAA 471
QY 185 CCAATTACATTAAGCTGAGAGCAAAATTAATTATGCTATGAGTGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACAATTAAGCTGAGAGCAAAATTAATTATGAGTGGCTATTCGATCCCTTCA 531
QY 245 ATGGCAATTAAGTGGCTGATCAATATTTAATGATATTAACAAGCAGGACGCACTGATG 304
DB 532 AAACCAATTAATGCTGTTACCAATATCTTAAATGATATCTCAGGATGAAAGCGCAAGATG 591
QY 305 TGGAGAAATCTCTTGGCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTATACATA 364
DB 592 TAGAGACTACTCTTTGGCCAAATGCGCAATCTCGTGTAGTAAATAAATTAACCTTTGATA 651
QY 365 GCTTATATCCGACATGGAAGAAAGCAAGTAACTCAAGAAATCAAGTCCATTTGG 424
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Db 652 GTCCATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAGTCAGGTCACATCG 711
 Qy 425 GAATTCAAATCTCAGCGAGTACATTTGAAAAATCTCT 462
 Db 712 GAATTCAAATCTCAGCGAGTAAATTTGAAAAATTTCT 749

RESULT 10

US-09-005-273-3
 ; Sequence 3, Application US/09005273
 ; Patent No. 6137030
 ; GENERAL INFORMATION:
 ; APPLICANT: Tumer, Nilgun E.
 ; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
 ; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LERNER, DAVID, LITENBERG, KRUMHOLZ &
 ; STREET: 600 South, Avenue West
 ; CITY: Westfield
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07090
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/005,273
 ; FILING DATE: 09-JAN-1998
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/500,611
 ; FILING DATE: 11-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/500,694
 ; FILING DATE: 11-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/11546
 ; FILING DATE: 11-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foley, Shawn P.
 ; REGISTRATION NUMBER: 33,071
 ; REFERENCE/DOCKET NUMBER: OCTRS 3.3-034
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-654-5000
 ; TELEFAX: 908-654-7866
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1379 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 225..1163
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 225..290
 ; US-09-005-273-3

Query Match 64.1%; Score 298; DB 3; Length 1379;
 Best Local Similarity 78.2%; Pred.No.3-5e-77;
 Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 5 TAAATACATACCTTTGATGCTGAATGCGACCATTAACCAATATGCGACCTTTATG 64
 Db 292 TGAATACATCATCTTCAATGTGGAGTACCAACATTAGCAATACGCCACTTTTCGA 351

Qy 65 AATCTTCTGTATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTAC 124
 Db 352 ATGATCTTGTATGAAAGCGAAAGATCCAAAGTTAAATGCTATGAAATACCAATGCTGC 411
 Qy 125 CTGATTAATTTGCAACCCCTTAAGTATTTGTTAGCTCAAGTGCCTCAAACTTAAAA 184
 Db 412 CCAATACAAATACAAATCCAAAGCAGTGTGTTAGCTCCAAAGTTCAATATAAAAA 471
 Qy 185 CCATTAACCTAATGCTGAGACGAATTAATTATACGTATGAGGCTATTCTGATCCCTTCA 244
 Db 472 CCATCACACTAATGCTGAGACGAATTAATTATGAGGCTATTCTATCCCTTGTG 531
 Qy 245 ATGCAATPAAGTGTGATACCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 304
 Db 532 AAACCAATTAATGCTGATACCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 591
 Qy 305 TGAAGATATCTTTGCTCAAGTCTGATGCTGTTGCAATGCTCAATTAATCAATA 364
 Db 592 TAGAGACTACTCTTGGCCCAATGCCAATCTCGTGTATGATTAATAAACAATTAATTTGATA 651
 Qy 365 GCTATATCCGACCATGGAAGAAAGAGCAAGTAACTCAAGAAATCAATCCCAATTG 424
 Db 652 GTGATATCCCAACTGTGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 711
 Qy 425 GAATTCAAATCTCAGCGAGTACATTTGAAAAATCTCT 462
 Db 712 GAATTCAAATCTCAGCGAGTAAATTTGAAAAATTTCT 749

RESULT 11

US-08-138-636-1
 ; Sequence 1, Application US/08138636
 ; Patent No. 5348865
 ; GENERAL INFORMATION:
 ; APPLICANT: Moon, Young-Ho
 ; APPLICANT: Jeon, Hong-Seoh
 ; APPLICANT: Choi, Kyu-Mhan
 ; APPLICANT: Lee, Kwan Ho
 ; TITLE OF INVENTION: No. 5348865el Genome Coding Phyloceca Antiviral
 ; TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DARBY & DARBY
 ; STREET: 805 THIRD AVE.
 ; CITY: NEW YORK
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/138,636
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, S. Peter
 ; REGISTRATION NUMBER: 25,351
 ; REFERENCE/DOCKET NUMBER: 0136/08818
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 527-7700
 ; TELEFAX: (212) 753-6237
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 918 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA

HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATACGATCCTTTGAGCTGGAATGCCACATTACAAATATGCCACTTTATGG 64
DB 68 TGAATACCATCATCTACCATGTTGGAAGTACACCATATGAACTATGCACTTTGGAT 127
QY 65 AATCTTCTGTAATCAAGCGAAGATCCAAACTAAATGTATGCGATTCATCTAC 124
DB 128 A---CTTCGACTGAAGGCGAAGATCCAG--TTATGTCTATGAAATACCAATGCTGC 181
QY 125 CTGATTAATTCGACCCCTTAAGTACTTATTTGTTAAGCTCAAGTGCATAAATA 184
DB 182 CCAATATTTGATCAAAATCCAAATATCATTTGGTTGAGCTCAAGGTTCAAAATGAAGA 241
QY 185 CCAATTAAGTATGCTGAGAGCAAAATTAAGTATGAGGAGGCTATTTCTGATCCCTCA 244
DB 242 GCATCACTTAATGCTAAGAGCAAAATTAATATGATGAGGCTATTTCTGATCCCTCA 301
QY 245 ATGGCAATAGTGTCTGATCATATATTTAATGATTAACAAGCAGCAAGCACTGATG 304
DB 302 A---CAATAGGTGTGTTTCAATCTCTTAAGGCTATCTCGATCAAGCAAGCAAGATG 358
QY 305 TGGAGAACTCTTTGCTCAAGTCTAGTTCTCGTTGCAATGTCATTAACTACATA 364
DB 359 TAGAGACTACTCTTTGCGCAATGCGATTCGCTGTGTTGTTAAACATTAATCATATGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCAATTGG 424
DB 419 GTGATATCCAACTGGAATCAAAAGCAGAGTAATTCAGAAAGTGCAGTCAACTGG 478
QY 425 GAATTCAAATCTCAGAGTGAATGGAATTAATCTCT 462
DB 479 GAATTCGAATCTCAGAGTGAATGGAATTAATCTCT 516

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/0A445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATACGATCCTTTGAGCTGGAATGCCACATTACAAATATGCCACTTTATGG 64
DB 68 TGAATACCATCATCTACCATGTTGGAAGTACACCATATGAACTATGCACTTTGGAT 127
QY 65 AATCTTCTGTAATCAAGCGAAGATCCAAACTAAATGTATGCGATTCATCTAC 124
DB 128 A---CTTCGACTGAAGGCGAAGATCCAG--TTATGTCTATGAAATACCAATGCTGC 181
QY 125 CTGATTAATTCGACCCCTTAAGTACTTATTTGTTAAGCTCAAGTGCATAAATA 184
DB 182 CCAATATTTGATCAAAATCCAAATATCATTTGGTTGAGCTCAAGGTTCAAAATGAAGA 241
QY 185 CCAATTAAGTATGCTGAGAGCAAAATTAAGTATGAGGAGGCTATTTCTGATCCCTCA 244
DB 242 GCATCACTTAATGCTAAGAGCAAAATTAATATGATGAGGCTATTTCTGATCCCTCA 301
QY 245 ATGGCAATAGTGTCTGATCATATATTTAATGATTAACAAGCAGCAAGCACTGATG 304
DB 302 A---CAATAGGTGTGTTTCAATCTCTTAAGGCTATCTCGATCAAGCAAGCAAGATG 358
QY 305 TGGAGAACTCTTTGCTCAAGTCTAGTTCTCGTTGCAATGTCATTAACTACATA 364
DB 359 TAGAGACTACTCTTTGCGCAATGCGATTCGCTGTGTTGTTAAACATTAATCATATGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCAATTGG 424
DB 419 GTGATATCCAACTGGAATCAAAAGCAGAGTAATTCAGAAAGTGCAGTCAACTGG 478
QY 425 GAATTCAAATCTCAGAGTGAATGGAATTAATCTCT 462
DB 479 GAATTCGAATCTCAGAGTGAATGGAATTAATCTCT 516

RESULT 13

US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 572326

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 572326el Genome Coding Phytoleuca Antiviral

TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phycolacca inuellaris
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATAGATGACCTTATGATGCTGAATGCGACCATTAACCAAAATATGCCACTTTATG 64
DB 68 TGAATACCATATCTACCATGATGTGAACTACCACTTAAAGAACTATCACTTTTGAT 127
QY 65 AATCTCTGTAATCAAGCAAGATCCAAATTAATGCTATGAGTACCAATGCTAC 124
DB 128 A-----CTTGTACTGAGAGCGAAGATCCAG--TTATGTGCTATGAAATACCAATGCTGC 181
QY 125 CTGATTAATTTGACCCCTTAAGTACTTATGTTAGCTCCAAAGTCAAACTTAATA 184
DB 182 CCAATATATGATCAAAATCAAAATATCATATTTGTTGAGCTCAAGCTTCAATGAAAG 241
QY 185 CCATTACGTAATGCTGAGAGAAATACTTATAGTATGAGGCTATTTGATCCCTTCA 244
DB 242 GCATACACATATGCTAAGAGAAACATTTATATGATGAGGCTATTTCTATCTTCA 301
QY 245 ATGCAATAGATGCTGATACCATATATTAATGATATTAACAAGCAGCAAGCTATG 304
DB 302 A---CAATAGAGTGTGTTTTCATCTTTAAGGCTATCTCAGTACTGAAGCAAGATG 358
QY 305 TGGAGATATCTTTGCTCAAGTTTGAATTTCTGTTGCTCAATGCTCAATTAACAATA 364
|||||

DB 359 TAGAGACTACTCTTTGCCCAATATGCGCATCTCGTGTGTAATAAATCAATATAGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGAGTAATCTCAAGAAATCAAGTCCATATG 424
DB 419 GTGATATTCGAACATTTGAATCAAAAGAGATTAATTCAGAAAGTGAAGTCAACTGG 478
QY 425 GAATTCAAATACTGACGATGATGGAATTAATCTCT 462
DB 479 GAATTCGAATACTGACGATGATGGAATTAATCTCT 516
|||||

RESULT 14

US-08-718-904-80
Sequence 80, Application US/08718904
Patent No. 6037329

GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPY
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS
LOCATION: 1..1230
OTHER INFORMATION: /product= "E. coli codon optimized"
OTHER INFORMATION: FGF-SAP"
US-08-718-904-80

Query Match 9.3%; Score 43.2; DB 3; Length 1233;
Best Local Similarity 48.7%; Pred. No. 0.0093;
Matches 148; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 1 ATGTAATATGCAATCCTTGAATGCTGGAATATGCCACATTAACAATATATGCCACTTT 60
DB 469 ATGATCACTTATATACGCTGATCTGTCAACCCGACCGTGTGATACAGCTCGTTT 528
QY 61 ATGGAATCTCTTCTTAATCAAGCAAGATCCAAATTAATGCTATGAGTACCAATG 120
DB 529 GTGATTAAGATGCTTAATTAATGTAAGATCGAATTTAAATACGATGCAAGATAT 588
QY 121 CTACTGATTAATTTGACCCCTTAAGTACTTATGTTAAGCTCAAGGTCAAACTTA 180
DB 589 GCAATGATATGCGCCGCGCTTAAGAAAGTTCTTGTGATTTAACTTCAAGCTCTGCG 648
|||||

QY 181 AAAACATTACCTAATGCTGAGACGAATACTTATACGTATGGGCTATTCTGATCCC 240
Db 649 GGCACTGTGCTCTGGGCTTAAAGCGATATTTGTACGTTGTAGCGTACCTGGCGATG 708
QY 241 TTCAATGGCAAT---AAGTGTGCTTACCATATTTATGATATTTACAGACCGAAGCC 297
Db 709 GATATATCCATGTAAACCGCTTACTATTTCAAAAGCGAATAATTAACCTGTGCTGAATG 768
QY 298 ACTG 301
Db 769 ACTG 772

RESULT 15

US-09-449-249-80
; Sequence 80, Application US/09449249
; Patent No. 6503886
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; Chandler, Lois Ann
; Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/449,249
; FILING DATE: 24-No. 6503886-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6503886tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1230
; OTHER INFORMATION: /product= "E. coli codon optimized
; RGR-SAP"
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-449-249-80

Query Match 9.3%; Score 43.2; DB 3; Length 1233;
Best Local Similarity 48.7%; Pred. No. 0.0093;
Matches 148; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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Db 469 ATGTCACCTTCTATCAAGCTGATGTGTCAACCCGACCGCTGTGTCAGTACAGCTCGTTT 528
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Db 529 GTCCATTAAGATTCTGAATTAATGTGAAGATCCGAATTTAAATACGGTGCACCGAATTT 588
QY 121 CTACCTGATCTAATTTGACCCCTAAGTACTTATTTGTATAGCTTCAAGTGCAAACTTA 180
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QY 181 AAAACATTACCTAATGCTGAGACGAATACTTATACGTATGGGCTATTCTGATCCC 240
Db 649 GGCACTGTGCTCTGGGCTTAAAGCGATATTTGTACGTTGTAGCGTACCTGGCGATG 708
QY 241 TTCAATGGCAAT---AAGTGTGCTTACCATATTTATGATATTTACAGACCGAAGCC 297
Db 709 GATATATCCATGTAAACCGCTTACTATTTCAAAAGCGAATAATTAACCTGTGCTGAATG 768
QY 298 ACTG 301
Db 769 ACTG 772

Search completed: April 8, 2006, 09:48:54
Job time : 162.42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 537.272 Seconds
(without alignments)
7157.007 Million cell updates/sec

Title: US-09-978-274A-5
Perfect score: 465
Sequence: 1 atgataatacagtcacacct.....acattggaataatctctta 465

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	465	100.0	465	US-09-978-274A-5	Sequence 5, Appli
2	462	99.4	792	US-09-978-274A-3	Sequence 3, Appli
3	462	99.4	1092	US-09-978-274A-19	Sequence 19, Appli
4	459	98.7	945	US-09-978-274A-1	Sequence 1, Appli
5	301.2	64.8	1379	US-09-978-274A-30	Sequence 30, Appli
6	301.2	64.8	1379	US-11-106-187-1	Sequence 31, Appli
7	298	61.7	1368	US-09-978-274A-31	Sequence 31, Appli
8	286.8	64.1	1376	US-10-467-009-1	Sequence 1, Appli
9	54.6	11.7	855	US-11-106-187-20	Sequence 20, Appli
10	54.6	11.7	934	US-09-978-274A-32	Sequence 32, Appli
11	54.6	11.7	934	US-11-106-187-3	Sequence 3, Appli
12	46.6	10.0	765	US-09-792-793A-66	Sequence 66, Appli
13	46.6	10.0	765	US-10-375-209A-66	Sequence 66, Appli
14	46.6	10.0	984	US-09-792-793A-60	Sequence 60, Appli
15	46.6	10.0	984	US-10-375-209A-60	Sequence 60, Appli
16	46.6	10.0	993	US-09-792-793A-63	Sequence 63, Appli
17	46.6	10.0	993	US-10-375-209A-63	Sequence 63, Appli
18	46.6	10.0	999	US-09-792-793A-54	Sequence 54, Appli
19	46.6	10.0	999	US-09-792-793A-57	Sequence 57, Appli
20	46.6	10.0	999	US-10-375-209A-54	Sequence 54, Appli
21	46.6	10.0	999	US-10-375-209A-57	Sequence 57, Appli
22	43.2	9.3	1233	US-09-861-257-24	Sequence 24, Appli
23	43.2	9.3	1233	US-10-189-360-80	Sequence 80, Appli

c	24	41.6	8.9	9723	6	US-10-311-455-2353	Sequence 2353, Ap
	25	39.6	8.5	1230	6	US-10-189-360-53	Sequence 53, Appl
	26	39.6	8.5	1251	6	US-09-861-257-77	Sequence 77, Appl
	27	39.6	8.5	1251	6	US-10-189-360-74	Sequence 74, Appl
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	30	39.6	8.5	1266	6	US-09-861-257-78	Sequence 78, Appl
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	32	39.6	8.5	1269	3	US-09-861-257-78	Sequence 81, Appl
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	36	39.6	8.5	1299	3	US-09-861-257-80	Sequence 80, Appl
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	38	39.6	8.5	1320	6	US-10-189-360-76	Sequence 76, Appl
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	40	38.2	8.2	765	4	US-09-861-257-73	Sequence 23, Appl
	41	38	8.2	765	6	US-10-189-360-79	Sequence 79, Appl
	42	38	8.2	588	4	US-09-925-065A-793731	Sequence 793731,
	43	37.6	8.1	804	3	US-09-861-257-22	Sequence 22, Appl
	44	37.6	8.1	804	3	US-09-861-257-35	Sequence 35, Appl
	45	37.6	8.1	804	3	US-09-861-257-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1	US-09-978-274A-5	Sequence 5, Application US/09978274A
Sequence 5, Appli	Patent No. US20020116737A1	GENERAL INFORMATION:
APPLICANT: Thomas, Christopher	APPLICANT: McPherson, Michael	APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil	TITLE OF INVENTION: PLANT CELL DEATH SYSTEM	FILE REFERENCE: 9341-028
CURRENT FILING DATE: 2001-10-15	PRIOR APPLICATION NUMBER: 0025225.4	PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32	SOFTWARE: PatentIn version 3.1	SEQ ID NO 5
LENGTH: 465	TYPE: DNA	ORGANISM: Phylocacca americana
US-09-978-274A-5	Query Match	100.0%; Score 465; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.7e-123;	Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB 301 GATGTGAGAACTCTTTGCTCAAGTTCAGTTCCTGTTGCAATGTCATTACTAC 360
QY 361 AATGCTTAATCCGACCAATGAAAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCCA 420
DB 361 AATGCTTAATCCGACCAATGAAAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCCA 420
QY 421 TTGGGAATTCAAATTAATCTCAGCAATGACATTGGAAAAATCTCTTAA 465
DB 421 TTGGGAATTCAAATTAATCTCAGCAATGACATTGGAAAAATCTCTTAA 465

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RESULT 2
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phylocacca americana
US-09-978-274A-3

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Query Match 99.4%; Score 462; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 TTGGGAATTCAAATTAATCTCAGCAATGACATTGGAAAAATCTCT 462
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RESULT 3
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

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Query Match 99.4%; Score 462; DB 3; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.9e-122;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 TTGGGAATTCAAATTAATCTCAGCAATGACATTGGAAAAATCTCT 462
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RESULT 4
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM

```

FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 945
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274a-1

Query Match 98.7%; Score 459; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 1,3e-121;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 373 GTGAGATATCTCTTGTCTCAAGTTCTAGTTCTGCTGTGCAATGTCATTAACTA 432
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DB 433 AGCTTAATCCGACCATGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAAT 492
QY 424 GGAATTCATAATCTCAGAGTGACATTTGAAAAATCTCT 462
DB 493 GGAATTCATAATCTCAGAGTGACATTTGAAAAATCTCT 531
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RESULT 5
US-09-978-274a-30
Sequence 30, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1379
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274a-30

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
Best Local Similarity 78.6%; Pred. No. 5e-76; Mismatches 98; Indels 0; Gaps 0;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 65 AATCTCTGCTAATCAAGCCGAAAGATCCAAATCTAAATATGCTATGCAATGCTAC 124
DB 352 AATCTCTGCTAATCAAGCCGAAAGATCCAAATCTAAATATGCTATGCAATGCTAC 411
QY 125 CTGATCTAATTCGACCCCTAATGATCTAATGTTAGCTCAAGGTCGAACTTAA 184
DB 412 CCATTAACAAATCAATCAAGTACGTTGTTAGCTCAAGGTCGAACTTAA 471
QY 185 CCATTAACAAATCAAGTACGTTGTTAGCTCAAGGTCGAACTTAA 244
DB 472 CCATTAACAAATCAAGTACGTTGTTAGCTCAAGGTCGAACTTAA 531
QY 245 ATGCAATTAATGCTGCTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 304
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DB 592 TGAAGAAATCTCTTGTCTCAAGTTCTAGTTCTGCTGTGCAATGTCATTAACTA 651
QY 365 GCTTAATCCGACCATGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAAT 424
DB 652 GTCATATCCCAATGGAATCAAAAGGGAGTAAATCAAGAAAGTCAAGTCAAT 711
QY 425 GAATTCATAATCTCAGAGTGACATTTGAAAAATCTCT 462
DB 712 GAATTCATAATCTCAGAGTGACATTTGAAAAATCTCT 749
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RESULT 6
US-11-106-187-1
Sequence 1, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILDUN E.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 1379
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURES:
NAME/KEY: CDS
LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 64.8%; Score 301.2; DB 10; Length 1379;
Best Local Similarity 78.6%; Pred. No. 5e-76; Mismatches 98; Indels 0; Gaps 0;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 125 CTGATCTTAATTCAGCCCTTAAGTACTTATGTTAGCTCCAGGTGCAAACTTAATAA 184
DB 412 CCAATTAACAAATACAAATTCGAAAGTACGTTGTTGAGCTCCAGGTTCGAATTAATAA 471
QY 185 CCATTACACTATGCTGAGAGAAATTAATTATAGTATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACTATGCTGAGAGAAATTCGATATGATGATGATGATGATGATGATGATGAT 531
QY 245 ATGCGAATAAGTGTGCTTACCAATATTTAATGATATTAACAAGCAGCACTGATG 304
DB 532 AAACCAATAAATGCTGTTACCAATATCTTAATGATATCTGAGTACTGAACGCCAAGATG 591
QY 305 TGGGAATATCTCTTGTCTCAAGTCTTACTTCTCGTGTGCAATGCTTCACTTAACATA 364
DB 592 TAGGACTACTCTTGTGCGCAATATCCAAATCTCTGTTAGTAAACATAAATCTTGTATA 651
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAAAGTAACTCAAGAAATCAAGTCAATG 424
DB 652 GTCATATCCAACTTGAATTCAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTG 711
QY 425 GAATTCAAATATCTGAGAGTCACTTGGAAAAATCTCT 462
DB 712 GAATTCAAATATCTGAGAGTCACTTGGAAAAATCTCT 749
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RESULT 7

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US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US2002011673A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIORITY FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIORITY FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Phytolacca americana
; US-09-978-274A-31
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Query Match 64.1%; Score 298; DB 3; Length 1368;

Best Local Similarity 78.2%; Pred. No. 4.1e-75;

Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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QY 65 AATCTCTTGGTAATCAAGCGAAAGATCCAAAATAAAATGCTATGCGATACCAATGCTAC 124
DB 352 ATGATCTTCGTAAATGGAAGCGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTGC 411
QY 125 CTGATCTTAATTCAGCCCTTAAGTACTTATGTTAGCTCCAGGTGCAAACTTAATAA 184
DB 412 CCAATTAACAAATACAAATTCGAAAGTACGTTGTTGAGCTCCAGGTTCGAATTAATAA 471
QY 185 CCATTACACTATGCTGAGAGAAATTAATTATAGTATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACTATGCTGAGAGAAATTCGATATGATGATGATGATGATGATGATGATGAT 531
QY 245 ATGCGAATAAGTGTGCTTACCAATATCTTAATGATATTAACAAGCAGCACTGATG 304
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DB 532 AAACCAATAAATGCTGTTACCAATATCTTATGATATCTGAGTACTGAAGCGCAAGATG 591
QY 305 TGGGAATATCTCTTGTCTCAAGTCTTACTTCTCGTGTGCAATGCTTCACTTAACATA 364
DB 592 TAGGACTACTCTTGTGCGCAATATCCAAATCTCTGTTAGTAAACATAAATCTTGTATA 651
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAGAAAGTAACTCAAGAAATCAAGTCAATG 424
DB 652 GTCATATCCAACTTGAATTCAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTG 711
QY 425 GAATTCAAATATCTGAGAGTCACTTGGAAAAATCTCT 462
DB 712 GAATTCAAATATCTGAGAGTCACTTGGAAAAATCTCT 749
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RESULT 8

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US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467, 009
; PRIORITY FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIORITY FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1
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Query Match 61.7%; Score 286.8; DB 8; Length 1376;

Best Local Similarity 78.2%; Pred. No. 7.1e-72;

Matches 358; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

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QY 5 TAAATACGATCACCTTGTGATGCTGAAATGCGACCATTAACAATATGCACTTATAG 64
DB 292 TGAATACATCATCTACAAATGTTGGAAGTACACCATTAAGCAAAATGCGCACTTTGGA 351
QY 65 AATCTCTTGGTAATCAAGCGAAAGATCCAAAATAAAATGCTATGCGATACCAATGCTAC 124
DB 352 ATGATCTTCGTAAATGGAAGCGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTGC 411
QY 125 CTGATCTTAATTCAGCCCTTAAGTACTTATGTTAGCTCCAGGTGCAAACTTAATAA 184
DB 412 CCAATTAACAAATACAAATTCGAAAGTACGTTGTTGAGCTCCAGGTTCGAATTAATAA 471
QY 185 CCATTACACTATGCTGAGAGAAATTAATTATAGTATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACTATGCTGAGAGAAATTCGATATGATGATGATGATGATGATGATGATGAT 531
QY 245 ATGCGAATAAGTGTGCTTACCAATATTTAATGATATTAACAAGCAGCACTGATG 304
DB 532 AAACCAATAAATGCTGTTACCAATATCTTAATGATATCTGAGTACTGAACGCCAAGATG 591
QY 305 TGGGAATATCTCTTGTCTCAAGTCTTACTTCTCGTGTGCAATGCTTCACTTAACATA 364
DB 592 TAGGACTACTCTTGTGCGCAATATCCAAATCTCTGTTAGTAAACATAAATCTTGTATA 648
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAGAAAGTAACTCAAGAAATCAAGTCAATG 424
DB 649 GTCATATCCAACTTGAATTCAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTG 708
QY 425 GAATTCAAATATCTGAGAGTCACTTGGAAAAATCTCT 462
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OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
NAME/KEY: CDS
LOCATION: (1)..(984)
US-09-792-793A-60

Query Match 10.0%; Score 46.6; DB 3; Length 984;
Best Local Similarity 49.2%; Pred. No. 0.012;
Matches 152; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 1 ATGATTAATACATGACCTTTGATGCTGAAATGCGACCATTAACAAATATGCGACCTTT 60
DB 220 ATGGTACTAGATTATACCTGAGCCTGTGCAATCGACCGCGCAATATGCGACCTTC 279
QY 61 ATGGAATCTCTGATATCAAGCAAGATCCAAAATTAATGCTATGCGATACCAATG 120
DB 280 GTGGATTAAGATTCGTACCAAGCTAAAGATCCGAATTCGAATAGCGTGATCTGATATT 339
QY 121 CTACCTGATCTAATTCGACCCCTAGTACTTATTTGTTAAGCTCCAAAGTCAAACTTA 180
DB 340 GCGGTATCGGTCCCGCGCAAGAAAGTTCTGCGCATTAACCTTCAAGCTCCGT 399
QY 181 AAAACATTAACATGATGAGAGCAAAATTAATTAAGTATGCGCTATTTGATCCC 240
DB 400 GGCACGTGTTCTCTGCGCCTGAAGCGCATTAACCTGATGTTGCTATCTGCGCATG 459
QY 241 TTCATATGCAATTAAGTGTCT--TACCATATATTAATGATTAATTAAGACGACGACGC 297
DB 460 GATAATACGAACGTGAACCGCGCTACTACTTCTGTAAGGAGATTACGAGCGGAATCC 519
QY 298 ACTGATGTG 306
DB 520 ACTGCTCTG 528

RESULT 15

US-10-375-209A-60
Sequence 60, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 60
LENGTH: 984
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(984)
US-10-375-209A-60

Query Match 10.0%; Score 46.6; DB 6; Length 984;
Best Local Similarity 49.2%; Pred. No. 0.012;
Matches 152; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 1 ATGATTAATACATGACCTTTGATGCTGAAATGCGACCATTAACAAATATGCGACCTTT 60
DB 220 ATGGTACTAGATTATACCTGAGCCTGTGCAATCGACCGCGCAATATGCGACCTTC 279
QY 61 ATGGAATCTCTGATATCAAGCAAGATCCAAAATTAATGCTATGCGATACCAATG 120
DB 280 GTGGATTAAGATTCGTACCAAGCTAAAGATCCGAATTCGAATAGCGTGATCTGATATT 339
QY 121 CTACCTGATCTAATTCGACCCCTAGTACTTATTTGTTAAGCTCCAAAGTCAAACTTA 180

DB 340 GCGGTATCGGTCCCGCGCAAGAAAGTTCTGCGCATTAACCTTCAAGCTCCGT 399
QY 181 AAAACATTAACATGATGAGAGCAAAATTAATTAAGTATGCGCTATTTGATCCC 240
DB 400 GGCACGTGTTCTCTGCGCCTGAAGCGCATTAACCTGATGTTGCTATCTGCGCATG 459
QY 241 TTCATATGCAATTAAGTGTCT--TACCATATATTAATGATTAATTAAGACGACGACGC 297
DB 460 GATAATACGAACGTGAACCGCGCTACTACTTCTGTAAGGAGATTACGAGCGGAATCC 519
QY 298 ACTGATGTG 306
DB 520 ACTGCTCTG 528

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Job time: 539.272 secs

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GenCore version 5.1.7
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OW nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278038 residues

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Listing first 45 summaries

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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301.2	64.8	1360	US-11-010-795-19	Sequence 19, Appl
2	54.6	11.7	934	US-11-010-795-21	Sequence 21, Appl
3	41.6	8.9	1471	US-10-750-185-27060	Sequence 27060, A
4	41.6	8.9	1471	US-10-750-623-27060	Sequence 27060, A
5	38.2	8.2	588	US-09-925-065A-793732	Sequence 793732, A
6	37.8	8.1	588	US-09-925-065A-793731	Sequence 793731, A
7	35.6	7.7	994	US-10-301-480-611379	Sequence 611379, A
8	35.6	7.7	994	US-10-301-480-1224788	Sequence 1224788, A
9	35	7.5	647	US-09-925-065A-409152	Sequence 409152, A
10	35	7.5	650	US-10-301-480-475630	Sequence 475630, A
11	35	7.5	650	US-10-301-480-475630	Sequence 475630, A
12	35	7.5	18930	US-10-995-561-13213	Sequence 13213, A
13	34.6	7.4	650	US-10-301-480-219992	Sequence 219992, A
14	34.6	7.4	650	US-10-301-480-833401	Sequence 833401, A
15	34.6	7.4	655	US-09-925-065A-121758	Sequence 121758, A
16	34.4	7.4	700	US-09-925-065A-64273	Sequence 64273, A
17	34.4	7.4	1048	US-09-925-065A-64273	Sequence 64273, A
18	34.4	7.4	1048	US-10-301-480-165511	Sequence 165511, A

19	34.4	7.4	1048	US-10-301-480-778920	Sequence 778920, A
20	34.4	7.4	1708	US-10-750-185-44263	Sequence 44263, A
21	34.4	7.4	1708	US-10-750-623-44263	Sequence 44263, A
22	34	7.3	598	US-10-301-480-98532	Sequence 98532, A
23	34	7.3	598	US-10-301-480-711941	Sequence 711941, A
24	34	7.3	700	US-09-925-065A-671816	Sequence 671816, A
25	34	7.3	1341	US-10-750-185-57064	Sequence 57064, A
26	34	7.3	1341	US-10-750-623-57064	Sequence 57064, A
27	33.8	7.3	503	US-09-925-065A-214054	Sequence 214054, A
28	33.8	7.3	510	US-10-301-480-300908	Sequence 300908, A
29	33.8	7.3	510	US-10-301-480-914317	Sequence 914317, A
30	33.8	7.3	1951	US-10-750-185-45758	Sequence 45758, A
31	33.8	7.3	1951	US-10-750-623-45758	Sequence 45758, A
32	33.8	7.3	2784	US-11-129-741-2922	Sequence 2922, A
33	33.8	7.3	2784	US-11-129-741-2930	Sequence 2930, A
34	33.8	7.3	2784	US-11-129-741-4242	Sequence 4242, A
35	33.8	7.3	2900	US-10-750-185-50117	Sequence 50117, A
36	33.8	7.3	2900	US-10-750-623-50117	Sequence 50117, A
37	33.8	7.3	29942	US-10-895-064-3	Sequence 3, Appl
38	33.8	7.3	29942	US-10-895-064-34	Sequence 34, Appl
39	33.8	7.3	29942	US-10-895-064-457	Sequence 457, Appl
40	33.8	7.3	29942	US-10-895-064-724	Sequence 724, Appl
41	33.8	7.3	29942	US-10-895-064-1319	Sequence 1319, Appl
42	33.8	7.3	29942	US-10-895-064-1908	Sequence 1908, Appl
43	33.8	7.3	29942	US-10-895-064-2454	Sequence 2454, Appl
44	33.8	7.3	29942	US-11-129-741-3	Sequence 3, Appl
45	33.8	7.3	29942	US-11-129-741-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NITGUN B.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 64.8%; Score 301.2; DB 14; Length 1360;
Best Local Similarity 78.6%; Pred. No. 1.3e-67;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
DB 5 TAAATAGACACCTTGATGCTGGAATGCAACATTAACAAATATGACCTTTATG 64
274 TGAATACATCATATCAATGTTGAAATGCAACATTAACAAATATGACCTTTTGA 333
65 AATCTTCTGTAATCAAGCAAGCAAAATCAATTAATGCTATGCAATGCTATC 124
334 ATGATCTTCTGTAATCAAGCAAGCAAAATCAATTAATGCTATGCAATGCTATC 393
125 CTGATTAATTAATGCAAGCAAGCAAAATCAATTAATGCTATGCAATGCTATC 184
394 CCAATTAATTAATCAAGCAAGCAAAATCAATTAATGCTATGCAATGCTATC 453

Qy	185	CCATTACACTATAGCTGAGACGAATAACTTAACTGATAGGGCTATTGATCCCTTCA	244
Db	454	CCATCAACTATAGCTGAGACGAACAAATTGTATGTGATGGTATTTCGATCCCTTGG	513
Qy	245	ATGGCAATAGTGTGCTTACCAATATTTAAATGATATTTACAGACCGAAGCGACTGATG	304
Db	514	AAACCAATAAAAGTGGTACCAATCTTTAAATGATATTCACGGTACTGAAACGCAAGATG	573
Qy	305	TGGAGATATCTTTTGCTCAAGTTCAGTTCAGTTCGATGCAATGTCCATTAACTACAAATA	364
Db	574	TAGAGACTACTCTTTTGCCAAATGCGCAATTCCTGTGTAGTATAAAACATTAACCTTGATA	633
Qy	365	GCTTATATCCGACCATGAAAAAGAAAGCAGAAAGTAAACTCAGAAATCAAGTCCAAATTGG	424
Db	634	GTCGATATCCAACTATGGAATCAAAAACGGGAGTAAATCAAGAAAGTCAGGTCCAACTGG	693
Qy	425	GAAATCAATATCTCAGACGATGACATTGGAAAAATGCTCT	462
Db	694	GAATTCMAATCTCCAGACGTAAATATTGGAAAGATTTCT	731

RESULT 2
US-11-010-795-21
; Sequence 21, Application US/11010795
; Publication No. US20060005271A1
CENTRAL INTELLIGENCE AGENCY

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1  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
2  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
3  TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
4  FILE REFERENCE: OCIRS 3.0-085
5  CURRENT APPLICATION NUMBER: US/11/010,795
6  CURRENT FILING DATE: 2004-12-13
7  PRIOR APPLICATION NUMBER: 60/529,348
8  PRIOR FILING DATE: 2003-12-12
9  NUMBER OF SEQ ID NOS: 44
10 SOFTWARE: PatentIn Ver. 3.3
11 SEQ ID NO 21
12
13 LENGTH: 934
14
15 TYPE: DNA
16
17 ORGANISM: Phytolacca americana
18
19 FEATURES:
20
21 NAME/KEY: CDS
22
23 LOCATION: (1)..(930)
24
25 OS-11-010-795-21

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Query Match	11.7%	Score 54.6	DB 14	Length 934
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Best Local Similarity 55.9%; Pred. No. 0.00034;
Matches 146; Conservative 0; Mismatches 109; Indels 6; Gaps 2;

Oy 19 TTTGATGCTGAGAAATGGCCACCTTACCAATATAGCACCTTATNGAAATCTCTCGAAT 78
 Db 85 TTTGACGTTTGAGAAATGCCACACCAAAACCTACTTAAATTTCTGACTAGTTGGCGAA 144
 Oy 79 CAAGGAAAGATCCAAACTAAATAGCTATGGCATACCAATGCTACCTGATTAATTCG 138
 Db 145 GCTGTGAAAGACAGAAATTTGCATGCTCATGTAGATGTAATGGCCAAACCTTCACGAA 204
 Oy 139 ACCCTTAAGTACTTATTTGGTTAAGCTCCAAAGGCAAAACCTAAATACCTTACACTAATG 198
 Db 205 CAACCCAAATAGTGTGTGGTGAAGCTCCAAATTTGGATCTGAAACATTC---ACATTGCA 261
 Oy 199 CTGAGACGAATACTTATACGATGATGGGCTATTCTGATCCCTCAATGGCAATAAAGTG 258
 Db 262 ATCAGAAAGGGAACCTTATATTATTTGAGGGCTATTCTGACATTTACAAATGG---AAATGT 318
 Oy 259 CGTTACACTATATTTAATGAT 279
 Db 319 CGTTATCGATCTTCAAGAT 339

RESULT 3
US-10-750-185-27060/c

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: Sequence 27060, Application US/10750185
: Publication No. US20050260603A1
: GENERAL INFORMATION:
: APPLICANT: MMI GENOMICS, INC.
: APPLICANT: DENISE, Sue K.
: APPLICANT: KERR, Richard
: APPLICANT: ROSENFELD, David
: APPLICANT: HOLM, Tom
: APPLICANT: BATES, Stephen
: APPLICANT: FANTIN, Dennis
: TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
: FILE REFERENCE: MM1100-2
: CURRENT APPLICATION NUMBER: US/10/750,185
: CURRENT FILING DATE: 2003-12-31
: PRIOR APPLICATION NUMBER: US 60/437,482
: PRIOR FILING DATE: 2002-12-31
: NUMBER OF SEQ ID NOS: 64922
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 27060
: LENGTH: 1471
: TYPR: DNA
: ORGANISM: Bovine 19866880349638
US-10-750-185-27060

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Query Match	8.9%	Score 41.6;	DB 8;	Length 1471;
Best Local Similarly	59.2%	Fred. NO. 0.88;		
Matches 71; Conservative	0;	Mismatches 49;	Indels 0;	Gaps 0;

Accession	Sequence	Position
QY	GCATGTCCTTAATCTCAATAGCTTATATCCGACCTGTGAAAAAGAAAGCAAGTAAC	402
Db	1377 GCATGCTAAAGCATACTAAAGCTTGATACCTCCATAGGATGAAGGCTATGTATAA	1318
QY	403 TCACGAATCAAGTCCATTTGGGAATCCAAATACACGACGTGACATTTGAAAAATCTCT	462
Db	1317 GGTGAATAATTAGTATATAAGGATTTTGAACTCTCTTCGTATATACTGAAAAATTTCT	1258

Introduction

RESULT 4
US-10-750-623-27060/c
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; sequence 2/060, Application US/10/50623
; Publication No. US20050287531A1
; GENERAL INFORMATION.

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; GENERATED INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.

APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David

```

; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

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; FILE REFERENCE: MML100-1
; CURRENT APPLICATION NUMBER: US/10/750.623
; CURRENT FILING DATE: 2003-12-31

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! CURRENT FILING DATE: 2003-12-31
! PRIOR APPLICATION NUMBER: US 60/437,482
! PRIOR FILING DATE: 2002-12-31

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; NUMBER OF SEQ ID NOS: 64922
;-----
; SOFTWARE: Patentin version 3.1

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; SEQ ID NO 27060
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; LENGTH: 1471

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; TYPE: DNA
; ORGANISM: Bovine 1986680349638
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OS-10-/50-623-27060
Qwen: Match 0 08. Score 41 6. DB 8. Length 1471.

Query match	0.54	Score	41.07	DB	01	Accession	1711
Best Local Similarity	59.24	Pred.	No. 0.88				
Matches	71	Conservative	0	Mismatches	49	Indels	0
							Gaps
							0

343 GCAATGCTTAATCAATATGCTTATATCCGACCATGAAAAGAACGAGTTAAC 402

Db 1377 GCACTGCTAAGCATACTAAAGCTTGATATCTTCATAGGCGATGAAGCCATTGTAAAA 1318

403 TCAGAATCAAGTCCAATTGGGATTCAAATACCTCAGCAGTGACATTTGGAAAAATCTCT 462

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US-10-301-480-1224/88/C
; Sequence 1224788, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21, 598
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1224788
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1224788

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Best Local Similarity 7.7%; Score 35.6; DB 10; Length 994;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 342 TGCATGTCATTAATACATATGATCCGACCATGGAAGAAGCAAGTAA 401
DB 278 TGAAGGCTATTAATCTCAAGCTTCATGAAAAAAGAAAGAAAGCA 219
QY 402 CTCAGAATCAAG 415
DB 218 AATAAGAAAGCCAG 205

RESULT 9
US-09-925-065A-409152/c
; Sequence 409152, Application US/0925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 409152
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-409152

Query Match
Best Local Similarity 7.5%; Score 35; DB 6; Length 647;
Matches 92; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

QY 240 CTTCAATGCGAATAGTGTCTTACCATATTTAATATTTCAAGCAGCAAGCAG 299
DB 483 CTATCAGAAATTCAGATAGAACTAGATATTTGATATATTAAGAAATTAAGTAA 424
QY 300 TGATGTGAGAAATCTTTGCTCAAGTTCTAGTTCGTGTCGATGTCATTAAC 359
DB 423 TTTAGTTAGTGAAGAAAGTATGAGTTTGAATCGAATTTTAATTTAATTACTA 364
QY 360 CAATAGCTTATATCGACCATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCA 419
DB 363 GGCTCAATATATCTTTATTAATTAATGTAGAACCAATTAATCAACATTTTGGCA 304
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QY 420 ATTGGGAAT 428
DB 303 ATGAGAAAT 295

RESULT 10
US-10-301-480-475630
; Sequence 475630, Application US/10301480
; Publication No. US2006005564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475630
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-475630

Query Match
Best Local Similarity 7.5%; Score 35; DB 10; Length 650;
Matches 92; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

QY 240 CTTCAATGCGAATAGTGTCTTACCATATTTAATATTTCAAGCAGCAAGCAG 299
DB 168 CTATCAGAAATTCAGATAGAACTAGATATTTGATATTAAGAAATTAAGTAA 227
QY 300 TGATGTGAGAAATCTTTGCTCAAGTTCTAGTTCGTGTCGATGTCATTAAC 359
DB 228 TTTAGTTAGTGAAGAAAGTATGAGTTTGAATCGAATTTTAATTTAATTACTA 287
QY 360 CAATAGCTTATATCGACCATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCA 419
DB 288 GGCTCAATATATCTTTATTAATTAATGTAGAACCAATTAATCAACATTTTGGCA 347
QY 420 ATTGGGAAT 428
DB 348 ATGAGAAAT 356
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RESULT 11
US-10-301-480-1089039
; Sequence 1089039, Application US/10301480
; Publication No. US2006005564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089039
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1089039
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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121758
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-121758

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Query Match      7.4% Score 34.6; DB 6; Length 655;
Best Local Similarity 67.1%; Pred. No. 43;
Matches 49; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 42 TAACAAATATGCCACTTATGGAATCTCTGTAATCAAGCAAGATCCAAACTTAA 101
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DB 458 TAACAAATATGCCACTTATGGAATCTCTGTAATCAAGCAAGATCCAAACTTAA 101
    |||||
QY 102 ATGCTATGCCATA 114
    |||||
DB 398 ATGAGGGGGGCATA 386
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Search completed: April 9, 2006, 04:47:48
 Job time : 406.834 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using ~~fasta~~ p2n model

Run on: April 9, 2006, 01:20:32 ; Search time 3516 Seconds
(without alignments)
2489.732 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793
Sequence: 1 MINITTFDAGNATINKYATF.....SRNOVQLGIQLISDGIKIS 154

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=genbank1 -QFMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELTEXT=7

Database :

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10: gb_sbs: *
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13: gb_vi: *
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15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	465	6	AX427706 Sequence
2	793	100.0	792	6	AX427704 Sequence
3	793	100.0	1092	6	AX427720 Sequence

4	788	99.4	945	6	AX427702
5	788	99.4	1249	15	PAPAPSRIP
6	773	97.5	786	15	AB071855
7	670.5	84.6	783	15	AB071854
8	613	77.3	882	6	A67183
9	608	76.7	714	15	AY603354
10	605	76.3	939	15	AY327475
11	598	75.4	711	15	AF338910
12	596	75.2	714	15	AY603352
13	596	75.2	942	15	AY547315
14	596	75.2	942	15	AY572976
15	596	75.2	1195	6	AY2103
16	596	75.2	1195	6	AY2103
17	596	75.2	1195	6	AY2103
18	596	75.2	1195	6	AY2103
19	596	75.2	1195	6	AY2103
20	596	75.2	1195	6	AY2103
21	596	75.2	1195	6	AY2103
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23	596	75.2	1195	6	AY2103
24	594	74.9	714	15	AY603353
25	590	74.4	1195	6	AY2103
26	589	74.3	1114	15	AF533515
27	588	74.1	1378	6	AX427732
28	588	74.1	1379	6	AR136705
29	559.5	70.6	2472	15	BO5033
30	559.5	70.6	2472	15	FTCAPAP
31	554.5	69.9	1052	15	AY137202
32	542.5	68.4	951	6	A67185
33	542.5	68.4	2369	15	AF141331
34	527	66.5	1113	15	AY071928
35	463.5	58.4	918	6	AA3003
36	463.5	58.4	918	6	AA8150
37	463.5	58.4	918	6	160482
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39	399	50.3	1226	15	CAANTIPR
40	399	50.3	1226	15	CAANTIPR
41	278.5	35.1	1180	15	MCUR0072
42	274	34.6	902	15	AF533516
43	261	32.9	934	6	AX427733
44	261	32.9	1187	15	PAPAPIT
45	247	31.1	1667	15	PAPAPITIN

ALIGNMENTS

RESULT 1	AX427706	465 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427706	Sequence 5 from Patent WO0233107.			
DEFINITION	AX427706				
ACCESSION	AX427706.1	GI:21537817			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE					
AUTHORS	Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J. R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 5 25-APR-2002;				
	CAMBRIDGE ADVANCED TECH (GB)				
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	/organism="Phytolacca americana"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:3527"				
	1..3				
	/note="Initiation codon added via PCR primer"				
	462..465				
	/note="Stop codon added via PCR primer"				
misc_feature					
misc_feature					
ORIGIN					

Alignment Scores:
Pred. No.: 3,38e-74 Length: 465
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427706 (1-465)

QY 1 MetIleAenThrlleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyraLathrPhe 20
DB 1 ATGATTAATACGATCACCCTTGATGCTGGAATGCCACATTACAATATGCCACCTTT 60
QY 21 MetGluSerLeuAArgAngInAlaLysAspProLysLeuLysCysTyrglyIlePromet 40
DB 61 ATGGATCTCTTCTGTAATCAAGCAAGATCCAAAATCAATATGCGATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTACCTAATACTAATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
QY 61 LysThrIleThrlleuMetLeuAArgAsnAsnLeuTyraLmetGlyTyrsAspPro 80
DB 181 AAAACATTACACTAATGCTGAGAGCAAAATTAATTATCGATGGGCTATTGATGCC 240
QY 81 PheAngLysAnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGGCAATTAAGTGTGCTTACCATATTAATGATTAATACCAAGCAAGCAAGCACT 300
QY 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrr 120
DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGTCCATTACTAC 360
QY 121 AsnSerLeuTyrrProThrMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTAATTCGACCATGAGAAAGAAACAGAAAGTAACTCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 TTGGGAATTCAAATTAATCTCAGCAGTGACATTGGAAAAATCTCT 462

RESULT 2
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704.1 GI:21537816
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Source location/Qualifiers
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/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
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misc_feature /note="Initiation codon added via PCR primer"
misc_feature complement(436..462)
misc_feature /note="Binding site for primer PS1SR"
463..492
/note="Binding site for primer PS2BF"

variation 612
/note="Nucleotide change from published sequence"
variation 681..686
/note="Sequence replacing removed XbaI site"
misc_feature /note="Sequence (765..792)
complement(765..792)
misc_feature /note="Binding site for primer PS2SR"
790..792
/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:
Pred. No.: 6.03e-74 Length: 792
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427704 (1-792)

QY 1 MetIleAenThrlleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyraLathrPhe 20
DB 1 ATGATTAATACGATCACCCTTGATGCTGGAATGCCACATTACAATATGCCACCTTT 60
QY 21 MetGluSerLeuAArgAngInAlaLysAspProLysLeuLysCysTyrglyIlePromet 40
DB 61 ATGGATCTCTTCTGTAATCAAGCAAGATCCAAAATCAATATGCGATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTACCTAATACTAATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
QY 61 LysThrIleThrlleuMetLeuAArgAsnAsnLeuTyraLmetGlyTyrsAspPro 80
DB 181 AAAACATTACACTAATGCTGAGAGCAAAATTAATTATCGATGGGCTATTGATGCC 240
QY 81 PheAngLysAnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGGCAATTAAGTGTGCTTACCATATTAATGATTAATACCAAGCAAGCAAGCACT 300
QY 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrr 120
DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGTCCATTACTAC 360
QY 121 AsnSerLeuTyrrProThrMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTAATTCGACCATGAGAAAGAAACAGAAAGTAACTCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 TTGGGAATTCAAATTAATCTCAGCAGTGACATTGGAAAAATCTCT 462

RESULT 3
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Source location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:35630"
/note="PAP-S/Cystatin fusion"

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/note="Binding site for primer PS1BP"
variation 681..686
/note="Modified XbaI site"
misc_feature complement(742..786)
misc_feature /note="Binding site for primer PCS-PAPSR"
766..806
/note="Binding site for primer PCS-Delta86P"
766..786
/note="REV NIA protease cleavage site"
misc_feature complement(1066..1092)
/note="Binding site for primer SYNPDelta86SR"

ORIGIN

Alignment Scores:

Pred. No.: 8,54e-74 Length: 1092
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427720 (1-1092)

QY 1 MettIeaenThrlEthrPheaspaIaGlyAsnaIaThrlEaenlyTyraIaThrPhe 20
DB 1 ATGATTAATACATACATCTTGATGCTGGAATGCAACATTAACAAATATGCACTTT 60
QY 21 MetGIuSerIeuArgaAngIaIaIyAspProIyIeulYcTyrgIyIleProMet 40
DB 61 ATGGAATCTCTTGATACAGGAAAGATCCAAATGCTAATGCGCATACCAATG 120
QY 41 IeuProApThrAsnSerThrProIyTyrlEuleuValIyIeGInGlyIaIaenIeu 60
DB 121 CTAAGTATACATTAATTCAGCCCTTAAGTACTTAATGTTAGCTCCAAAGTGAACCTTA 180
QY 61 IyethrlEthrIeuleuMetIeuArgaAsnaIeulYrValMetGlyTySerAspPro 80
DB 181 AAAACATTAACATTAATGCTGAGCAAGAAATTAATTAAGTATGAGGCTATTCATCCC 240
QY 81 PheAngIyAsnIyGcAaIyTyrlHisIlePheAsnaIleThrSerThrGIuArgThr 100
DB 241 TTCAATGCGCAATTAAGTGTGTTACCATATTAATTAATTAATTAATTAATTAATTA 300
QY 101 AspValGIuAsnThrlEuleuCySerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GATGGAATTAATCTTTGCTCAAGTTCTAGTTCGATGCAATGTCATTAATTAATC 360
QY 121 AsnSerIeuTyProThrMetGIuIyIyIaIaIuValAsnSerArgaAngIaIaGIn 140
DB 361 AATACCTTAATATCCGACCATGGAAGAAAGCAAGAAATTAATTAATTAATTAATTA 420
QY 141 IeuGIyIleGInIleIeuSerSerSerSerSerSerSerSerSerSerSerSer 154
DB 421 TTGGGAATTCATTAATCTCAGCAGTGCATTAATTAATTAATTAATTAATTAATCTCT 462

RESULT 4
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 1 from Patent WO0233107.
DEFINITION AX427702
ACCESSION AX427702.1 GI:21537815
VERSION
KEYWORDS
SOURCE
ORGANISM

Phytolacca americana (American pokeweed)

Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Neelam A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCB TECH (GB)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:3527"

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complement(735..776)
misc_feature /note="Binding site for primer PSXPR"
736..777
/note="Binding site for primer PSXDP"
750..759
/note="Sequence replacing removed XbaI site"
variation complement(922..945)
/note="Binding site for primer PPS2SR"

ORIGIN

Alignment Scores:

Pred. No.: 2,45e-73 Length: 945
Score: 768.00 Matches: 153
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427702 (1-945)

QY 2 IleaenThrlEthrPheaspaIaGlyAsnaIaThrlEaenlyTyraIaThrPheMet 21
DB 73 ATTAATTAACATACATCTTGATGCTGGAATGCAACATTAACAAATATGCACTTTATG 132
QY 22 GIuSerIeuArgaAngIaIaIyAspProIyIeulYcTyrgIyIleProMetIeu 41
DB 133 GATCTCTTGATTAATCAAGCAAGAAATCCAAATGCTAATGCGCATACCAATGCTTA 192
QY 42 ProApThrAsnSerThrProIyTyrlEuleuValIyIeGInGlyIaIaenIeuYs 61
DB 193 CCTGATACATTAATTCAGCCCTTAAGTACTTAATGTTAGCTCCAAAGTGAACCTTA 252
QY 62 ThrIleThrIeuleuMetIeuArgaAsnaIeulYrValMetGlyTySerAspProPhe 81
DB 253 ACCATTAACATTAATCTGAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 312
QY 82 AsnGIyAsnIyGcAaIyTyrlHisIlePheAsnaIleThrSerThrGIuArgThr 101
DB 313 AATGCAATTAATGTTGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTA 372
QY 102 ValGIuAsnThrlEuleuCySerSerSerSerSerSerSerSerSerSerSer 121
DB 373 GTGGGAATTAATCTTTGCTCAAGTTCTAGTTCGATGCAATGTCATTAATTAATC 432
QY 122 SerIeuTyProThrMetGIuIyIyIaIaIuValAsnSerArgaAngIaIaGInIeu 141
DB 433 AGCTTAATTCGACCATGGAAGAAAGCAAGAAATTAATTAATTAATTAATTAATTA 492
QY 142 GIyIleGInIleIeuSerSerSerSerSerSerSerSerSerSerSerSer 154
DB 493 GGAATTCATTAATCTCAGCAGTGCATTAATTAATTAATTAATTAATTAATTAATCTCT 531

RESULT 5
PAPAPSRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS P.americana mRNA for pokeweed antiviral protein.
DEFINITION PAPAPSRIP
ACCESSION X98079
VERSION X98079.1 GI:1707648
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.

Phytolacca americana (American pokeweed)

Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1

AUTHORS Poyet, J.L. and Hoeveler, A.
TITLE cDNA cloning and expression of pokeweed antiviral protein from seeds in *Escherichia coli* and its inhibition of protein synthesis in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet, J.L.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES location/Qualifiers
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 /mol_type="mRNA"
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 106..1050
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 /protein_id="CAA66702.1"
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 /db_xref="GOA:P93444"
 /db_xref="InterPro:IPR001574"
 /db_xref="UniProt/TREMBL:P93444"
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 polyA_site
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 Score: 788.00 Matches: 153
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.4% Indels: 0
 DB: 15 Gaps: 0
 US-09-978-274A-6 (1-154) x PAPAPSRIP (1-1249)
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 Db 178 ATAAATACGATCACTTTGATGCTCGAAATGACACATTAAACAAATATGCCCTTTATG 237
 Oy 22 GluSerLeuArgAenGlnAlaIyAaPProlySleuLySvCyTyGlyllePProMetLeu 41
 Db 238 GAATCTCTTCGTAATCAAGCGAAGATCCAAATGCTAATGCTATGACCAATGCTA 297
 Oy 42 ProAaPThrAaenSerThrProLySryLeuLeuValIySleuGlnGlyAlaAaenLyS 61
 Db 298 CCTGATCTAATTCGACCCCTTAAGTACTTATTGGTTAAGCTCCAAAGTCCAAACTAAA 357
 Oy 62 ThrilleThrLeuMetLeuArgAaenAenlyeTyValMetGlyTySerAaPProPhe 81
 Db 358 ACCATTACACTAATGCTGAGACGAATATACTTATACGTATGGGCTATTCTGATCCCTTC 417

Oy 82 AaenIyAaenLySvCyArgTyRhllePheAaenAaPilleThrSerThrluArgThrAaP 101
 Db 418 AATGCAATAGTGTCTGTTACCATATTTATATATTTACACACGACGACATGAT 477
 Oy 102 ValGluAaenThrlleuCySerSerSerSerSerArgValAlaMetSerlleAaenTyAaen 121
 Db 478 GTGAGATACTCTTTGCTCAAGTTAGTTCTGCTGTGCAATGTCATTAACTCAAT 537
 Oy 122 SerleuTyProThrMetGluLyLyAlaGluValAaenSerAaenGlnValGlnleu 141
 Db 538 AGCTTAATTCGACCAAGAAAGAAAGCAAGATAAATCAAGAAATCAAGTCAATG 597
 Oy 142 GlylleGlnlleuSerSerAaPilleGlyTySerleuSer 154
 Db 598 GGAATTCAAATCTCAGCAGTACGATTCGAAATATCTCT 636

RESULT 6
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana paps2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855.1 GI:19570839
VERSION AB071855.1
KEYWORDS Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS 1
TITLE Honjo, E. and Watanabe, K.
JOURNAL Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
REFERENCE 2 (bases 1 to 786)
AUTHORS Watanabe, K. and Honjo, E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail: watekei@cc.saga-u.ac.jp, Tel: 81-952-28-8774, Fax: 81-952-28-8774)
 Location/Qualifiers

FEATURES
SOURCE 1..786
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gene

CDS 1..786
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 /db_xref="GI:19570840"

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ORIGIN

Alignment Scores:
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 Query Match: 97.5% Indels: 0
 DB: 15 Gaps: 0

US-09-978-274A-6 (1-154) x AB071855 (1-786)

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OY	22	giuserleuargasninalalyaspprolyseulyscyslylleprometleu	41
Db	61	GAATCTCTTCGTAAATCAACGAAGAAGTCCAAACTAAATGCTATGGCATACCAATGCTA	120
OY	42	ProAspThrAsnSerThrProlystryleuleuVallyleuGlnGlyAlaasneulysc	61
Db	121	CCTGATACCTAATTCGACCCTTAAGTACTTAATGGTTAACTCCAAAGTCAAACTTAAAA	180
OY	62	ThrilethrleumetleuargasnaleuIyrValmetGlyTyrSerAspprophe	81
Db	181	ACCATTACACTAATGCTGAGCAAGAAATACTTATACGTATGGGCAATTCATGCCCTTC	240
OY	82	AenglyasulyscysargtyrthiisileleasnapilrthSerThrGluargthraap	101
Db	241	AATGGCAATTAAGTGTGCTGTTACCAATTAATTAAATGATTAACAAGCCCAAGCACTGAT	300
OY	102	ValGluAsnThrLeuCyseSerSerSerSerArgValAlaMetSerilleasnyrzan	121
Db	301	GTGAGGAATACCTTTTGCTCAGAGTTCTAAGTTCTCGATGCAATGTCATTAACATCAAT	360
OY	122	SerleuIyrProthMetGlnulysalysalagluValasnsSerArgasnInValGlnleu	141
Db	361	AGCTAATATTCGCACCTTGGAAAAGAAAGACAGAAATTAATCAAGAAGTCAATTCCAATTG	420
OY	142	GlyIleGlnIleLeuSerSerSeraspIleGlyIysIleSer	154
Db	421	GGAAATCAAAATACAGCAAGTACATTTGGAAAAAATCTCT	459

RESULT 7					
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LOCUS	Phytolacca americana papstl gene for PAP-S1, partial cds.				
DEFINITION					
ACCESSION	AB071854				
VERSION	AB071854.1	GI:19570837			
KEYWORDS					
SOURCE	Phytolacca americana (american pokeweed)				
ORGANISM	Phytolacca americana				

REFERENCE

1. Bukacynska, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

AUTHORS	Honjo, E. and Watanabe, K.
TITLE	Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 783)
AUTHORS	Watanabe, K. and Honjo, E.
TITLE	Direct Submision
JOURNAL	Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,

Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: wakabe@cc.saga-u.ac.jp,
Tel: 01-952-28-8774, Fax: 01-952-28-8774)

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ORIGIN

Alignment Scores:	
Pred. No.:	4,58e-61
Score:	670.50
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Best Local Similarity:	86.3%
Query Match:	84.6%
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US-09-978-274A-6 (1-154) x AB071854 (1-783)	
	Length: 783
	Matches: 132
	Conservative: 8
	Mismatches: 12
	Indels: 1
	Gaps: 1

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Db 1 ATCAATACGATACGTTGACGCTGGAATACCACTTAAACAATGACCTTATATG 60

Qy 22 GluSerLeuArgAsnGlnAlaIysAspProLysLeuLysCysTyrGlyIleProMetLeu 41

Db 61 GAATCTCTTCGTAAGAGGAGGAAAGATCCAACTTAAAGGTATVAGAAATACCAATGTTG 120

Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlnVal1aAsnLeuLys 61

Db 121 CCCAAATCAATTCACACATCAAGTACTGTGTGTAAAGCTCCCAAGGTGCAAGCTTAAAA 180

Qy 62 Thr11eThrMetLeuArgArgAsnLeuLysTyrValMetGlyTyrSerAspProPhe 81

Db 181 ACCATCACTAATATCTAAGACGAACAACCTTATATGATGGGCTATTTGGATTCCTTAC 240

[illegible]

Db 358 GGCCTATATCCAACTTTGGAAAAAGCAGAGTAACCTCAGAAATCAAGTCAACTA 417

Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154

Dn		418	GGAATTCGAAATTCTCAGCGACGTGCATTGGAAAAATTTCTT	456
RESULT 8				
A67183				
LOCUS	A67183			
DEFINITION	Sequence 1 from Patent EP0808902.	882 bp	DNA	linear
ACCESSION	A67183			
VERSION	A67183.1	GI:4756167		
KEYWORDS	.			

SOURCE ORGANISM	Phylogenetic Group
<i>Phytolacca insularis</i>	Phytolacaceae
<i>Phytolacca insularis</i>	Phytolacaceae
<i>Eukaryota</i>	Eukaryota
<i>Viridiplantae</i>	Viridiplantae
<i>Streptophyta</i>	Streptophyta
<i>Embryophyta</i>	Embryophyta
<i>Tracheophyta</i>	Tracheophyta
<i>Spermatophytes</i>	Spermatophytes
<i>Magnoliophyta</i>	Magnoliophyta
<i>eudicotyledons</i>	eudicotyledons
<i>core eudicotyledons</i>	core eudicotyledons
<i>Carroviellales</i>	Carroviellales
<i>Phytolaccaceae</i>	Phytolaccaceae
<i>Phytolacca</i>	Phytolacca

REFERENCE
1 (bases 1 to 882)
Moon, Y., Choi, J., Yun, Y., Jih, J., Hong, E., Lee, J., Choi, K., Lee, J., Song, S., Choi, Y., Kim, C. and Kim, M.
TITLE
Novel genes encoding antiviral proteins of *Phytolacca inularis*
Nakai and recombinant microorganisms expressing the same proteins
JOURNAL
Patent: JP 0808902-A 1 26-NOV-1997

COMMENT	FEATURES
JINRO LTD (KR)	
Other publication JP 9308489 19971102	
Other publication CA 2186303 19971123	
Other publication AU 6570696 19971127.	
Location/Qualifiers	
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source	

ORIGIN /db xref="taxon:63744"
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Score: 613.00 Matches: 114
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Best Local Similarity: 74.0% Mismatches: 19
Query Match: 77.3% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x A67183 (1-882)

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QY 21 MetGluSerIleuArgAsnGlnAlaIleAspProIleuIleYsCySyrGlyIlePromet 40
Db 61 CTGATTAATCTTCTGTAATGAAGCAAAAGATCCAACTTTAAATGCTATGGAATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProIleYrIleuValIleuGlnGlyAlaAsnIleu 60
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Db 241 TTTGATACCAATTAAGTCTGTTACATATCTTTAATGATATCTCAGTACGAAAGCCAA 300
QY 101 AspValGluAsnThrIleuCySerSerSerSerSerSerArgValAlaMetSerIleAsnYr 120
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QY 121 AsnSerIleuYrProThrMetGluIleYsAlaGluValAsnSerArgAsnGlnValGln 140
Db 361 GATAGTCATATCCAAATCTGGAATCAAAAGCGGAGTAAATCAAAAGTCAAGTTCAA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 421 CTGGGAATTCAAATCTCGACAGTACATTGGAAGATTCT 462

RESULT 9
AY603354 714 bp DNA linear PLN 17-MAY-2004
LOCUS PhytoIacca acinosa antiviral protein PAPA2 (papa2) gene, papa2-s

DEFINITION
AY603354
AY603354
AY603354.1 GI:47175558

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
PhytoIacca acinosa (food pokeweed)

REFERENCE
AUTHORS
TITLE
JOURNAL
PhytoIacca acinosa anti-viral protein PAP (PAPA2) DNA
Unpublished
2 (bases 1 to 714)
Chen, G., Lei, J., Zeng, G. and Cao, B.
Direct Submission
Submitted (20-Apr-2004) Horticultural College, South China
Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR
China

FEATURES
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US-09-978-274A-6 (1-154) x AY603354 (1-714)
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Db 1 GTGAAATCAATCAATCTACATGTTGGAAGTACCAATGCAATAGCCCACTTTCTG 60
QY 22 GluSerLeuArgAsnGlnAlaIleAspProIleuIleYsCySyrGlyIlePrometIleu 41
Db 61 GATATATCTTCTGTAATGAAGCAAAAGATCCAAATGCTATGGAATCCAAATGTTG 120
QY 42 ProAspThrAsnSerThrProIleYrIleuValIleuGlnGlyAlaAsnIleu 61
Db 121 CCCAATCAATCCAAATCCAAAGTACGTTGTTAAGCTCCAAAGTTCAATGAA 180
QY 62 ThrIleThrIleuMetIleuArgAsnAsnIleuYrValMetGlyIleProMetPro 81
Db 181 ACCATCAACATTAATGCTGAGAGCAAAATTTGATGATGAGGCTATTCGATCCCTT 240
QY 82 AsnGlyAsnIleYsCySyrGlyIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 241 GATACCAATTAAGTCTGTTACATATCTTTAATGATATCTCAGTACGAAAGCCCAAGAT 300
QY 102 ValGluAsnThrIleuCySerSerSerSerSerSerArgValAlaMetSerIleAsnYrAsn 121
Db 301 GTAGAGACTACTCTTGGCCCAATCCCAATCTCGTGTAGTAAACCAATAACTATAT 360
QY 122 SerIleuYrProThrMetGluIleYsAlaGluValAsnSerArgAsnGlnValGlnIleu 141
Db 361 AGTCATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAAAGTCAAGTTCACTG 420
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 421 GGAATTCAAATCTCGACAGTACATTGGAAGATTCT 459

RESULT 10
AY327475 939 bp mRNA linear PLN 01-JUL-2004
LOCUS PhytoIacca heterotepala anti-viral protein PAP (RIP1) mRNA,
DEFINITION complete cds.
ACCESSION AY327475
VERSION AY327475.1 GI:37625511

KEYWORDS

SOURCE	ORGANISM	REFERENCE	TITLE	AUTHORS	JOURNAL	FEATURES	LOCATION
Phytolacca heterotepala	Phytolacca heterotepala	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.	1 (bases 1 to 939)	Delli Bovi, P. and Corrado, G.	Direct Submission	Submitted (23-JUN-2003) Department of Soil, Plants and Environmental Sciences, University of Naples 'Federico II', via	University
100, Portici, Naples 80055, Italy							
Location/Qualifiers							
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Alignment Scores:	
Pred. No.:	4,33e-54
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Percent Similarity:	87.6%
Best Local Similarity:	73.28
Query Match:	76.38
DB:	15
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QY 22 GluSerLeuArgasnGlnAlaLysAspProLysLeuLysCysTyGlyIleProMetLeu 41
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QY 42 ProAspThrAsnSerThrProLysTyIleuLeuValLysLeuGlnGlyAlaAsnLys 61
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QY 82 AsnGlyAsnLysCysArgTyPheAlaPheaAsnAspIleThrSerThrGluArgThrAsp 101
Db 307 GATACCAAGTAAGTGTCTTACCAATCTTTAAATGATATCTCAAGTATCGAACGCCAAGAT 366

QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyAsn 121
Db 367 GTAGAAGACTACTCTTGTCCAAATTCCAATTCTCGTGTAAATAAACAATAAATCATGAT 426

QY 122 SerLeuTyIleProThrMetGluLysLysAlaLeuValAsnSerArgasnGlnValGlnLeu 141
Db 427 AGTGAATATCCAAATGTGAATCAAAAGTGGAGATTAATAATCAAGAGTCAAAGTCCAAGT 486

QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154

DB	487	GGAATTCAAAATCTCGACAGTACATTGGAAAGATTTC	525
RESULT 11			
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LOCUS	711 bp	mRNA	linear
DEFINITION	Phytolacca americana antiviral protein (mpap) mRNA,		PLN 21-MAR-2001
ACCESSION	AF338910		partial cds.
VERSION	AF338910.1	GI:13398616	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			

ORIGIN	
Alignment Scores:	
Pred. No.:	1.75e-53
Score:	598.00
Percent Similarity:	86.9%
Best Local Similarity:	71.9%
Query Match:	75.4%
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Matches:	110
Conservative:	23
Mismatches:	20
Indels:	0
Gaps:	0

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 Db 1 GTGAATCATTCAATCAATGTTGGAAAGTACCAACATTGCAAAATACGCACTTTCTG 60
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 QY 62 ThrIlethrIeuleuIeAargAargAsnleuIleTyValMetgIyrYsraaProPhe 81
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 QY 82 AsngIYAsnIscYsAargIYrHsIlePheAsnAspIleThrSerThrGluAargThrAsp 101

Db 241 GAACCAATAAATGCTGTTACCATATCTTTATGATATCTCAGGTAAGCAAGCCCAAGAT 300

Qy 102 ValGluAnthrIleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 301 GTAAAGACTACTCTTTGCCCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 360

Qy 122 SerLeuTyrProThrMetGluLysLeuAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 361 AGTGATATTCACATTCGATTCGAAAGCCGGAGTAAATCAAGAGTCAGTCCAACTG 420

Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 421 GGAATTCAAATATCTCGACATTAATATTGGAAGAATTCT 459

RESULT 12
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LOCUS PhytoIacca americana antiviral protein PAP (pap) gene, pap-s
DEFINITION
ACCESSION AY603352
VERSION AY603352.1 GI:47175554
KEYWORDS
SOURCE PhytoIacca americana (American pokeweed)
ORGANISM
REFERENCE
AUTHORS Chen, G., Lei, J., Cao, B. and Zeng, G.
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 714)
AUTHORS PhytoIacca americana antiviral protein (PAP) DNA
TITLE
AUTHORS Chen, G., Lei, J., Cao, B. and Zeng, G.
JOURNAL Direct Submission
Submitted (20-APR-2004) Horticultural College, South China
Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR
China

FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 2.85e-53 Length: 714
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Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 15 Gaps: 0

US-09-978-274A-6 (1-154) x AY603352 (1-714)

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Db 1 GTGAATCAATCATCTCAATGTTGGAAGTACCAATTCAGCAATACGCACTTTCTG 60

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Db 61 AATGATCTTGATATGAAAGGAAAGATCCGAGTTTAAATGCTATGGAATACCAATGCTG 120

Qy 42 ProAnThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 181 ACCATCACTAATGCTGAGACGAAACAAATTTGATATGATGGGTATTTGATCCCTTT 240

Qy 82 AsnGlyAsnLysCyAspGlyThrIleIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 241 GAACCAATAAATGCTGTTACCATATCTTTATGATATCTCAGGTAAGCAAGCCCAAGAT 300

Qy 102 ValGluAnthrIleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 301 GTAAAGACTACTCTTTGCCCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 360

Qy 122 SerLeuTyrProThrMetGluLysLeuAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 361 AGTGATATTCACATTCGATTCGAAAGCCGGAGTAAATCAAGAGTCAGTCCAACTG 420

Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 421 GGAATTCAAATATCTCGACATTAATATTGGAAGAATTCT 459

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LOCUS PhytoIacca americana antiviral protein gene, complete cds.
DEFINITION
ACCESSION AY547315
VERSION AY547315.1 GI:44889055
KEYWORDS
SOURCE PhytoIacca americana (American pokeweed)
ORGANISM
REFERENCE
AUTHORS Zhao, Y., Wang, X., Zhou, G. and Li, H.
TITLE A pokeweed antiviral protein gene in roots of PhytoIacca americana
JOURNAL Acta Virol. 48 (2), 131-132 (2004)
PUBMED 15462289
REFERENCE 2 (bases 1 to 942)
AUTHORS
AUTHORS Zhao, Y., Wang, X. and Li, H.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-2004) Plant Virology, Institute of Plant
Protection, CAAS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
China

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KNGVLPRLELVDSGAKW"

AUTHORS Lin, Q., Chen, Z.C., Antoniw, J.F. and White, R.F.
TITLE Isolation and characterization of a cDNA clone encoding the
JOURNAL anti-viral protein from Phytolacca americana
PUBLISHED Plant Mol. Biol. 17 (4), 609-614 (1991)
REFERENCE 1912488
AUTHORS 2 (bases 1 to 1164)
TITLE Antoniw, J.F.
JOURNAL Direct Submission
Submitted (05-NOV-1990) Antoniw, J.F., AFRC Inst of Arable Crops
Research, Dept. of Plant Pathology, Rothamsted Experimental
Station, Harpenden, Hert, AL5 2JQ, UK

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Alignment Scores:

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US-09-978-274A-6 (1-154) x PAPAP (1-1164)

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Db GTGAATCAATCATCTCAATGTTGGAAGTACCAACATTAGCAATAACGCCATTTCCTG 127
QY 22 GluSerLeuArgaenGlnAlaLyaspProLyseuLyCybTyrgLyIleProMetLeu 41
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QY 128 AATGATCTTCGTATGAAAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 187
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QY 42 ProAspThrAsnSerThrProLyseTyLeuLeuValLyLeuGlnGlyAlaAsnLeuLyS 61
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QY 188 CCCAATACAAATACAAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATAAAAA 247
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QY 62 ThrIleThrLeuMetLeuArgArgaenAsnLeuTyValMetGlyTySerAspProPhe 81
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QY 248 ACCATCACACTAATCTGAGACGAACAATTTGTATGATGGGTTATTCGATCCCTTT 307
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QY 82 AenGlyAenLyCybArgTyHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
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QY 308 GAAACCAATTAATGTCGTTACCAATCTTTAATGATATCTCAGGTACTGAACGCCAAGAT 367
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QY 368 GTAGAGACTACTCTTTGCCAAATGCCAATTCCTCGTGTAGTAAACATAAATTGAT 427
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QY 142 GlyIleGlnIleLeuSerSerSerAspIleGlyLyseIleSer 154
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Search completed: April 9, 2006, 07:31:32
Job time : 3518 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 408.713 Seconds
(without alignments)
2511.204 Million cell updates/sec

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Perfect score: 793
Sequence: 1 MINTTPDAGNATINKYATP.....SRNOVGLQILSSDIGKIS 154

Scoring table:
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes03h
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11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	100.0	465	6 AAD42717	Aad42717 Pokeweed
2	793	100.0	792	6 AAD42716	Aad42716 Pokeweed
3	793	100.0	1092	6 AAD42729	Aad42729 Pokeweed
4	788	99.4	945	6 AAD42715	Aad42715 Pokeweed

5	613	77.3	882	2 AAT99556	Aat99556 Phytolacc
6	596	75.2	1378	12 ADG76061	Adg76061 American
7	596	75.2	1379	3 AAZ45197	Aaz45197 Wild-type
8	596	75.2	1379	3 AAZ59220	Aaz59220 Pokeweed
9	596	75.2	1379	4 AAC87929	Aac87929 P. ameriec
10	596	75.2	1379	6 AAD42738	Aad42738 Pokeweed
11	596	75.2	1379	10 ADI05787	Adi05787 DNA encod
12	595	75.0	1164	11 ADM74765	Adm74765 HIV-1 inh
13	592	74.7	1164	11 ADM74751	Adm74751 HIV-1 inh
14	590	74.4	1195	6 AAQ56672	Aaq56672 Sequence
15	588	74.1	1378	6 AAD42739	Aad42739 Pokeweed
16	588	74.1	1379	3 AAZ59221	Aaz59221 Variant p
17	580	73.1	1195	2 AAQ81457	Aaq81457 Phytolacc
18	559.5	70.6	2472	2 AAQ43967	Aaq43967 Pokeweed
19	542.5	68.4	2369	2 AAT99557	Aat99557 Phytolacc
20	542.5	68.4	2369	2 ABA95543	Ab95543 Phytolacc
21	463.5	58.4	918	2 AAQ64893	Aaq64893 Antiviral
22	463.5	58.4	918	2 AAT04782	Aat04782 DNA pLMC2
23	344.5	43.4	603	2 ABA96547	Ab96547 Cloning v
24	301.5	38.0	600	2 ABA96716	Ab96716 Cloning v
25	261	32.9	934	3 AAZ45198	Aaz45198 Wild-type
26	261	32.9	934	6 AAD42740	Aad42740 Pokeweed
27	196.5	24.8	765	3 AAZ61131	Aaz61131 DNA encod
28	196.5	24.8	984	3 AAZ61125	Aaz61125 DNA encod
29	196.5	24.8	993	3 AAZ61128	Aaz61128 DNA encod
30	196.5	24.8	999	3 AAZ61122	Aaz61122 DNA encod
31	196.5	24.8	999	3 AAZ61119	Aaz61119 DNA encod
32	191.5	24.1	864	1 AAN91504	Aan91504 DNA of r1
33	190.5	24.0	804	2 AAQ53896	Aaq53896 Saporin c
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36	190.5	24.0	804	2 AAT17964	Aat17964 Saporin c
37	190.5	24.0	804	3 AAA12862	Aaa12862 Saporin D
38	190.5	24.0	804	9 ACD67205	Adc67205 Common so
39	190.5	24.0	804	10 ADC34589	Adc34589 Common so
40	190.5	24.0	804	10 ADH92013	Adh92013 DNA encod
41	188.5	23.8	765	3 AAA12895	Aaa12895 Mammalian
42	188.5	23.8	765	9 ACD27612	Adc27612 Common so
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45	188.5	23.8	783	2 AAT18231	Aat18231 Amplified

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XX	AAD42717;
AC	
XX	15-NOV-2002 (first entry)
DT	
XX	
XX	Pokeweed PAP-Salpa protein encoding DNA.
DE	
XX	Neurotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW	PAP-Salpa; ds.
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XX	Phytolacca americana.
OS	
XX	
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XX	WO200233107-A2.
PD	
XX	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-GB004593.
XX	
XX	14-OCT-2000; 2000GB-00025217.
XX	

Accession	Sequence	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DB
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.						
XX							
PI	Thomas CUR, Mcpherson MJ, Atkinson HU, Neelam A,						
XX							
DR	WPI; 2002-483891/52.						
DR	P-PSDB; AAE25920.						
XX							
PT	Inducing necrotic effect in specific cells of plant by transforming plant						
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter						
PT	which acts in response to application of specific stimulus to plant.						
XX							
PS	Claim 3; Page 77; 87bp; English.						
XX							
CC	The invention relates to a method of inducing a necrotic effect in						
CC	specific cells of a plant. The method involves transforming the plant						
CC	with chimeric gene(s) which encode a pokeweed antiviral protein namely						
CC	PAP, PAP1 and PAP-5, where the gene(s) comprises a promoter which acts						
CC	in response to the application of a specific stimulus to the plant so as						
CC	to facilitate expression of the pokeweed antiviral protein in specific						
CC	cells of the plant. The method is useful for inducing a necrotic effect						
CC	in specific cells of a plant. The present sequence is pokeweed PAP-Salpa						
CC	protein encoding DNA						
XX							
XX	Sequence 465 BP; 165 A; 97 C; 76 G; 127 T; 0 U; 0 Other;						
Alignment Scores:							
Pred. No.:	1,428-91	Length:	465				
Score:	793.00	Matches:	154				
Percent Similarity:	100.0%	Conservative:	0				
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DB:	6	Gaps:	0				
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DB	121 CTACCTGATCAATTCGACCCCTAGTACTTATGTTAAGCTCCAAAGTCAAACTTA	180					
QY	61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyIleValMetGlyIleSerAspPro	80					
DB	181 AAACCATTAACCTATATGTCGAGACCAAAATTAATTAAGTCGATATTCGATCC	240					
QY	81 PheAsnGlyAsnIleCysArgTyIleIlePheAsnAspIleIleSerThrGluArgThr	100					
DB	241 TTCAATGGCAATTAAGTGTGTTATCAATATTAATTAAGATTAACAAGCAACGCACT	300					
QY	101 AspValIleAsnThrIleuCysSerSerSerSerSerSerSerArgValAlaMetSerIleAsnTyI	120					
DB	301 GATGGGGAATACTCTTGTCTCAAGTTCTAGTTCCTGCTTCGATTCATATGTCATTAC	360					
QY	121 AsnSerLeuTyIleProThrMetGluIleValAlaGluValAsnSerArgAsnGlnValGln	140					
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QY	141 LeuGlyIleGlnIleLeuSerSerAspIleGlyIleIleSer	154					
DB	421 TTGGGAATCAATTAATCTCAGCAGTGCATTGGAAAAATCTCT	462					
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XX							
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[illegible]

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Db 61 ATGGAAATCTCTTGATATACAGGAAAGATCAAAATCAAAATGATGAGCATTAACCAATG 120
Qy 41 LeuProAspThrAsnSerThrProLybTyrLeuLeuValYsLeuGlnGlyAlaAsnLeu 60
Db 121 CTACCTGATTAATTTGACCCCTTAAGTACTTATGTTAGCTCCAGGTCCAAAGCTTA 180
Qy 61 LybThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
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Qy 81 PheAsnGlyAsnLybCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
Db 241 TTCAATGGCAATAGATGCTGTTACCAATATTAATTAATTAACAAGCACCAAGCACT 300
Qy 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyr 120
Db 301 GATGAGGAATATCTTTGCTCAAGTTCTACTTCCTCGTTGCAATGTCATTAACCTAC 360
Qy 121 AsnSerLeuTyrProThrMetGluYsLybAlaGluValAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTATATCCACCATGGAAGAAAGAAAGCAAGAAATCAAGAAATCAAGTCCAA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyYsIleSer 154
Db 421 TTGGAAATTCAAATATCTCAGCAGTGAATGGAAATTAATCTCT 462

RESULT 3

AAD42729
ID AAD42729 standard; DNA; 1092 BP.

XX AAD42729;

XX 29-AUG-2003 (revised)

DT 15-NOV-2002 (first entry)

XX Pokeweed PAP-S/rice cystatin delta D86 fusion DNA.

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;

KW chimeric; rice; cystatin delta D86; NIA protease cleavage site; PCS; da.

XX PhytoIacca americana.

OS Oryza sativa.

OS Tobacco; Etch virus.

OS Chimeric.

XX Key Location/Qualifiers

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XX WO200233107-A2.

XX 25-APR-2002.

PD

XX 15-OCT-2001; 2001WO-GB004593.
PF 14-OCT-2000; 2000GB-00025217.
XX (ADVE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PA Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
PI WPI, 2002-489891/52.
XX

XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.

PS Disclosure; Page 83; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
CC on 29-AUG-2003 to standardise OS field)

XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.87e-91 Length: 1092
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274a-6 (1-154) x AAD42729 (1-1092)

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Db 1 ATGATTAATAATACATCACTTTGATGCTGGAAATGACCACTTAACAAATATGCGACCTTT 60
Qy 21 MetGluSerLeuArgAsnGlnAlaYsAspProLybLeuYsCysTyrGlyIleProMet 40
Db 61 ATGGAAATCTCTTGATATACAGGAAAGATCAAAATCAAAATGATGAGCATTAACCAATG 120
Qy 41 LeuProAspThrAsnSerThrProLybTyrLeuLeuValYsLeuGlnGlyAlaAsnLeu 60
Db 121 CTACCTGATTAATTTGACCCCTTAAGTACTTATGTTAGCTCCAGGTCCAAAGCTTA 180
Qy 61 LybThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
Db 181 AAACCATTAACATATGCTGAGACGAATAACTTAATAGTATGAGGCTATTCGATCC 240
Qy 81 PheAsnGlyAsnLybCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
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Qy 121 AsnSerLeuTyrProThrMetGluYsLybAlaGluValAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTATATCCACCATGGAAGAAAGAAAGCAAGAAATCAAGAAATCAAGTCCAA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyYsIleSer 154
Db 421 TTGGAAATTCAAATATCTCAGCAGTGAATGGAAATTAATCTCT 462

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RESULT 4
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ID AAD42715 standard; DNA; 945 BP.
XX
XX AAD42715;
AC
XX 15-NOV-2002 (first entry)
DT
XX
DE Pokeweed pro-PAP-S protein encoding DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM gene; ds.
XX
XX Phytoacca americana.
OS
XX
XX Key Location/Qualifiers
FH 1..945
FT /*tag= a
FT /product= "Pro-PAP-S protein"
FT primer_bind 1..24
FT /*tag= b
FT /bound_molecety= "primer PPS1BF"
FT complement(735..776)
FT primer_bind /*tag= c
FT /bound_molecety= "primer PSXDR"
FT 736..777
FT /*tag= d
FT /bound_molecety= "primer PSXDP"
FT 750..759
FT /*tag= e
FT /note= "Sequence replacing removed XbaI site"
FT primer_bind complement(922..945)
FT /*tag= f
FT /bound_molecety= "primer PPS2BR"

W0200233107-A2.
XX
XX 25-APR-2002.
PD
XX
XX 15-OCT-2001; 2001MO-GB004593.
PF
XX 14-OCT-2000; 2000GB-00025217.
PR
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PA
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
PI
XX WPI; 2002-489891/52.
DR
XX P-PSDB; AAE25918.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 24; Page 73-74; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC protein encoding DNA
XX
XX
SQ Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.72e-90 Length: 945
Score: 788.00 Matches: 153
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
```

```
Query Match: 99.4% Indels: 0
DB: 6 Gaps: 0
US-09-978-274A-6 (1-154) x AAD42715 (1-945)

QY 2 TLeaAnthrilleThrPheAepAlaGlyAsnAlaThrIleAsnlyTYraIaThrPheMet 21
Db 73 ATAAATACGATCACTTGTGATGCGAAATGCCACCTTAACAATATGCGACCTTATG 132
QY 22 GluSerLeuArgAngAlaIlyAspProlyLeuIlyCysTYRGIYIleProMetLeu 41
Db 133 GAATCTCTGCTAATCAAGGAAGATCCAAACTAAATGCTATGCGATACCAATGCTA 192
QY 42 ProAspThrAsnSerThrProlyTYRLeuLeuValIlySleuGInGIYAlaAsnLeuIlyS 61
Db 193 CCGATATCTAATTCGACCCCTTAAGTACTTATGTTAGCTCCAGGTGCAAACTTAAAA 252
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTYRValMetGIYTYRSerAspProPhe 81
Db 253 ACCATTACACTAATGCTGAGACGAAATATACCTTATACGTGAGGCTATCTGATCCCTTC 312
QY 82 AsnGIYAsnIlyCysArgTYRHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 313 AATGGCAATAGAGTGTCTTACCATATTAATGATATACAGCACCGAAGCACTGAT 372
QY 102 ValGIUAnthrIleuCYsSerSerSerSerSerArgValAlaMetSerIleAsnTYRAsn 121
Db 373 GTGGAGAAATCTCTTCTCTCAAGTTCTAGTTCTCGTGTTCGATTCGAATGTCATTATCAAT 432
QY 122 SerIleTYRProThrMetGIUlyGlyAlaGIUValAsnSerArgAngInValGIUleu 141
Db 433 AGCTTATATCCGACCATGAGAAAGAAAGAGTAACATCAAGAAATCAAGTCCAATTG 492
QY 142 GlyIleGIUleuIleuSerSerAspIleGIYlySerIleSer 154
Db 493 GGAATCAAAATCACTCAGCAGTGAATGACATTGGAAAAATCTCT 531

RESULT 5
AAT99556
ID AAT99556 standard; DNA; 882 BP.
XX
XX AAT99556;
AC
XX 17-OCT-2003 (revised)
DT 08-JUN-1998 (first entry)
DT
XX
XX Phytoacca insularis antiviral protein gPIP2 gene.
DE
XX
XX Antiviral protein; gPIP2 gene; virucide; transgenic plant;
KW virus resistance; immunconjugate; AIDS; cancer; therapy; ss.
XX
XX Phytoacca insularis; Nakai.
OS
XX
XX Key Location/Qualifiers
FH 1..882
FT /*tag= a
FT CDS /transl_except= (pos:715..717, aa:Ile)

EP808902-A2.
XX
XX 26-NOV-1997.
PD
XX
XX 30-SBP-1996; 96EP-00307159.
PF
XX 22-MAY-1996; 96KR-00017404.
PR
XX
XX (JINR-) JIN RO LTD.
PA
XX
XX Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J;
PI Song S, Choi Y, Kim C, Kim M;
XX
XX WPI; 1998-001788/01.
DR P-PSDB; AAM26773.
```

XX Antiviral proteins of Phytoecia insularis Nakai and their genes - useful
PT in plant antiviral agents and immunocoujugates for the treatment of AIDS
PR and cancer.

PS Claim 2; Page 10-12; 26pp; English.

XX This polynucleotide comprises the coding region of the Phytoecia
CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
CC designated gp12 (see AAM26773). The gp12 gene was isolated from leaf
CC genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
CC AAT99557), encoding a 35.7 kDa protein (see AAM26774) designated gp150,
CC has also been isolated from P. insularis Nakai. Also claimed are vectors
CC encoding these antiviral proteins and host cells transformed or
CC transfected with these vectors. R. coli XL1-Blue MRF⁺ gp12 (KCCM-10080)
CC host cells are claimed, as is a process for preparing antiviral protein
CC bodies. The antiviral proteins and recombinant proteins inhibit protein
CC synthesis. They can be used as active ingredients of antiviral agents of
CC plant viruses, and employed in the manufacture of immunocoujugates for
CC the treatment of AIDS and cancer. The isolated genes can be used in the
CC breeding of transgenic plants having viral resistance. (Updated on 17-0CT
CC -2003 to standardise OS field)

SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.67e-68 Length: 882
Score: 613.00 Matches: 114
Percent Similarity: 87.7% Conservative: 21
Best Local Similarity: 74.0% Mismatches: 19
Query Match: 77.3% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-6 (1-154) x AAT99556 (1-882)

QY 1 MetIleanthrilethPhaAspAlaGlyAsnAlaThrIleAsnLysTyraLathRhe 20
DB 1 ATGGGAAATCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 60
QY 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrglyIleProMet 40
DB 61 CTGATATATCTTCGTAATGAAGCAAAAGATCCAGCTTAAATGCTAATGCAATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyraValLysLeuGlnAlaLysAsnLeu 60
DB 121 TTGCCCAATACCAATCCAAATCCAAAGTACGTTGTTAGCTTCAAGTTCAATGAA 180
QY 61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyraValMetGlyTyrSerAspPro 80
DB 181 AAAACCAATCACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 240
QY 81 PheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTTGATACCAATGAATGTTGTTACCATATCTTATGATATCTCAAGTACGAAGCCAA 300
QY 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTy 120
DB 301 GATGTAGACCTACTCTTTCGCCCAATCCCAATCTCGTGTAAATAAACAATAACTAT 360
QY 121 AsnSerLeuTyrrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
DB 361 GATGTGATATCCAAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 CTGGGAATTCAAATACTCGACAGTGAATGTAAGATTTC 462

RESULT 6
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
AC ADG76061;

XX 11-MAR-2004 (first entry)
DT American pokeweed antiviral protein (PAP) DNA Seqid 1.
XX

XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KW nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KW american pokeweed; retroviral.
XX

OS Phytoecia americana.

XX WO2003106479-A2.

XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019141.

XX 17-JUN-2002; 2002US-0389649P.

XX (PARK-) PARKER HUGHES INST.

XX Uckun FM;

XX WPI; 2004-082156/08.

XX P-PSDB; ADG76064.

PT Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC depurinating viral RNA. This polynucleotide sequence (PAP) of the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX

SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.04e-65 Length: 1378
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 12 Gaps: 0

US-09-978-274A-6 (1-154) x ADG76061 (1-1378)

QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyraLathRhe 21
DB 290 GTGAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 349
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrglyIleProMetLeu 41
DB 350 AATGATCTTCGTAATGAAGCAAGATCCAGTTAAATGCTAATGCAATACCAATCTG 409
QY 42 ProAspThrAsnSerThrProLysTyraValLysLeuGlnGlnAlaLysLeuLys 61
DB 410 CCCAATCAATATCAATCCAAAGTACGTTGTTGAGCTTCAAGTTCAATAAATAA 469
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyraValMetGlyTyrSerAspProPhe 81

```
Db 470 ACCATCACTAAAGCTGAGAGCGAACAATTGATGATGGGTATTTCGATCCCTTT 529
Cc 82 AenGlyanLysCybaATGTYRHIIePheanAapIleHrSerThnGluarThraP 101
Cc 530 GAAACCAATAAATATCGTTACCATATCTTATATATCTCAGGACTGAAAGCGCAAGAT 589
Cc 102 ValGluAnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
Cc 590 GTAGAGACTACTCTTTGCCCAATGCGCAATTCGTGTTAGTAAACATTAACCTTGAT 649
Cc 122 SerLeuTYrProThrMetGluLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Cc 650 AGTCGATATCCAACTTGGAATCAAAAGCGGAGTAATAATCAAGAACTCAAGTCAACTG 709
Cc 142 GylIleGlnIleLeuSerSerApIleGlyLysIleSer 154
Cc 710 GGAATTCAAATATCTGACAGTAATATGGAAGAATTCT 748
Db 710 GGAATTCAAATATCTGACAGTAATATGGAAGAATTCT 748

RESULT 7
AAZ45197
ID AAZ45197 standard; DNA; 1379 BP.
XX
AC AAZ45197;
XX
DT 29-FEB-2000 (first entry)
XX
DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
KW Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
KW tomato yellow leaf curl virus.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT CDS 225..1166
FT /*tag= a
FT /product= "PAP"
FT /note= "Pokeweed antiviral protein"
XX
XX
XX MO9960843-A1.
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-US011301.
XX
XX 22-MAY-1998; 98US-0066374P.
XX
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Turner NE, Wang P,
XX
XX MPI; 2000-062555/05.
XX
XX P-PSDB; AAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43pp; English.
XX
XX This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX Phytolacca americana (pokeweed). It is a single polypeptide chain that
XX catalytically removes a specific adenine residue from a highly conserved
XX stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX activities to plants. A DNA molecule encoding a PAP II protein with an
XX intact catalytic active site amino acid residue (E172) is useful for
XX generating transgenic plants. PAP II DNA is useful for generating a
XX transgenic plants (especially cereal crops) through transforming a
XX protoplast or introducing the DNA directly into a plant part prior to
```

```
Cc regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
Cc activity thus have increased resistance to viruses and/or fungi. Viruses
Cc include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
Cc yellow leaf curl virus, and fungi include Pythium, Phytophthora,
Cc Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
Cc other plants pests including insects, bacteria and nematodes. PAP II DNA
Cc is also useful for identifying a PAP II protein having reduced
Cc cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
Cc unlike PAP transgenic plants which are stunted and sterile, PAP II
Cc transgenic plants have a normal and fertile phenotype
XX
XX SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1,04e-65 Length: 1379
XX Score: 596.00 Matches: 110
XX Percent Similarity: 86.9% Conservative: 23
XX Best Local Similarity: 71.9% Mismatches: 20
XX Query Match: 75.2% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-978-274a-6 (1-154) x AAZ45197 (1-1379)
XX
XX QY 2 IleAnThrIleThrPheAapAlaGlyAsnAlaThrIleAnLysTYraIerHrPheMet 21
XX ::::::::::::::::::::
XX Db 291 GTGAATCAATCATCTCAATCAATGTGGAAGTACCAACCATTAAGCAACTTTCTG 350
XX
XX QY 22 GluSerLeuArgAnGlnAlaLysAapProLysLeuLysCybTYrGylIleProMetLeu 41
XX ::::::::::::::::::::
XX Db 351 AATGATCTTGTAATGAAGCGAAGATCAAGTTAAATGCTAATGGAATACCAATGCTG 410
XX
XX QY 42 ProAspHrAsnSerThrProLysTYrLeuValLysLeuGlnGlyAlaAsnLeuLys 61
XX ::::::::::::::::::::
XX Db 411 CCCAATCAATATCAATCCAAATGACGTGTGTTAGCTCCAAAGTCCAAATTAATAA 470
XX
XX QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTYrValMetGlyTYrSerAapProPhe 81
XX ::::::::::::::::::::
XX Db 471 ACCATCACTAAAGCTGAGAGCGAACAATTGATGATGGGTATTTCGATCCCTTT 530
XX
XX QY 82 AenGlyanLysCybaATGTYRHIIePheanAapIleHrSerThnGluarThraP 101
XX ::::::::::::::::::::
XX Db 531 GAAACCAATAAATATCGTTACCATATCTTATATATCTCAGGACTGAAAGCGCAAGAT 590
XX
XX QY 102 ValGluAnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
XX ::::::::::::::::::::
XX Db 591 GTAGAGACTACTCTTTGCCCAATGCGCAATTCGTGTTAGTAAACATTAACCTTGAT 650
XX
XX QY 122 SerLeuTYrProThrMetGluLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
XX ::::::::::::::::::::
XX Db 651 AGTCGATATCCAACTTGGAATCAAAAGCGGAGTAATAATCAAGAACTCAAGTCAACTG 710
XX
XX QY 142 GylIleGlnIleLeuSerSerApIleGlyLysIleSer 154
XX ::::::::::::::::::::
XX Db 711 GGAATTCAAATATCTGACAGTAATATGGAAGAATTCT 749
XX

RESULT 8
AAZ59220
ID AAZ59220 standard; cDNA; 1379 BP.
XX
XX AAZ59220;
XX
XX 20-APR-2000 (first entry)
XX
XX Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX DE Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX KW pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX OS Phytolacca americana.
XX
XX PN US6015940-A.
XX
```

PD 18-JAN-2000.
 XX 07-APR-1992; 92US-00865169.
 XX 07-APR-1992; 92US-00865169.
 PR (MONS) MONSANTO CO.
 PA Kaniewski WK, Turner NE, Lodge JK,
 XX WPI: 2000-126326/11.
 DR
 XX Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX
 PS Claim 6; Fig 4; 30pp; English.
 XX
 CC This is the coding sequence for the spring leaf form of the pokeweed
 CC antiviral protein (PAP) which is used to generate transgenic potato
 CC plants. PAP is able to confer resistance to infection by potato virus X
 CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
 CC potato plant or tuber expressing PAP
 XX
 SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 Gaps: 0
 DB: 3
 US-09-978-274a-6 (1-154) x AAC59220 (1-1379)
 QY 2 Ileaanthrillethrpheaspalaaglyasnaalathrilleasnytyralathrphemet 21
 DB 291 GTGAATCAATCATCTACATGTTGGAAGTACCAATGATGCAATGACCAATGACCACTTTCTG 350
 QY 22 GluserleuarganglialysaspProlylsleuyscytytyglylleprometleu 41
 DB 351 AATGATCTTGTAATGAAGCGAAGATCAAGTTAAATGCTATGGAATACCAATGCTG 410
 QY 42 ProasphrhaenSerThrProlystytleuValysleuGlnGlyAlaasnlleuys 61
 DB 411 CCCAATCAATACCAATCAAGTACCTGTTGGTGAAGCTCCAGAGTTCAATATAAAA 470
 QY 62 ThrillethreuleuarganglialysaspProlystytleuValysleuGlnGlyAlaasnlleuys 81
 DB 471 ACCATCACTAATGCTGAAGCAAGCAATTTGTATGATGAGGTTATTCGATCCCTT 530
 QY 82 AsnGlyasnllyscysaagtythrislethephensaapliethrSerThrGluargThrasp 101
 DB 531 GAAACCAATTAATGCTGTTACCATATCTTATATGATATCAAGTACCAAGCCCAAGAT 590
 QY 102 ValGluasnthrleuCyserSerSerSerSerArgValAlaMetSerIleAsnTyran 121
 DB 591 GTAGAGACTACTCTTTGCCAATGCCAATCTCTGCTGTTAGTAAAAACAATAACTTTCAT 650
 QY 122 SerleutytyrProthmetGlnlysuValagluValansSerArgasnglnValGlnleu 141
 DB 651 AGTCGATATCCAAATTCGAATGCAAAAGCGGAGTAATAAACAAGAAGTCAGTCCAACTG 710
 QY 142 GlylleGlnleleuSerSerapliGlylyser 154
 DB 711 GGAATTCAAATACCTGACAGTAATATGGAAGATTTCT 749
 RESULT 9
 ID AAC87929 standard; DNA; 1379 BP.
 AC AAC87929;
 XX

DT 06-MAR-2001 (first entry)
 XX
 DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
 XX
 KW Phytoleuca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
 KW biotherapeutic; fusion protein; immunocjugate; mutant; cytostatic;
 KW anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
 KW brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
 XX
 OS Phytoleuca americana.
 XX
 FH Key Location/Qualifiers
 FT 225..1166
 FT CDS /tag=a
 FT /product="pokeweed antiviral protein (PAP)"
 XX
 XX US6146628-A.
 XX
 XX 14-NOV-2000.
 XX
 XX 11-JUL-1995; 95US-00501253.
 XX
 XX 11-JUL-1995; 95US-00501253.
 XX
 XX (MINU) UNIV MINNESOTA & RUTGERS.
 XX (UNNE-) UNIV STATE NEW JERSEY.
 XX
 XX Uckun FM, Turner NE;
 XX WPI: 2001-040422/05.
 XX P-PSDB; AAB36500.
 XX
 PT Immunocjugates useful for treating cancer and acquired immunodeficiency
 PT syndrome, comprises mutant pokeweed anti-viral protein and a targeting
 PT moiety that binds a cell surface receptor.
 XX
 PS Disclosure; Col 47-50; 32pp; English.
 XX
 CC The present invention describes a fusion protein or an immunocjugate
 CC (1), comprising mutant Pokeweed Anti-viral protein (PAP) having an amino
 CC acid substitution at residue 75, 97 or 176 of native PAP and a targeting
 CC moiety that binds a cell surface receptor. (1) can have cytostatic and
 CC anti-HIV activities, and is an inhibitor of cellular RNA or protein
 CC synthesis. (1) is useful for treating AIDS and cancers including
 CC leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
 CC tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
 CC colon cancer. Immunocjugates prepared using PAP mutants exhibit an
 CC improved therapeutic index over immunocjugates containing either wild-
 CC type PAP or variant PAP. The present sequence encodes the wild-type PAP,
 CC which is given in the exemplification of the present invention
 XX
 SQ Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 Gaps: 0
 DB: 4
 US-09-978-274a-6 (1-154) x AAC87929 (1-1379)
 QY 2 Ileaanthrillethrpheaspalaaglyasnaalathrilleasnytyralathrphemet 21
 DB 291 GTGAATCAATCATCTACATGTTGGAAGTACCAATGATGCAATGACCAATGACCACTTTCTG 350
 QY 22 GluserleuarganglialysaspProlylsleuyscytytyglylleprometleu 41
 DB 351 AATGATCTTGTAATGAAGCGAAGATCAAGTTAAATGCTATGGAATACCAATGCTG 410
 QY 42 ProasphrhaenSerThrProlystytleuValysleuGlnGlyAlaasnlleuys 61
 DB 411 CCCAATCAATACCAATCAAGTACCTGTTGGTGAAGCTCCAGAGTTCAATATAAAA 470

```

Db      411  CCCAATACAAATACAAATCCAAAGTACGTGTGGTTCAGCTCAAGGTTCAAAATAAAAA 470
Qy      62  ThrIleThrlleuMetLeuAArgAAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db      471  ACCATTCACACTAATGCTGAGACGAAACAAATTTGATGTGATGGGTATTTTCGATCCCTTT 530
Qy      82  AAsnGlyAsnIlySvAsArgTyrH1sIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db      531  GAAACCAATTAATATTCCTTACCAATCTTTATATGATATCTCAGGTACTGAACGCCAAGAT 590
Qy      102  ValGluAsnThrlleuCySvSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db      591  GTAGAGACTACTCTTTGCCCAATTCGCAATTCGTGTAGTAAACATTAACCTTGAT 650
Qy      122  SerLeuTyrProThrlMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
Db      651  AGTCGATATTCACAAATTCGAAATCAAAAGCGAGATTAATAATCAAGAGTCGACGTCG 710
Qy      142  GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db      711  GGAATTCAAATCTCGACAGATTAATTTGAAAAGATTTCT 749

RESULT 10
AAD42738
ID  AAD42738 standard; DNA; 1379 BP.
XX
AC  AAD42738;
XX
DT  15-NOV-2002 (first entry)
XX
DE  pokeweed PAP' DNA #1.
XX
KM  Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS  Phytolacca americana.
XX
FH  Key location/Qualifiers
FT  misc_feature 290..1076
FT  /*tag= a
FT  /note= "Mature PAP' sequence"
XX
XX  WO200233107-A2.
XX
XX  25-APR-2002.
XX
PD  15-OCT-2001; 2001WO-GB004593.
XX
PR  14-OCT-2000; 2000GB-00025217.
XX
XX  14-OCT-2000; 2000GB-00025217.
XX
PA  (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX  Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
PI  WPI; 2002-489891/52.
XX
DR  WPI; 2002-489891/52.
XX
XX  Inducing necrotic effect in specific cells of plant by transforming plant
PT  with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT  which acts in response to application of specific stimulus to plant.
XX
XX  Claim 5; Page 86; 87p; English.
XX
XX  The invention relates to a method of inducing a necrotic effect in
CC  specific cells of a plant. The method involves transforming the plant
CC  with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC  PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
CC  in response to the application of a specific stimulus to the plant so as
CC  to facilitate expression of the pokeweed antiviral protein in specific
CC  cells of the plant. The method is useful for inducing a necrotic effect
CC  in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ  Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Alignment Scores:

```

```

Pred. No.: 1,04e-65 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AAD42738 (1-1379)
Qy      2  ILeAsnThrlleThrlPheAspAlaGlyAsnAlaThrlleAsnIlySvTyrAlaThrlPheMet 21
Db      291  GTGAATACAAATCAATCTACCAATGTTGGAAGTACCAACATTAAGCAATACGCACTTTCTG 350
Qy      22  GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCySvTyrGlyIleProMetLeu 41
Db      351  AATGATCTTCTGTATGAGAGCGAAAGATCCAAAGTTAAAGCTATGGAATACCAATGCTG 410
Qy      42  ProAspThrAsnSerThrlProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db      411  CCCAATACAAATACAAATCCAAAGTACGTGTGGTTCAGCTCCAAAGGTTCAAAATAAAAA 470
Qy      62  ThrIleThrlleuMetLeuAArgAAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db      471  ACCATTCACACTAATGCTGAGACGAAACAAATTTGATGTGATGGGTATTTCTGATCCCTTT 530
Qy      82  AAsnGlyAsnIlySvAsArgTyrH1sIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db      531  GAAACCAATTAATATTCCTTACCAATCTTTATATGATATCTCAGGTACTGAACGCCAAGAT 590
Qy      102  ValGluAsnThrlleuCySvSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db      591  GTAGAGACTACTCTTTGCCCAATTCGCAATTCGTGTAGTAAACATTAACCTTGAT 650
Qy      122  SerLeuTyrProThrlMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
Db      651  AGTCGATATTCACAAATTCGAAATCAAAAGCGAGATTAATAATCAAGAGTCGACGTCG 710
Qy      142  GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db      711  GGAATTCAAATCTCGACAGATTAATTTGAAAAGATTTCT 749

RESULT 11
AD105787
ID  AD105787 standard; DNA; 1379 BP.
XX
XX  AD105787;
XX
DT  15-APR-2004 (first entry)
XX
DE  DNA encoding the wild-type pokeweed antiviral protein.
XX
XX  ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
KM  cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
KM  medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
KM  B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX  ds.
XX
XX  Phytolacca americana.
XX
XX  Key location/Qualifiers
XX  CDS 225..1166
XX  FT /*tag= a
XX  /product= "wild-type pokeweed antiviral protein"
XX
XX  WO200262952-A2.
XX
XX  15-AUG-2002.
XX
PD  01-FEB-2002; 2002WO-US002792.
XX
PR  02-FEB-2001; 2001US-0266396P.
XX
XX  (RUTE ) UNIV RUTGERS STATE NEW JERSEY.

```


XX Tumor NE, Hudak KA, Parikh B;
 XX WPI: 2003-156656/15.
 DR P-PSDB; ADI05788.
 XX
 PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 XX or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 1; 51pp; English.
 XX
 CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer, AIDS, viral infection or autoimmune
 CC diseases associated with proliferation of unwanted T-cells or B-cells.
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.

Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 DB: 10 Gaps: 0

US-09-978-274A-6 (1-154) x ADI05787 (1-1379)

```

QY 2 ILeaNTThrlleThPhaSpAlaGlyAsnAlaThrIleAsnLysTyraLathrPhemec 21
DB 291 GGAATACCAATCATCTACCAATGTTGGAACTACCCATTAGCAAAATCCCACTTTTCG 350
QY 22 GluSerLeuAAGSnglnAlaLysAspProLysLeuLysCyTYGlyIleProMetLeu 41
DB 351 AATGATCTTCGTAATGAAGCGAAAGATCCAACTTTAAATGCTAAGATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyreuleuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 411 CCCAATACAAATACCAATCCAAATGACGTTGGTTGAGCTCCAAAGTTCAATATMAAAA 470
QY 62 ThrIleThrlleuMetLeuArgArgAsnLeuLysValMetGlyTyrSerAspProPie 81
DB 471 ACCATACCACTAATCTGAGCAAAATGCAATTTGTAATGATGGTTATTCATCCCTTT 530
QY 82 AsnGlyAsnLysCyArgTyrisIlePhaAsnAlaIleThSerThGlnuArgThrAsp 101
DB 531 GAAACCAATTAATGCTGTTACCAATCTTTAATGATATCTGAGTACGAAACGCCAAGAT 590
QY 102 ValGluAsnThrLeuCySerSerSerSerSerSerValAlaMetSerIleAsnTyraAsn 121
DB 591 GTAGAGACTACTCTTGGCCCAATATCTCGGTTAGTAAATAACATAAATTTGAT 650
QY 122 SerLeuTyrrProThrMetGlnLysLysAlaGluValaAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCATATCCCAATCAATTCGTAATCAAAAGCGGAGTAAATCAAGAAGTCAGGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 711 GGAATTCAAATCTGACAGTAATATGGAAGAATTTCT 749

```

RESULT 12
 ADM74765

ID ADM74765 standard; cDNA; 1164 BP.

XX AC ADM74765;

XX DT 03-JUN-2004 (first entry)

XX DE HIV-1 inhibition activity related Tat cDNA.

XX KW human immunodeficiency virus; HIV-1; tumour; plant;

XX KW Chinese phytoacta leaf; trans-acting activation factor; Tat; mutant;

XX KW gene; ss.

XX OS Human immunodeficiency virus 1.

XX FH Key Location/Qualifiers

XX FT CDS 2..943

XX FT /tag= a

XX FT /product= "Tat HIV-1 protein"

XX PD CN1400220-A.

XX PF 05-MAR-2003.

XX PF 02-AUG-2001; 2001CN-00123911.

XX PF 02-AUG-2001; 2001CN-00123911.

XX PR (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.

XX PA Peng X, Bai L, Yin B;

XX PI WPI: 2003-469263/45.

XX DR P-PSDB; ADM74765.

XX PT Two kinds of cDNA with activity capable of extensively inhibiting HIV and

XX PT its expression, separation and purification method in protokaryon.

XX PS Example 9; Page 11-12; 17pp; Chinese.

XX The present invention relates to two kinds of cDNA which can inhibit

XX human immunodeficiency virus (HIV-1) activity, including separation clone

XX CC and application of the cDNA in preparation of preparation for curing the

XX CC virus and tumour. One of the described cDNAs is obtained by separation

XX CC and cloned from a plant Chinese phytoacta leaf, and one from the trans-

XX CC acting activation factor (Tat) mutant coded by human immunodeficiency

XX CC virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA

XX CC used in the HIV-1 inhibition activity of the invention.

XX SQ Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.09e-65 Length: 1164
 Score: 595.00 Matches: 110
 Percent Similarity: 87.6% Conservative: 24
 Best Local Similarity: 71.9% Mismatches: 19
 Query Match: 75.0% Indels: 0
 DB: 11 Gaps: 0

US-09-978-274A-6 (1-154) x ADM74765 (1-1164)

```

QY 2 ILeaNTThrlleThPhaSpAlaGlyAsnAlaThrIleAsnLysTyraLathrPhemec 21
DB 68 GGAATACCAATCATCTACCAATGTTGGAACTACCCATTAGCAAAATCCCACTTTTCG 127
QY 22 GluSerLeuAAGSnglnAlaLysAspProLysLeuLysCyTYGlyIleProMetLeu 41
DB 128 GATATATCTTCGTAATGAAGCGAAAGATCCAACTTTAAATGCTAAGATACCAATGCTG 187
QY 42 ProAspThrAsnSerThrProLysTyreuleuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 188 CCCAATACAAATACCAATCCAAATGACGTTGGTTGAGCTCCAAAGTTCAATATMAAAA 247

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Qy 62 ThrIleThrlleuMetleuArgArgAsnAsnleuTyValMetGlyTYrSerAspProPhe 81
Dd 248 ACCATCAACATAAGCTGAGAGCAAACTTGTATGTATGGGATATTCGATCCCTT 307
Qy 82 AsnGlyAsnLysCyBAgTYrHleIlePheAsnAspIleThrSerThGluArgThrAsp 101
Dd 308 GATACCAATAGTGTCTGATCAATCTTGTAGTATCTCAGGACTGAACGCCAAT 367
Qy 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnThrAsn 121
Dd 368 GTAGAGACTACTCTTGTCCCAATCCCAATTCCTGTGTAGTAAACATTAACATGAT 427
Qy 122 SerleuTYrProthMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnleu 141
Dd 428 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCAACTG 487
Qy 142 GlyIleGlnIleleuSerSerAspIleGlyLysIleSer 154
Dd 488 GGAATTCAAATATCTGACAGTAAATTTGAAAGATTCT 526

RESULT 13
ADM74751
ID ADM74751 standard; cDNA; 1164 BP.
XX
AC ADM74751;
XX
DT 03-JUN-2004 (first entry)
XX
DE HIV-1 inhibition activity related cDNA.
XX
KW human immunodeficiency virus; HIV-1; tumour; plant;
KM Chinese phytoacca leaf; trans-acting activation factor; Tac; mutant;
XX gene; ss.

OS Human immunodeficiency virus 1.
XX
XX Key Location/Qualifiers
XX FT 1..1164
XX FT CDS /*tag= a
XX FT /product= "HIV-1 related protein"
XX
XX CN1400220-A.
XX
XX 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX PA Peng X, Bai L, Yan B;
XX
XX PI WPI; 2003-469263/45.
XX
XX DR P-PSDB; ADM74752.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
XX its expression, separation and purification method in protokaryon.
XX
XX Example 8; Page 9-10; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
XX human immunodeficiency virus (HIV-1) activity, including separation clone
XX of two kinds of cDNA, external mutation, fusion expression in prokaryons
XX and application of the cDNA in preparation of preparation for curing the
XX virus and tumours. One of the described cDNAs is obtained by separation
XX and cloned from a plant Chinese phytoacca leaf, and one from the trans-
XX acting activation factor (Tac) mutant coded by human immunodeficiency
XX virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
XX the HIV-1 inhibition activity of the invention.
XX
XX Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;
XX
XX
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```
Alignment Scores:
Pred. No.: 2.65e-65 Length: 1164
Score: 592.00 Matches: 109
Percent Similarity: 87.6% Conservative: 25
Best Local Similarity: 71.2% Mismatches: 19
Query Match: 74.7% Indels: 0
DB: 11 Gaps: 0

US-09-978-274a-6 (1-154) x ADM74751 (1-1164)
Qy 2 IleaenThrlleThrllePheAsnAlaGlyAsnAlaThrlleAsnLysTYrValThrllePheMet 21
Dd 289 GTGATATCAATCAATCAATGTTGGAAGTCCCACTTACCAATTCGCCACTTTCTG 348
Qy 22 GluSerleuArgAsnGlnAlaLysAspProLysleuLysCyTYrGlyIleProMetleu 41
Dd 349 GATATATCTGTAATGAAAGCAAAAGATCCAGTTTAAAGCTATGGATATCCAAATGTTG 408
Qy 42 ProAspThrAsnSerThrProLysTYrleuLeuValLysleuGlnGlyAlaAsnLys 61
Dd 409 CCAATCAATCAATCAATCCAAAGTACGTTGTGAGCTCCAAGGTTCAATTAATAA 468
Qy 62 ThrIleThrlleuMetleuArgArgAsnAsnleuTyValMetGlyTYrSerAspProPhe 81
Dd 469 ACCATCAACATAAGCTGAGAGCAAACTTGTATGTATGGGCTATTCTGATCCCTT 528
Qy 82 AsnGlyAsnLysCyBAgTYrHleIlePheAsnAspIleThrSerThGluArgThrAsp 101
Dd 529 GATACCAATAGTGTCTGATCAATCTTGTAGTATCTCAGGACTGAACGCCAAT 588
Qy 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnThrAsn 121
Dd 589 GTAGAGACTACTGTTGTCCCAATCCCAATTCCTGTGTAGTAAACATTAACATGAT 648
Qy 122 SerleuTYrProthMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnleu 141
Dd 649 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCAACTG 708
Qy 142 GlyIleGlnIleleuSerSerAspIleGlyLysIleSer 154
Dd 709 GGAATTCAAATATCTGACAGTAAATTTGAAAGATTCT 747

RESULT 14
AA056672
ID AA056672 standard; cDNA; 1195 BP.
XX
XX AC AA056672;
XX
XX DT 16-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 04-SEP-1994 (first entry)
XX
XX DE Sequence of Phytoacca antiviral protein (PAP) cDNA.
XX
XX KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX
XX OS Phytoacca americana; L.
XX
XX FH Key Location/Qualifiers
XX FT 33..974
XX FT CDS /*tag= a
XX
XX PN BP58554-AL.
XX
XX PD 09-MAR-1994.
XX
XX PF 30-JUN-1993; 93BP-00110445.
XX
XX PR 16-AUG-1992; 92KR-00014895.
XX
XX (JINR-) JIN RO LTD.
XX
XX Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
XX
```

XX WPI; 1994-076002/10.
DR P-PSDB; AAR46548.
XX
PT Expression vector for phytolecta antiviral protein - used for producing
transgenic virus-resistant plants and for producing the antiviral agent.
XX
PS Disclosure; Fig 1; 15pp; English.
XX
CC To isolate PAP gene, total cellular mRNA was purified from leaves of
Phytolecta americana L. obd. in Korea. A cDNA library was constructed.
The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC A deletion mutant was prep. from the isolated PAP gene, and the DNA
sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1195 BP, 420 A, 201 C, 230 G, 344 T, 0 U, 0 Other;
Alignment Scores:
Pred. No.: 4.95e-65 Length: 1195
Score: 590.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.4% Indels: 0
DB: Gaps: 0
US-09-978-274A-6 (1-154) x AAG56672 (1-1195)
QY 2 11eantthrllethrpheapalagllyasnalaathrlleasnlytyralatthrphe 21
DB 99 GTGAATCAATCATCTCAATGTTGGAAGTACCAATTCAGCAATATGCGCACTTTCTG 158
QY 22 GluserleuarganglinalyaspProlyseuCystrglyllepromeleu 41
DB 159 AATGATCTTGGTAAGGCAAGATCCAGTTAAATGCTATGGAATCCAAATGCTG 218
QY 42 ProaspthrznseSerThrpolystrleuValyleuGlnlyalaasnleuys 61
DB 219 CCCAATACAAATCAATCAAGTACGTTGTTGTTGCTTCAAGTTCATTAATAA 278
QY 62 ThrllethleuMetleuarganglinalyasnleuTyralMetglytyrSeraspProphe 81
DB 279 ACCATCACTAATGCTGAGACGAACCAATTTGTTGATGAGTATTCGATCCCTTT 338
QY 82 AsnglyasnlyCybarglytyrhillepheasnspillethrsertthgluargthrasp 101
DB 339 GAAACCACTAATATGCTTACCATATCTTAAATGATATCTCAGTACGCAAGAT 398
QY 102 ValgluasnThrlleuCyseSerSerSerSerSerArgValalametSerilleasntyrasn 121
DB 399 GTAGAGACTACTCTTTGCCCAATGCCAATCTCGTGTGAGTAAACATTAACCTTGAT 458
QY 122 SerleuTytrProthMetGluylslyalaagluValaasnSerArgasnGlnValglu 141
DB 459 AGTCGATTCACAACTTGAATCAAAACGGGAATGAATCAAGAGTCAAGTCCAACTG 518
QY 142 GlylleGlnlleuSerSeraspilleglytyrSileser 154
DB 519 GGAATTCAAATATCTGACAGTAATATTTGAAAGATTCT 557
RESULT 15
AAD42739
ID AAD42739 standard; DNA; 1378 BP.
XX
AC AAD42739;
XX
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP' DNA #2.
DM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
KM
XX Phytolecta americana.
OS

XX
FH Key Location/Qualifiers
FT misc_feature 290..1076
FT /*tag= a
FT /note= "Mature PAP' sequence"
XX
PN W0200233107-A2.
XX
PD 25-APR-2002.
XX
PP 15-OCT-2001; 2001WO-GB004593.
XX
PR 14-OCT-2000; 2000GB-00025217.
XX
PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
F1 Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
DR WPI; 2002-489891/52.
XX
PT Inducing necrotic effect in specific cells of plant by transforming plant
with a chimeric gene encoding pokeweed antiviral protein and a promoter
which acts in response to application of specific stimulus to plant.
XX
PS Claim 5; Page 86-87; 87pp; English.
XX
CC The invention relates to a method of inducing a necrotic effect in
specific cells of a plant. The method involves transforming the plant
with chimeric gene(s) which encodes a pokeweed antiviral protein namely
PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
in response to the application of a specific stimulus to the plant so as
to facilitate expression of the pokeweed antiviral protein in specific
cells of the plant. The method is useful for inducing a necrotic effect
in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.1e-64 Length: 1378
Score: 588.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.1% Indels: 0
DB: Gaps: 0
US-09-978-274A-6 (1-154) x AAD42739 (1-1378)
QY 2 11eantthrllethrpheapalagllyasnalaathrlleasnlytyralatthrphe 21
DB 291 GTGAATCAATCATCTCAATGTTGGAAGTACCAATTCAGCAATATGCGCACTTTCTG 350
QY 22 GluserleuarganglinalyaspProlyseuCystrglyllepromeleu 41
DB 351 AATGATCTTGGTAAGGCAAGATCCAGTTAAATGCTATGGAATCCAAATGCTG 410
QY 42 ProaspthrznseSerThrpolystrleuValyleuGlnlyalaasnleuys 61
DB 411 CCCAATCAATACAAATCAAGACGATGTTGTTGCTTCAAGTTCATTAATAA 470
QY 62 ThrllethleuMetleuarganglinalyasnleuTyralMetglytyrSeraspProphe 81
DB 471 ACCATCACTAATGCTGAGACGAACAAATTTGATGTGATGTTTCTGATCCCTTT 530
QY 82 AsnglyasnlyCybarglytyrhillepheasnspillethrsertthgluargthrasp 101
DB 531 GAAACCACTAATATGCTTACCATATCTTAAATGATATCTCAGTACGCAAGAT 590
QY 102 ValgluasnThrlleuCyseSerSerSerSerSerArgValalametSerilleasntyrasn 121
DB 591 GTAGAGACTACTCTTTGCCCAATGCCAATCTCGTGTGAGTAAACATTAACCTTGAT 650
QY 122 SerleuTytrProthMetGluylslyalaagluValaasnSerArgasnGlnValglu 141

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 2798.92 seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793
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Ygapop 10.0 , Ygapext 0.5	
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Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=BSR -QFMT=fasted -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45
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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
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9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	23.6	498	5	B0588134 E012337-0
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3	171.5	21.6	489	2	BN782289 EST00385
4	151.5	19.1	841	7	BN130330 L48-484T3
5	151.5	19.1	903	7	CO121195 GR_EB02E
6	150	18.9	1021	2	CO103587 GR_EB003
7	149	18.8	639	2	BE036639 MP03B03 M
					BE037217 MP18B02 M

8	138.5	17.5	603	5	B0590856
9	138	17.4	811	2	BE034055
10	136	17.2	837	1	AM053634
11	125	15.8	661	6	CF227046
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14	121	15.3	621	7	CV052755
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17	120	15.1	678	6	CA840373
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19	118.5	14.9	698	6	CA838926
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21	112.5	14.2	497	5	B0488214
22	110	13.9	494	7	CA8600715
23	104.5	13.2	1310	1	AJ922191
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25	101.5	12.8	419	6	CF226983
26	100.5	12.7	949	1	AJ927358
27	99	12.5	658	5	B0583480
28	98.5	12.4	671	7	CN846973
29	98	12.4	672	10	CG167941
30	98	12.4	636	1	AM053585
31	97	12.2	472	8	DN953953
32	97	12.2	504	5	B0594182
33	97	12.2	665	6	CF227084
34	95.5	12.0	669	7	CN848288
35	92.5	11.7	491	8	DN142823
36	92.5	11.7	611	5	B0490182
37	92	11.6	503	8	DN142727
38	91.5	11.5	317	8	CG110999
39	91	11.5	573	6	CD930847
40	91	11.5	632	7	CN010200
41	90.5	11.4	1038	2	BE033546
42	89.5	11.3	463	2	BE605223
43	89.5	11.3	813	10	CL957625
44	88.5	11.2	665	10	CE458462
45	88.5	11.2	875	2	BG369793

ALIGNMENTS

RESULT 1
B0588134
LOCUS B0588134 498 bp mRNA linear EST 06-DEC-2002
DEFINITION E012337-024-009-G14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-G14 5-PRIME, mRNA sequence.
ACCESSION B0588134
VERSION B0588134.1 GI:26117717
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNALS Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0049215062851
Email: weisshaar@mpi-z-koeln.mpg.de
Insert Length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTGCTGACACTATAG.
Location/Qualifiers

FEATURES

|||
ACCESSION BE130330
VERSION BE130330.1 GI:8577693
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 489)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-5 row: G column: 12
Seq primer: T3
High quality sequence stop: 350
POLY-A-No.

FEATURES
SOURCE
Location/Qualifiers
1..489
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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-484"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 48 hours NaCl treatment"
/note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site_1:
EcoRI, Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 1,21e-11 Length: 489
Score: 171.50 Matches: 43
Percent Similarity: 56.4% Conservative: 14
Best Local Similarity: 42.6% Mismatches: 35
Query Match: 21.6% Indels: 9
DB: 2 Gaps: 4
US-09-978-274A-6 (1-154) x BE130330 (1-489)

QY 2 l l e a n t h r i l e t h r p h e a p a l a g l y a s n a l a t h r - - - - - l l e a s n l y e t y r a l a t h r 19
Db 150 A T A A C A C T A A T A C C T G G A C A T C T C A G A G A A G C T A C C T G C G A T A C A T A C C A T A C A 209
QY 20 P h e m e t G u s e r l e u A r g A n G l a l a l y a s p p r o l y s l e u l y s c y t y r g l y l e r o 39
Db 210 T T C C T G A A T C T T A C G A A T G A A C T G A A G A T C C A T G A A A C C C A T A G T A T A T A C A 269
QY 40 M e t l e u - - - - - P r o a s p T h r a s n - - - - - s e r t h r p r o l y s t y r l e u l e u V a l l y s l e u 55
Db 270 G T A T G G A A A A C C T A C A C T T C C A A G A T G A C A A C G A T A C T A T C T T T G T A G A G C T G 329
QY 56 G l n G l y l a a s n l e u l y e t h r i l e t h r l e u M e t l e u A r g A s n a s n l e u T y r V a l m e t 75
Db 330 C A G C G A G C A C C C A A A G T C A T A T T A T C T A G A C A G A A G C A A T T A T A T T C A T G 389
QY 76 G l y T y r s e r a s p - - - - - P r o p h e a s n l y a s n l y s c y a r g t y r H i s l l e p h e a s n 92
Db 390 G G C T A C A G T G A C A T T G G A T T A T A A A A T A A A A A A T G C G C A C C A T G T G T C A A G 449
QY 93 A s p 93

|||
Db 450 GAT 452

RESULT 4
LOCUS CO121195
DEFINITION GR_EB02E11.f GR_EB Gossypium raimondii cDNA clone GR_EB02E11 5',
mRNA sequence.
ACCESSION CO121195
VERSION CO121195.1 GI:48819882
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; eustroside II; Malvales; Malvaceae; Malvaceae; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 841)
AUTHORS Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
Wing, R.A.
TITLE Global assembly of Cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 02 row: B column: 11.

FEATURES
SOURCE
Location/Qualifiers
1..841
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_EB02E11"
/tissue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_EB"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Alignment Scores:
Pred. No.: 1.08e-08 Length: 841
Score: 151.50 Matches: 43
Percent Similarity: 46.5% Conservative: 30
Best Local Similarity: 27.4% Mismatches: 65
Query Match: 19.1% Indels: 19
DB: 7 Gaps: 5
US-09-978-274A-6 (1-154) x CO121195 (1-841)

QY 2 l l e a n t h r i l e t h r p h e a p a l a g l y a s n a l a t h r l l e a s n l y s t y r a l a t h r p h e m e t 21
Db 34 A T T A C A C A G T A C A G A T T A C C A C T G A A A G C C A C G A A C T C T T A T C G A T T A T A T G 93
QY 22 G l u s e r l e u A r g A n G l a l a l y a s p p r o l y s l e u l y s c y t y r g l y l e r o M e t l e u 41
Db 94 A A G G A T C T G A C A A T G A T G A C A G C G T G C A A G C G A G A C A T G C C A T A T T G 153
QY 42 P r o a s p T h r a s n s e r t h r p r o - - - - - l y s t y r l e u l e u V a l l y s l e u G l n g l y 57
Db 154 C C T C C C G A T C T G A C A C C C T A C G A T C C T C G G A A A T G T C T G T A G A G C T T C A A T 213
QY 58 A l a a s n l e u l y t h r i l e t h r l e u M e t l e u A r g A s n a s n l e u l y t y r V a l m e t G l y t y r 77
Db 214 - - - - - G T T A C C A A A C T G C A C A T T A G C C T G C A T C A G T A G T G A T G T A T C T T G G T T A T 270
QY 78 S e r a s p P r o p h e a s n l y a s n l y s c y a r g t y r H i s l l e p h e a s n a s p l l e t h s e r t h r 97

Db 271 CGGCAAGTGGGGCTCC-----TATTCTTAGCGATGCCAGAC--- 312
Qy 98 GUAAGThraApValGuaenThrluCySerSerSerSerArgValAlaMetSer 117
Db 313 -----GATGACGTAATGCTTTGTTCCAGGCGACT-----GGC 348
Qy 118 IleaenTyraenSerleuTyProthMetGluValysAlaGluValaenSerArgAsn 137
Db 349 CTACCCCTTACAGGACATATGGGCACTTGAAGGCTCTGCGGAGTAAATGACAGAAG 408
Qy 138 GlnValGlnleuGlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 409 GAATCCCTCTGGGAATGATGAACACTACGCAACATATTGATACTGAAT 459
RESULT 5
COL03587 903 bp mRNA linear EST 16-JUN-2004
LOCUS GR_EB0032E01.r_GR_Eb Gossypium raimondii cDNA clone GR_EB0032E01
DEFINITION 3'-UTR mRNA sequence.
ACCESSION COI03587
VERSION COI03587.1 GI:48802273
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; euroside II; Malvales; Malvaceae; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 903)
AUTHORS Klm,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
TITLE Global assembly of Cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0032 row: E column: 01.
FEATURES
source 1..903
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
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/tissue_type="floral"
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/lab_host="DH10B"
/clone_1lb="GR_Eb"
/note="Vector: pCMV.SPORT.6.1; Site 1: NotI; Site 2:
EcoRV; library made by invitrogen with RNA supplied by
Wendle lab. Directional clones into NotI-EV. Clones
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:
Pred. No.: 1,19e-08 Length: 903
Score: 151.50 Matches: 43
Percent Similarity: 46.5% Conservative: 30
Best Local Similarity: 27.4% Mismatches: 65
Query Match: 19.1% Indels: 19
DB: 7 Gaps: 5

US-09-978-274A-6 (1-154) x COI03587 (1-903)

Qy 2 IleaenThrluThraPheapAlaGlyAsnAlaThrluAsnTyralaThrPheMet 21
Db 172 ATTACACAGTGAATTCACCACTGAAGAGCCACCGAATCTTATTCGATCTTATG 231
Qy 22 GUSerleuArganGlnAlaTyAspProlyleuTyCyTrGlyIleProMetleu 41

Db 232 AACGATCTGTAACAATGATTCACAGACCGGAGATTAAGACCGAGATGATTTG 291
Qy 42 ProAspThraenSerThraPro-----LyTrIleuValValysleuGlnGly 57
Db 292 CTCCCGCATCTGACAGCGCTTACTGATCCCTCGGCAATATTTGTAAGACTCTCAAT 351
Qy 58 AlaaenleuTyhrlleThrluMetleuArgAsnAsnleuTyValMetGlyTy 77
Db 352 ---GGTTACAAACTGTCACATTAACCTTGATGCTGATGATGATGATGATGAT 408
Qy 78 SerAspProPheanGlnTyAsnTyCyArgTyHisIlePheanAspIleThrSer 97
Db 409 CGGCAAGTGGGGCTCC-----TATTCTTAGCGATGCCAGAC--- 450
Qy 98 GUAAGThraApValGuaenThrluCySerSerSerSerArgValAlaMetSer 117
Db 451 -----GATGACGTAATGCTTTGTTCCAGGCGACT-----GGC 486
Qy 118 IleaenTyraenSerleuTyProthMetGluValysAlaGluValaenSerArgAsn 137
Db 487 CTACCCCTTACAGGACATATGGGCACTTGAAGGCTCTGCGGAGTAAATGACAGAAG 546
Qy 138 GlnValGlnleuGlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 547 GAATCCCTCTGGGAATGATGAACACTACGCAACATATTGATACTGAAT 597

RESULT 6
BE036639 1021 bp mRNA linear EST 07-JUN-2000
LOCUS MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:9331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astrocaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 1021)
AUTHORS Bohner,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
Pereira,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
Palacio,C., Sears,G., Wheeler,M. and Zepeda,G.R.
TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michalowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu
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FEATURES
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/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_1lb="MP"
/note="3 d 500mM NaCl"

ORIGIN

Alignment Scores:
Pred. No.: 2,23e-08 Length: 1021
Score: 150.00 Matches: 50
Percent Similarity: 49.0% Conservative: 26
Best Local Similarity: 32.3% Mismatches: 59
Query Match: 18.9% Indels: 20
DB: 2 Gaps: 8

LOCUS	BQ590856	603 bp	mRNA	linear	EST 06-DEC-2002
DEFINITION	B012599-024-018-N14-SP6 MP1Z-ADIS-024-storage root Beta vulgaris				
ACCESSION	CDNA clone 024-018-N14 5'-PRIME, mRNA sequence.				
VERSION	BQ590856				
KEYWORDS					
SOURCE	BQ590856.1	GI:26120439			
ORGANISM	Beta vulgaris				
REFERENCE	Beta vulgaris				
AUTHORS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.				
	1 (bases 1 to 603)				
	Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radeflo,U.				
TITLE	Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes				
JOURNAL	Plant J. 32 (5), 845-857 (2002)				
PUBMED	12472698				
COMMENT	Contact: Weishaar B ADIS DNA core facility at MP1Z Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaa@mpiz-koeln.mpg.de Insert Length: 603 Std Error: 0.00 Plate: 18 row: N column: 14 Seq primer: SP6; CATACGATTTAGGTGCACCTAAG. Location/Qualifiers 1..603				
FEATURES					
source					

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzieler Saetzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SmaI-SalI-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator; Prof. Christian Jung, Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:
 Pred. No.: 3,34e-07 Length: 603
 Score: 138.50 Matches: 47
 Percent Similarity: 45.2% Conservative: 23
 Best Local Similarity: 30.3% Mismatches: 64
 Query Match: 17.5% Indels: 21
 DB: 5 Gaps: 7

US-09-978-274a-6 (1-154) x B0590856 (1-603)

QY 3 Aanthrillethrpheapalagly---AanlathrilleanthlytyrAlathrphemet 21
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 DB 174 AACCTGTGTATGGAGACTTTCACCTCTGATCTGTAAATGCTATCCAAATTTCTTG 233
 QY 22 GluserleuarganglinalyabapProlyseulyCyetyglyylePrometleu 41
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 DB 234 ACGAGACTGCGCAATCAAGTGAAGCTCGATCAGAGATCTGC-----GGCTTA 281
 QY 42 ProaethrAanSerThrPro-----LystryleuLeuValylseunglly 57
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 DB 282 CCATCCAGCGCAATGCTCCCTTAGAAGGCCAAAGATATATAACGTGACCTAAAGANT 341
 QY 58 AlaAanleulystrillethreuleuarganglinalyabapleulytyrValmetglytyr 77
 |||||:::|||||
 DB 342 AGCAACAGAAATTTGGGTGACCATAGAAATGATGTCATGATTTGATGATGAGGGTAT 401
 QY 78 SerAapProPhaangllyabnlyCyabarytyrHlellePhaAanleulythreSerThr 97
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 DB 402 CAAGCAAGTTTAAACGGG---ATACTTCGGTCCACTTGTATATACCTTCCCCAGGCT 458
 QY 98 GluArgThrAapValglubanthrleuCyserSerSerSerSerArgValAlaMetSer 117
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 DB 459 GCAAGG-----AACACCTTTTCCAGATGCGGCATTTAGAAAGAACACTAAT 506
 QY 118 Ile-----AanTyraAnSerleulytyrProThrMetGluLylValagluValaAnSer 135
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 DB 507 TTTCAGAGCAACTACGACGCTTTCAGCCATACGCTCGA-----ACAGAT 551
 QY 136 ArgAnglnValgluLeuglylleGlnlleLeuserSerAaplle 150
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 DB 552 AGAACAAAGCTTGATTTAGGTGTATAGCTACAGGGTGCATTC 596

RESULT 9 811 bp mRNA linear EST 07-JUN-2000
 BE034055
 LOCUS MG0405 MG Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION ribosome-inactivating protein gelonin, mRNA sequence.
 ACCESSION BE034055
 VERSION BE034055.1 GI:8329064
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Alceaceae; Mesembryanthemum.
 1 (bases 1 to 811)
 Bohmert,H.J., Borchert,C., Brazille,S., Broke,J., Baton,M.,
 Perret,H., Kawasaki,S., McColough,A., Michalowski,C.B.,
 Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 JOURNAL Unpublished (2000)

COMMENT

Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
 An open reading frame exists.
 Insert Length: 1 Std Error: 0.00.
 Location/Qualifiers
 1. 811

FEATURES

source

/organism="Mesembryanthemum crystallinum"
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 /db_xref="taxon:3544"
 /tissue_type="roots"
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 /note="grown in hydroponics, stress 400 mM NaCl (in 0.5 Hoagland's), 30 h stress"

ORIGIN

Alignment Scores:
 Pred. No.: 5.92e-07 Length: 811
 Score: 138.00 Matches: 51
 Percent Similarity: 48.7% Conservative: 25
 Best Local Similarity: 32.7% Mismatches: 59
 Query Match: 17.4% Indels: 21
 DB: 2 Gaps: 8

US-09-978-274a-6 (1-154) x BE034055 (1-811)

QY 3 AanthrillethrpheapalaglyAanlathrilleanthlytyrAlathrphemet 22
 |||||:::|||||
 DB 246 AACACCGGACCTTCAACCTC-----GCCAACCCAAACATATCCGATTCAGACA 299
 QY 23 SerleuarganglinalyabapProlyseulyCyetyglyylePrometleupo 42
 |||||:::|||||
 DB 300 TCTCTCCAGCTCAACCTCTCTGC---ACAACCGCATG-----CAAAATCCC 344
 QY 43 AapThraAnSerThr-----ProlystryleuLeuValylseungllyAla 58
 |||||:::|||||
 DB 345 GTGACACGGTCAACCGCACCGGATCTCCACGATTCCTGCTGACCTCAAAACACCC 404
 QY 59 AanthlyeThrillethreuleuarganglinalyabapleulytyrValmetglytyrSer 78
 |||||:::|||||
 DB 405 TCGAAAGACATCACTCCGATCGACGACGACGACGATCGTGTGCGCTGCGCC 464
 QY 79 AapProPhaangllyabnlyCyabarytyrHlellePhaAanleulythreSerThrglu 98
 |||||:::|||||
 DB 465 GACACCTT---GGCGAAAGACCGTCCCACTTCTTAGCGATCTCCACGCTCGCT 521
 QY 99 ArgThraAapValglubanthrleuCyserSerSerSerSerSerArgValAlaMetSerlle 118
 |||||:::|||||
 DB 522 AGG-----AACACCTTTCAAGGCGCGACGGTTCG-----MACATT 560
 QY 119 AanthTyraAnSerleulytyrProThrMetGluLylValagluValaAnSerAapAn-gl 138
 |||||:::|||||
 DB 561 GCGTTCGAGAGGAGTTTACATAGCCCTTAGAAAGAGCTGCAAG---CAAGCCGCAATGCA 617
 QY 138 nValGlnLeuglylleGlnlleLeuserSerAaplleGlylylle 153
 |||||:::|||||
 DB 618 ATATGAGTTAGGGGTGATTAATTAAGAAATTTGGCATGATCCGCT 663

RESULT 10

AM053634 837 bp mRNA linear EST 20-FEB-2001
 LOCUS L30-1401r3 Ice plant Lambda Uni-zap XR expression library, 30 hours
 DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-1401
 5', mRNA sequence.
 ACCESSION AM053634
 VERSION AM053634.1 GI:5916827
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 837)

Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
Poly(A) tail, 10 nt: 838..847
PCR Primers
FORWARD: T7
BACKWARD: T3
Insert Length: 847 Std Error: 5.00
Plate: L30-15 row: A column: 5
Seq primer: T3
High quality sequence stop: 450.
Location/Qualifiers
1..837

FEATURES
source
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L30-1401"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/note="Vector: lambda Uni-Zap XR, Bluescript SK-; Site_1:
BcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 1.13e-06 Length: 837
Score: 136.00 Matches: 45
Percent Similarity: 48.3% Conservative: 24
Best Local Similarity: 31.5% Mismatches: 56
Query Match: 17.2% Indels: 18
Gaps: 7

US-09-978-274A-6 (1-154) x AM053634 (1-837)

15 AenlyTYrAlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLys 34
5 AACACATATTCACATTCATGACATCTCCGAGCTCAACTCTCGCC--ACAACCGCA 61
35 CysTYrGlyIleProMetLeuProAspThrAsnSerThr-----ProLysTYr 50
62 TGT-----CAATCCCGCTGACACCGTCAACCGCAACCGATCTCCACAGCATTC 109
51 LeuLeuValLysLeuGlnGlyAlaLeuLeuLysThrIleThrLeuMetLeuArgArgan 70
110 GTCTCTCGTGCACCTCAAAACAACCTCGCAAAAGACCATACACTGCAATCAACGTCACA 169
71 AenLeuTYrValMetGlyTYrSerAspProPheAsnGlyAsnLysCysArgTYrHisIle 90
170 AGCGCTATGTCGTGGCTACCGGCAAGCTT---GGCGAAAGAACCGTCCCAACTTC 226
91 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 110
227 CTTACCGAGTCTCCACGCTCGCTAGG-----AACACCTCTTCAAGGCGCG 274
111 SerSerArgValAlaMetSerIleAsnSerIleAsnSerLeuTYrProThrMetGlnLysLys 130
275 ACGGTTCCG-----AACATTGCTTCCGAGGAGGAGTACATGACCTTACAGAGGCT 325
131 AlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIle 150

Db 326 GCAAG---CAAGCCGGAATGCAATAGACTTAGGGGTGAATTAAGATTGGGATC 382
Qy 151 GlyLysIle 153
Db 383 GAGTCGGTT 391

RESULT 11
CP227046

LOCUS CP227046 661 bp mRNA linear EST 04-AUG-2003
DEFINITION IH202 subtracted Iris tepal cDNA library Iris hollandica cDNA clone
IH202, mRNA sequence.

ACCESSION CP227046
VERSION CP227046.1 GI:33438082
KEYWORDS EST.

SOURCE
ORGANISM Iris hollandica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
Iris.

REFERENCE
1 (bases 1 to 661)

AUTHORS Van Doorn, W.G., Balk, P.A., van Houwelingen, A.M., Hoeberichts, P.A.,
Hall, R.D., Vorse, O., van der Schoot, C. and van Woudagen, M.F.
TITLE Gene expression during anthesis and senescence in Iris flowers
JOURNAL Plant Mol. Biol. 53 (6), 845-863 (2003)
PUBMED 15082930

COMMENT Contact: Wouter G. van Doorn
Institute for Agro technological Research (ARO)
Wageningen University and Research Centre
P.O. Box 17, 6700 AA, Wageningen, The Netherlands
Tel: 0031 317 475105
Fax: 0031 317 475347
Email: wouter.vandoorn@wur.nl.
Location/Qualifiers
1..661

FEATURES

source
/organism="Iris hollandica"
/mol_type="mRNA"
/cultivar="Blue Magic"
/db_xref="taxon:35876"
/clone="IH202"
/tissue_type="sepal"
/clone_lib="subtracted Iris tepal cDNA library"
/note="Vector: pGEMT-Basy; mRNA isolated from Iris sepals
was subtracted using pedicel material as the driver. Equal
amounts of mRNA from each developmental stage were pooled
for cDNA synthesis. The pGEM-T Basy Vector System
(Promega) was used to construct the cDNA library."

ORIGIN

Alignment Scores:

Pred. No.: 2.21e-05 Length: 661
Score: 125.00 Matches: 42
Percent Similarity: 46.0% Conservative: 27
Best Local Similarity: 28.0% Mismatches: 63
Query Match: 15.8% Indels: 18
Gaps: 5

US-09-978-274A-6 (1-154) x CP227046 (1-661)

2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTYrAlaThrPheMet 21
76 ATTGAACAGTGCAGTTCGCTGCTACCTGGACACACAGGCAAACTATAGCTTCTTA 135
22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTYrGlyIleProMetLeu 41
136 CAGACCTTACCAACGCTTAAGCAGTGAAGT---ACGTCAGATGATATCTTGTGCTG 192
42 Pro---AspThrAsnSerThrProLysTYrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
193 CTTGGGCAATCGGTTCCACAGAGATTGCTCTTGTCACACTCTTTGATTGGACACAC 252
61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTYrValMetGlyTYrSerAspPro 80
253 ACGCGATCACGCTGCTGCTTAATCGGCTCAATGCTTATCTGTAAGTATCA----- 306

QY 81 Pheannglyanlyscysargtyrhielpheanapilletserthngluargthr 100
 DB 307 -----GCTAAATCGTTATTACTGCTTCCGAC-----ACT 339
 QY 101 AspyalgluamthrlleuCyseSerSerSerSerargvalalmetserilleasntyr 120
 DB 340 CCGGCATCTCGAGCTTATGAGCAACCGCAGCTTATGTTTACAGGAGCTAC 399
 QY 121 Amsenleutyrrprothmetglulylalyalaenlvalaenlvalaenlvalaenl 140
 DB 400 ATTCGCTT-----CAAAATGTCGAAACAGTACGAAATTTGAT 444
 QY 141 LeuglyileglnlleuSerSeraspile 150
 DB 445 CTGGATCATCCACTTCGCAACGCGCATC 474

RESULT 12
 CF227047 662 bp mRNA linear EST 04-AUG-2003
 LOCUS IH215, mRNA sequence.
 DEFINITION IH215, mRNA sequence.
 ACCESSION CF227047.1 GI:33438083
 VERSION CF227047.1
 KEYWORDS EST.
 SOURCE Iris hollandica
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae; Iris.

REFERENCE 1 (bases 1 to 662)
 Van Doorn, W.G., Balk, P.A., van Houweijngen, A.M., Hoeberichts, F.A., Hall, R.D., Vorst, O., van der Schoot, C. and van Woudagen, M.F.
 Gene expression during anthesis and senescence in Iris flowers
 Plant Mol. Biol. 53 (6), 845-863 (2003)
 15082930
 CONTACT: Mouter G. van Doorn
 Institute for Agro technological Research (ATO)
 Wageningen University and Research Centre
 P.O. Box 17, 6700 AA, Wageningen, The Netherlands
 Tel: 0031 317 475105
 Fax: 0031 317 475347
 Email: wouter.vandoorn@wur.nl.
 Location/Qualifiers

FEATURES
 source 1..662
 /organism="Iris hollandica"
 /mol_type="mRNA"
 /cultivar="Blue Magic"
 /db_xref="taxon:35876"
 /clone="IH215"
 /issue_type="sepal"
 /clone_1lb="subtracted Iris tepal cDNA library"
 /note="Vector: pGEMT-Easy; mRNA isolated from Iris sepals was subtracted using pedicel material as the driver. Equal amounts of mRNA from each developmental stage were pooled for cDNA synthesis. The pGEMT-Easy Vector System (Promega) was used to construct the cDNA library."

ORIGIN
 Alignment Scores: 2.21e-05 Length: 662
 Pred. No.: 125.00 Matches: 42
 Score: 125.00 Conservative: 27
 Percent Similarity: 46.0% Mismatches: 63
 Best Local Similarity: 28.0% Indels: 18
 Query Match: 15.8% Gaps: 5

US-09-978-274A-6 (1-154) x CF227047 (1-662)

QY 2 IleanthrilethrlpheanapilgylasmlahrlleasnytyraltthPhemet 21
 DB 109 ATTGAACAGTGAGTCCGTGTCATCGGAGCACCGCAACCTATAGCTTTCTTA 168

QY 22 GlusertleuargannglnalalyaspprolyleuLyCytyrglyileprometleu 41
 DB 169 CAGACCTACGACGCGCTTACGAGTGAAGT---AGCGTGAATGATTTCTTCTG 225
 QY 42 Pro---AspThrAnserthrrprolytyrleuValylleuglnllyalaenleu 60
 DB 226 CTTGGCAATCCGGTCTCCAGCAGATTTGCTCTTGTGCAACTTTGATTGGAGCAAC 285
 QY 61 LythrillethrlleuMetleuArgArgAnleutyrrValmetglytyrSerAspPro 80
 DB 286 ACGCCGATCGCGTGGCTTATGCGTCAGTCTTATGCTGAGCTTACAA----- 339
 QY 81 Pheannglyanlyscysargtyrhielpheanapilletserthngluargthr 100
 DB 340 -----GCTAAATCGTTATTACTGCTTCCGAC-----ACT 372
 QY 101 AspyalgluamthrlleuCyseSerSerSerSerargvalalmetserilleasntyr 120
 DB 373 CCGGCATCTCGAGCTTATGAGCAACCGCAGCTTATGTTTACAGGAGCTAC 432
 QY 121 Amsenleutyrrprothmetglulylalyalaenlvalaenlvalaenlvalaenl 140
 DB 433 ATTCGCTT-----CAAAATGTCGAAACAGTACGAAATTTGAT 477
 QY 141 LeuglyileglnlleuSerSeraspile 150
 DB 478 CTGGATCATCCACTTCGCAACGCGCATC 507

RESULT 13
 B0588856 546 bp mRNA linear EST 06-DEC-2002
 LOCUS B0588856
 DEFINITION B012534-024-014-P10-SP6 MP12-ADIS-024-storage root Beta vulgaris cDNA clone 024-014-P10 5-PRIME, mRNA sequence.
 ACCESSION B0588856
 VERSION B0588856.1 GI:26118439
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 546)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U.
 Construction of a 'unique' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 12472698
 CONTACT: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50823 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mp12-koeln.mpg.de
 Insert length: 546 Std Error: 0.00
 Plate: 14 row: P column: 10
 Seq primer: Sp6; CATACGATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source 1..546
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:187113"
 /db_xref="taxon:161934"
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 /clone="024-014-P10"
 /issue_type="storage root"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzleben Saat-zucht AG Einbeck, Germany, contact:

ORGANISM

Mesembryanthemum crystallinum
Bakryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 644)

REFERENCE
AUTHORS
TITLE
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL
COMMENT
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: B column: 04
Seq primer: T3 20mer
High quality sequence stop: 644.
Location/Qualifiers

FEATURES
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1..644
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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016B04"
/feature_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
BclRI, Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 9.57e-05 Length: 644
Score: 120.00 Matches: 41
Percent Similarity: 45.7% Conservative: 28
Best Local Similarity: 27.2% Mismatches: 64
Query Match: 15.1% Indels: 18
DB: Gaps: 6

US-09-978-274a-6 (1-154) x CA638401 (1-644)

OY 3 AantThrlleThrPheAapAagIaAanAaAathrlleAanlyTyraAathrPheMetGlu 22
DB 205 AACACCGTGAATTCGACCTC-----GCCCAATCCGACACATATCCAAAGTTCATTGCC 258
OY 23 SerLeuArgAaangInAlaIyAaPProLyLeuLyCyerTyrlYleProMetLeuPro 42
DB 259 GATCTCCAAGTGAATCTCCGGCACAACCGCATGTCAA--ATCCCCGTGACACGG 315
OY 43 AspThrAaSerThr-----ProLyTyrlleuValLyAaangInAlaAan 59
DB 316 GCAACCGCAACCAATCCAAATGACCAAGATGCTCTCTGACCTCGAAACACCTCG 375
OY 60 LeuLyThrIleThrLeuMetLeuArgAaAanleuTyraAaMetGlyTySerAap 79
DB 376 CAAAAAACCATCACTCCGCAATGACGTACAGAGCTACGTCGCTATCGCGAC 435
OY 80 ProPheAaangIyAa-----LyCyAaTyrlleAaAaAaAaAaAaAaAaAaAa 95
DB 436 AAGTTCAAAGAAAGACGCAAAATGAAGACCGTCAACTTCCTCAAGATGATCT 495
OY 96 SerThrIuArgThrAaPValGluAaThrlleuCySerSerSerSerAaAaAaAa 115
DB 496 ACGGTTCGCAAG-----GAGAAATCTCTTCAATGAGCAACGTTCCGAACCTTCG 546

OY 116 MetSerIleAanTyraAaSerLeuTyProThrMetGluLyAaAaAaAaAaAaAaAaAa 135
DB 547 TTCAAAGCACTTACACATCTTA-----GAGAAATGCTGCAAAACCAACGA 591
OY 136 ArgAaangInValGluAaangIyrlleGluIleLeu 146
DB 592 CGAAGACCAATGAGTTAGGGGTGATANAATA 624

Search completed: April 9, 2006, 06:20:25
Job time: 2800.92 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 168.1 Seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793

Sequence: 1 MIMTTPDAGNATINKYATF.....SRNQVKGIGILSSDGKIS 154

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -OPMT=fastlap -SUFFIX=p2n.rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abses02p -USRR=US09978274 @CGN 1.1 718 @rumat 07042006 173037 28482
-NCPU=6 -ICPU=3 -NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	75.2	1195	2	US-08-373-858-1
2	596	75.2	1195	2	US-08-342-7868-1
3	596	75.2	1379	2	US-08-500-611-1
4	596	75.2	1379	2	US-08-500-694-1
5	596	75.2	1379	3	US-07-865-169-1
6	596	75.2	1379	3	US-09-005-273-1
7	596	75.2	1379	3	US-08-501-253A-1
8	596	75.2	1379	6	PCT-US96-11546-1
9	588	74.1	1379	3	US-07-865-169-2

10	588	74.1	1379	3	US-09-005-273-3	Sequence 3, Appli
11	463.5	58.4	918	2	US-08-138-636-1	Sequence 1, Appli
12	463.5	58.4	918	2	US-08-319-622A-1	Sequence 1, Appli
13	463.5	58.4	918	2	US-08-471-564-1	Sequence 1, Appli
14	190.5	24.0	804	2	US-08-356-161-7	Sequence 7, Appli
15	190.5	24.0	804	3	US-08-718-904-23	Sequence 23, Appli
16	190.5	24.0	804	3	US-09-449-249-23	Sequence 2, Appli
17	190.5	24.0	804	6	PCT-US93-05702-13	Sequence 7, Appli
18	190.5	24.0	804	6	PCT-US95-10973A-7	Sequence 7, Appli
19	188.5	23.8	765	3	US-08-718-904-79	Sequence 79, Appli
20	188.5	23.8	765	3	US-09-449-249-79	Sequence 79, Appli
21	188.5	23.8	1167	6	PCT-US95-1651-12	Sequence 57, Appli
22	188.5	23.8	1230	2	US-08-356-161-13	Sequence 12, Appli
23	188.5	23.8	1230	2	US-08-356-161-13	Sequence 13, Appli
24	188.5	23.8	1230	3	US-08-718-904-53	Sequence 53, Appli
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30	188.5	23.8	1233	3	US-08-718-904-80	Sequence 80, Appli
31	188.5	23.8	1233	3	US-09-449-249-80	Sequence 80, Appli
32	188.5	23.8	1251	3	US-08-718-904-74	Sequence 74, Appli
33	188.5	23.8	1251	3	US-09-449-249-74	Sequence 74, Appli
34	188.5	23.8	1260	3	US-08-718-904-72	Sequence 72, Appli
35	188.5	23.8	1260	3	US-09-449-249-72	Sequence 72, Appli
36	188.5	23.8	1266	3	US-08-718-904-75	Sequence 75, Appli
37	188.5	23.8	1266	3	US-09-449-249-75	Sequence 75, Appli
38	188.5	23.8	1269	3	US-08-718-904-78	Sequence 78, Appli
39	188.5	23.8	1269	3	US-09-449-249-78	Sequence 78, Appli
40	188.5	23.8	1275	3	US-08-718-904-73	Sequence 73, Appli
41	188.5	23.8	1275	3	US-09-449-249-73	Sequence 73, Appli
42	188.5	23.8	1299	3	US-08-718-904-77	Sequence 77, Appli
43	188.5	23.8	1299	3	US-09-449-249-77	Sequence 77, Appli
44	188.5	23.8	1299	6	PCT-US95-10973A-58	Sequence 58, Appli
45	188.5	23.8	1320	3	US-08-718-904-76	Sequence 76, Appli

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoacca
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
TITLE OF INVENTION: Plant Transformed Thereof.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/06/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

Db 339 GAAACCAATTAATGCTGTACCATATCTTTAATGATATCTCAGTACTGAACGCCAAGAT 398
Qy 102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrrAsn 121
Db 339 GTAGAGACTACTCTTGGCCCAATATCTCTGTGTAGTAAACATTAACCTTGAT 458
Qy 122 SerLeuTyrrProThrMetGluLysIleValAsnSerArgAsnGlnValGlnLeu 141
Db 459 AGTCATATCCAAATTCGAATCAAAAGCGGAGTAAATCAAGAACATCCAACTG 518
Qy 142 GlyIleGlnIleLeuSerSerArgIleGlyIleSer 154
Db 519 GGAATTCAAATATCTGACAGTAAATATGAAAGATTCT 557

RESULT 3
US-08-500-611-1
Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun B.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Wentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-6 (1-154) x US-08-500-611-1 (1-1379)
Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnTyrrAlaThrPheMet 21
Db 291 GTGAATCAATCAATCAATCAATGGAATGGAATGCAACATTAAGCAATCACTTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaValAspProlyLeuLysCyrrGlyIleProMetLeu 41
Db 351 AATGATCTTGTAATGAGCAAGAAAGATCAAGTTAAAGCTAATGAAATCCAACTG 410
Qy 42 ProAspThrAsnSerThrProlyrTyrrLeuValIysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCATATCAATATCAATATCCAAAGTACGTGTGTTGAGTCCAAAGGTCAATTAATAA 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrrValMetGlyTyrrSerAspProPhe 81
Db 471 ACCATCACTAAAGCTGAGCGAAGCAATTTGTATGTGATGGGTATTCGATCCCTTT 530
Qy 82 AsnGlyAsnLysCyrrGlyrIleIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATTAATATCTGTACCATATCTTTAATGATATCTCAGTACTGAACGCCAAGAT 590
Qy 102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrrAsn 121
Db 591 GTAGAGACTACTCTTGGCCCAATATCTCTGTGTAGTAAACATTAACCTTGAT 650
Qy 122 SerLeuTyrrProThrMetGluLysIleValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCATATCCAAATTCGAATCAAAAGCGGAGTAAATCAAGAACATCCAACTG 710
Qy 142 GlyIleGlnIleLeuSerSerArgIleGlyIleSer 154
Db 711 GGAATTCAAATATCTGACAGTAAATATGAAAGATTCT 749

RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun B.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Wentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
US-08-500-694-1

Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-6 (1-154) x US-08-500-694-1 (1-1379)

QY 2 ILeaenThrlleThrhepalepAlaGlyAenAlaThrlleAenlyTyrlaThrPheMet 21
DB 291 GTGAATACATCAATCTAACAATGTTGAAAGTACCACTTAGCAATACGCCACTTTCTG 350
QY 22 GUSerLeuArGaenGlnAlaLyAaPProLyLeuLyCyTyrgLyIlePProMetLeu 41
DB 351 AATGATCTTCGTATGAGCGAAGAAAGATCCAAAGTTTAAATGCTATGAAATACCAATCTG 410
QY 42 ProAepThraAenSerThrProLyTyrlleuLeuValyleuGlnGlyAlaAenLeuLy 61
DB 411 CCCAATACAAATCAATCAATCAAGTACGTTGGTTGACCTCCAAAGTTCAATTAATAAAA 470
QY 62 ThrlleThrlleuMetleuArGaenAenLeuTyrlaMetGlyTyrlSerAaPProPhe 81
DB 471 ACCATCACTAATGCTGAGACAAACAATTTGTATGTATGGTTATTCGATCCCTTT 530
QY 82 AenGlyAenLyCyArGlyrHsilePheAaAenPileThSerThrgIuArGThraP 101
DB 531 GAAACCAATTAATGCTGTTACCATATCTTTAATGATATCTCAAGTACTGAACGCCAAGAT 590
QY 102 ValGluAenThrlleuCySerSerSerSerSerArGValAlaMetSerIleAenTyraA 121
DB 591 GTAGAGACTACTCTTTGCCCAATATGCCAATTCCTGTTAGTAAACAAATTAACCTTGAT 650
QY 122 SerLeuTyProThrMetGlyLylyAlaGluValAenSerArGaenGlnValGlnLeu 141
DB 651 AGTCGATATCCAAATTCGAATCAAAACGCGAGATTAATCAAGAAAGTCAGTCCAACTG 710
QY 142 GlyIleGlnIleuSerSerAepIleGlyLyIleSer 154
DB 711 GGAATTCAAATACTCGACAGATTAATTTGAAAGATTTCT 749

RESULT 5
US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kaniewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Parkway No. 6015940th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/865,169
; FILING DATE: 19920407
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10547)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6047
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-865-169-1

Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-6 (1-154) x US-07-865-169-1 (1-1379)

QY 2 ILeaenThrlleThrhepalepAlaGlyAenAlaThrlleAenlyTyrlaThrPheMet 21
DB 291 GTGAATACATCAATCTAACAATGTTGAAAGTACCACTTAGCAATACGCCACTTTCTG 350
QY 22 GUSerLeuArGaenGlnAlaLyAaPProLyLeuLyCyTyrgLyIlePProMetLeu 41
DB 351 AATGATCTTCGTATGAGCGAAGAAAGATCCAAAGTTTAAATGCTATGAAATACCAATCTG 410
QY 42 ProAepThraAenSerThrProLyTyrlleuLeuValyleuGlnGlyAlaAenLeuLy 61
DB 411 CCCAATACAAATCAATCAATCAAGTACGTTGGTTGACCTCCAAAGTTCAATTAATAAAA 470
QY 62 ThrlleThrlleuMetleuArGaenAenLeuTyrlaMetGlyTyrlSerAaPProPhe 81
DB 471 ACCATCACTAATGCTGAGACAAACAATTTGTATGTATGGTTATTCGATCCCTTT 530
QY 82 AenGlyAenLyCyArGlyrHsilePheAaAenPileThSerThrgIuArGThraP 101
DB 531 GAAACCAATTAATGCTGTTACCATATCTTTAATGATATCTCAAGTACTGAACGCCAAGAT 590
QY 102 ValGluAenThrlleuCySerSerSerSerSerArGValAlaMetSerIleAenTyraA 121
DB 591 GTAGAGACTACTCTTTGCCCAATATGCCAATTCCTGTTAGTAAACAAATTAACCTTGAT 650
QY 122 SerLeuTyProThrMetGlyLylyAlaGluValAenSerArGaenGlnValGlnLeu 141
DB 651 AGTCGATATCCAAATTCGAATCAAAACGCGAGATTAATCAAGAAAGTCAGTCCAACTG 710
QY 142 GlyIleGlnIleuSerSerAepIleGlyLyIleSer 154
DB 711 GGAATTCAAATACTCGACAGATTAATTTGAAAGATTTCT 749

RESULT 6
US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
```

TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSEE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0
US-09-978-274A-6 (1-154) x US-09-005-273-1 (1-1379)
QY 2 11aantthrllethrphesapalaglYasna1athrlleasulytyrAlathrPhamc 21
DB 291 GTGATTCATCTTAATGAGCGAAGATCCAGTTTAAATCTATGGAATACCATGCTG 350
QY 22 GluSerleuArganglnalAlaYasPProlySleuYsCytyrGlyIleProMetIeu 41
DB 351 AATGATCTTCTTAATGAGCGAAGATCCAGTTTAAATCTATGGAATACCATGCTG 410
QY 42 ProaepthrasensertThrProlytyrIleuIeuValIysIleunglnGlyAlaAsnIeuYs 61
DB 411 CCGATATCAATATCAATCCAAAGTACGTGTGTGTCGTCGCAAGGTTCAAAATAAAAA 470
QY 62 ThrIlethrIeuMetIeuArgArgAsnAsnIeuYrValMetGlytyrSerAspProPhe 81

DB 471 ACCATCAACATTAAGCTGAGCGAACAATTGTATGTAGNGGCTTATTCGATCCCTT 530
QY 82 AsnGlyAsnIysCybaGtyrHisIlePheAsnApIlethrSerThrgIuArgThrAsp 101
DB 531 GAAACCAATTAATGCTGTTACCATATCTTATATATCTACAGTACGCAAGAT 590
QY 102 ValGluAsnThrIeuCyserSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
DB 591 GTAGAGACTACTCTTGCCCAATGCCAATCTCTGTGTAGTAAAAACATTAACCTTGAT 650
QY 122 SerIeuYrProthmetGluYsIyAlaGluValAsnSerArgAsnGlnValGlnIeu 141
DB 651 AGTGATATCCAAATTCGAATCAAAACCGGAGTAAATCAAGAACTCAGTCAACTG 710
QY 142 GlyIleGlnIleuSerSerAspIleGlyIysIleSer 154
DB 711 GGAATTCAAATTAATCGACAGTAATATTTGGAAGATTTCT 749
RESULT 7
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant Pap and Pap Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0
US-09-978-274A-6 (1-154) x US-08-501-253A-1 (1-1379)

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QY 2 115aantThrlleThrPheaspAlaGlyAsnAlaThr115aantYsYrAlaThrPheMet 21
Db 291 GTGATATCAATCATCTCAATGTTGGAAGTACCAACATTGACAAATACGCACTTTCTG 350
QY 22 GluSerLeuArgAnglnAlaYsAspProlybLeuLysCytyrGly11ePrometLeu 41
Db 351 AATGATCTTGTATGAGAGCGAAGATCCAGTTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlybTyrlLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATACCAATCAATCCAAAGTACGTTGTTGTTGCTCCAGGTTCAATTAATAA 470
QY 62 Thr11eThrlleuMetLeuArgAsnAsnLeuTyrlValMetGlyTyrlSerAspProPhe 81
Db 471 ACCATCACTAATAGCTGAGACGAAACAATTGTATGTATGGGTATTCGTATCCCTTT 530
QY 82 AsnGlyAsnLysCytyrGlyTyrl11ePheAsnAsp11eThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATTAATGTCCTTACCAATCTTAAATGATATCTCAGGTACTGAAACGCCAAGAT 590
QY 102 ValGluAsnThrLeuCytyrSerSerSerSerSerValAlaMetSer11eAsnTyrlAsn 121
Db 591 GTGAGACTACTCTTTGCCCCAATGCCAATCTCTGTATGTAATAAACAATAAATTGAT 650
QY 122 SerLeuTyrlProThrMetGluTyrlYsAlaGluValAsnSerArgAnglnValGlnLeu 141
Db 651 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAAGTCAGGTCCAACTG 710
QY 142 Gly11eGln11eLeuSerSerAsp11eGlybYs11eSer 154
Db 711 GGAATTCAAATACTCGACAGTAATATTGAAAGATTCTT 749
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RESULT 8

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PCT-US96-11546-1
; Sequence 1, Application PC/TUS9611546
; GENERAL INFORMATION:
; APPLICANT: Turner, Nigun E.
; TITLE OF INVENTION: DNAs Encoding Fokweed Antiviral Protein
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,694
; FILING DATE: 11-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; TELEX: 139-125
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
; PCT-US96-11546-1
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Alignment Scores:

Pred. No.:	1-5e-70	Length:	1379
Score:	596.00	Matches:	110
Percent Similarity:	86.9%	Conservative:	23
Best Local Similarity:	71.9%	Mismatches:	20
Query Match:	75.2%	Indels:	0
DB:	6	Gaps:	0

US-09-978-274a-6 (1-154) x PCT-US96-11546-1 (1-1379)

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QY 2 115aantThrlleThrPheaspAlaGlyAsnAlaThr115aantYsYrAlaThrPheMet 21
Db 291 GTGATATCAATCATCTCAATGTTGGAAGTACCAACATTGACAAATACGCACTTTCTG 350
QY 22 GluSerLeuArgAnglnAlaYsAspProlybLeuLysCytyrGly11ePrometLeu 41
Db 351 AATGATCTTGTATGAGAGCGAAGATCCAGTTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlybTyrlLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATACCAATCAATCCAAAGTACGTTGTTGTTGCTCCAGGTTCAATTAATAA 470
QY 62 Thr11eThrlleuMetLeuArgAsnAsnLeuTyrlValMetGlyTyrlSerAspProPhe 81
Db 471 ACCATCACTAATAGCTGAGACGAAACAATTGTATGTATGGGTATTCGTATCCCTTT 530
QY 82 AsnGlyAsnLysCytyrGlyTyrl11ePheAsnAsp11eThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATTAATGTCCTTACCAATCTTAAATGATATCTCAGGTACTGAAACGCCAAGAT 590
QY 102 ValGluAsnThrLeuCytyrSerSerSerSerSerValAlaMetSer11eAsnTyrlAsn 121
Db 591 GTGAGACTACTCTTTGCCCCAATGCCAATCTCTGTATGTAATAAACAATAAATTGAT 650
QY 122 SerLeuTyrlProThrMetGluTyrlYsAlaGluValAsnSerArgAnglnValGlnLeu 141
Db 651 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAAGTCAGGTCCAACTG 710
QY 142 Gly11eGln11eLeuSerSerAsp11eGlybYs11eSer 154
Db 711 GGAATTCAAATACTCGACAGTAATATTGAAAGATTCTT 749
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RESULT 9

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US-07-865-169-2
; Sequence 2, Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Turner, Nigun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kaniewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B34F
; STREET: 700 Chesterfield Parkway No. 6015940ch
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
```



```

: REGISTRATION NUMBER: 39,317
: REFERENCE/DOCKET NUMBER: 760100.415C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 682-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 804 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..804
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..804
: OTHER INFORMATION: /note="Nucleotide sequence
: OTHER INFORMATION: corresponding to the clone M13 mp18-G9 in Example I.B.2."
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 46..804
: OTHER INFORMATION: /product="Saporin"
: US-08-718-904-23

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Alignment Scores:
Pred. No.: 5.21e-16 Length: 804
Score: 190.50 Matches: 50
Percent Similarity: 55.0% Conservative: 38
Best Local Similarity: 31.2% Mismatches: 59
Query Match: 24.0% Indels: 13
DB: 3 Gaps: 6

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US-09-978-274A-6 (1-154) x US-08-718-904-23 (1-804)

```

QY 2 11leasnthrllethrphaspalaglYAsn1athrlleasnytyrAlathrPhamet 21
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 46 GTCAATCAATCACTTAGATCTAGTAAATCCGACCGGGTCAATCTCTTTGTG 105
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 22 GluSerleuArganglnAlaLysAspProlyleuLysCysTyrGlyIlePromet--- 40
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 106 GATAAAATCCGAAACAGTAAAGATCCAAACCTGAAATACGGGTGATCCGACATAGCC 165
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 41 LeuProAspThrAsnSerThrProlyTyrlleuLysVallyLysLeuGlnGlyAlaAsnleu 60
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 166 GTGTAGGCCCACTTCAAGAAATAATCTTAGAATTAAATTCCAAAGTCCCGA--- 222
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 61 LysThrIleThrIleuMetIleuArgAsnAsnleuTyrValMetGlyTyr-----Ser 78
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 223 GGAACGGTCTACTTGGCTTAAACGGCATTAATGTATGTGTGGCGTATCTTGCAATG 282
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 79 AspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGlu 98
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 283 GATAACACGAAATGTAATCGGCA---TATTACTTCAGATCAGAATTAATCTTCGCGCAG 339
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 99 ArgThrAspValGluAsnThrIleuCysSerSerSerSerSerArgValAlaMetSerIle 118
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 340 TTAACC-----GCCCTTTCCAGAGGCCCAACTGCCAATTCAGAAAGCTTTA 387
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 119 AsnTyrAsnSerLeuTyrProThrMetGluLysLysAlaGluVal-----Asn 134
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 388 GAATACACAGAAATTTATTCAGTTCATGAAAGAAATGCCAGATTAACACAAAGAGATCAA 447
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 135 SerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 448 AGTAGAAAGAAACTCGGGTTGGGATGACTTACTTCAACGTCATGGAAGCAGTAGAAC 507
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

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Search completed: April 8, 2006, 14:02:02
 Job time : 172.1 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 551.36 Seconds
(without alignments)
2309.713 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793

Sequence: 1 MINTITPDAGNATINKYATP.....SRNGVQKGIQLISDICKIS 154

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Xgapop 10.0 , Xgapext 0.5	
Xgapop 6.0 , Xgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWB.spool/US09978274/rnat_07042006_173040_28552/arp_query.faeta.1
-DB=Published.Applications.NA.Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blonum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MTELEN=0 -MAXLEN=2000000000 -HOST=abbs03h
-USER=US09978274.CCEN_1.1.2039 -RUNAT=07042006_173040_28552 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_NA.Main.*

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	465	3	US-09-978-274A-5
2	793	100.0	792	3	US-09-978-274A-3
3	793	100.0	1092	3	US-09-978-274A-19
4	788	99.4	945	3	US-09-978-274A-1
5	596	75.2	1379	3	US-09-978-274A-30
6	596	75.2	1379	10	US-11-106-187-1
7	588	74.1	1368	3	US-09-978-274A-31

8	584.5	73.7	1376	8	US-10-467-009-1	Sequence 1, Appl
9	261	32.9	934	3	US-09-978-274A-32	Sequence 32, Appl
10	261	32.8	934	10	US-11-106-187-20	Sequence 3, Appl
11	260	32.8	835	10	US-11-106-187-20	Sequence 20, Appl
12	196.5	24.8	765	3	US-09-792-793A-66	Sequence 66, Appl
13	196.5	24.8	765	6	US-10-375-209A-66	Sequence 66, Appl
14	196.5	24.8	984	3	US-09-792-793A-60	Sequence 60, Appl
15	196.5	24.8	984	6	US-10-375-209A-60	Sequence 60, Appl
16	196.5	24.8	993	3	US-09-792-793A-63	Sequence 63, Appl
17	196.5	24.8	993	3	US-10-375-209A-63	Sequence 63, Appl
18	196.5	24.8	999	3	US-09-792-793A-54	Sequence 54, Appl
19	196.5	24.8	999	3	US-09-792-793A-57	Sequence 57, Appl
20	196.5	24.8	999	6	US-10-375-209A-54	Sequence 54, Appl
21	196.5	24.8	935	6	US-10-375-209A-57	Sequence 57, Appl
22	191.5	24.1	804	3	US-10-861-257-38	Sequence 4, Appl
23	190.5	24.0	804	3	US-10-861-257-38	Sequence 4, Appl
24	190.5	24.0	804	6	US-10-189-360-23	Sequence 23, Appl
25	188.5	23.8	765	3	US-09-861-257-23	Sequence 23, Appl
26	188.5	23.8	765	6	US-10-189-360-79	Sequence 79, Appl
27	188.5	23.8	1230	6	US-10-189-360-53	Sequence 53, Appl
28	188.5	23.8	1233	3	US-09-861-257-24	Sequence 24, Appl
29	188.5	23.8	1233	6	US-10-189-360-80	Sequence 80, Appl
30	188.5	23.8	1251	3	US-09-861-257-77	Sequence 77, Appl
31	188.5	23.8	1251	6	US-10-189-360-74	Sequence 74, Appl
32	188.5	23.8	1260	3	US-09-861-257-75	Sequence 75, Appl
33	188.5	23.8	1266	6	US-10-189-360-72	Sequence 72, Appl
34	188.5	23.8	1266	3	US-09-861-257-78	Sequence 78, Appl
35	188.5	23.8	1266	6	US-10-189-360-75	Sequence 75, Appl
36	188.5	23.8	1269	3	US-09-861-257-81	Sequence 81, Appl
37	188.5	23.8	1269	6	US-10-189-360-78	Sequence 78, Appl
38	188.5	23.8	1275	3	US-09-861-257-76	Sequence 76, Appl
39	188.5	23.8	1275	6	US-10-189-360-73	Sequence 73, Appl
40	188.5	23.8	1299	3	US-09-861-257-80	Sequence 80, Appl
41	188.5	23.8	1299	6	US-10-189-360-77	Sequence 77, Appl
42	188.5	23.8	1320	3	US-09-861-257-79	Sequence 79, Appl
43	188.5	23.8	1320	6	US-10-189-360-76	Sequence 76, Appl
44	184.5	23.3	804	3	US-09-861-257-35	Sequence 35, Appl
45	184.5	23.3	804	3	US-09-861-257-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-978-274A-5
Sequence 5, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Ackinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 465
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-5

Alignment Scores:

Pred. No.: 6,78e-99
Score: 793.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 465
Matches: 154
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-978-274A-5 (1-465)

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QY 1 MetIleasanthrilethPheaspAlaGlyAsnaIatThrIleasnyTyraIatThrPhe 20
DB 1 ATGATTAATACGATCAGCTTGTGATGCTGGAATCCCATTAACAATATGCCACTTT 60
QY 21 MetGluserieuarganginalalyaspprolyleuIysCySTyrgIyIlePromet 40
DB 61 ATGGAATCTCTGCTATCAAGCGAAGATCCAAAATCTTAATGCGATGCCAATG 120
QY 41 LeuProaspThrAsnserThrProlyTyrlleuValIysleuIngIyAlaAsnleu 60
DB 121 CTACCTGATACATAATTCGACCCCTTAAGTACTTATGTAAGCTCCAAAGGCGAACTTA 180
QY 61 LysThrIleThreuleuMetleuargAsnaAsnleuTyraValMetGlyTyrsereAspPro 80
DB 181 AAAACCATTAACATAAGTGCAGAGCGAAATTAACGTAATGGGCTATTCGATCCC 240
QY 81 PheAsnGlyAsnlyscYsarGlyrHisIlePheAsnaAspIleThrsertHrgIuaIrgThr 100
DB 241 TTCATATGCAATAAGTCTGCTACATATATTATATATTAACACACCGAAGCGACT 300
QY 101 AspValGluAsnthrileuCysserSerSerSerSerArgValAlaMetSerIleAsnTy 120
DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTCTGCTGCTGCAATGTCATTAACTAC 360
QY 121 AsnSerleuTyxProThrmecGluIyAlaGluValAsnserArgAsnIngIyAla 140
DB 361 AATAGCTTATATCCGACCAATGAAAGAAAGCAAGTAATCAATAATCAAGTCCAA 420
QY 141 LeuGlyIleGlnIleleuSerSerAspIleGlyIyIleSer 154
DB 421 TTGGGAATTCAAATACTCAGCAGATGACATGTAAGTAATCTCT 462
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RESULT 2

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US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-3
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Alignment Scores:

Pred. No.:	1,578-98	Length:	792
Score:	793.00	Matches:	154
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-978-274A-6 (1-154) x US-09-978-274A-3 (1-792)

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QY 1 MetIleasanthrilethPheaspAlaGlyAsnaIatThrIleasnyTyraIatThrPhe 20
DB 1 ATGATTAATACGATCAGCTTGTGATGCTGGAATCCCATTAACAATATGCCACTTT 60
QY 21 MetGluserieuarganginalalyaspprolyleuIysCySTyrgIyIlePromet 40
DB 121 CTACCTGATACATAATTCGACCCCTTAAGTACTTATGTAAGCTCCAAAGGCGAACTTA 180
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DB 61 ATGGAATCTCTGCTATCAAGCGAAGATCCAAAATCTTAATGCGATGCCAATG 120

QY 41 LeuProaspThrAsnserThrProlyTyrlleuValIysleuIngIyAlaAsnleu 60

DB 121 CTACCTGATACATAATTCGACCCCTTAAGTACTTATGTAAGCTCCAAAGGCGAACTTA 180

QY 61 LysThrIleThreuleuMetleuargAsnaAsnleuTyraValMetGlyTyrsereAspPro 80

DB 181 AAAACCATTAACATAAGTGCAGAGCGAAATTAACGTAATGGGCTATTCGATCCC 240

QY 81 PheAsnGlyAsnlyscYsarGlyrHisIlePheAsnaAspIleThrsertHrgIuaIrgThr 100

DB 241 TTCATATGCAATAAGTCTGCTACATATATTATATATTAACACACCGAAGCGACT 300

QY 101 AspValGluAsnthrileuCysserSerSerSerSerArgValAlaMetSerIleAsnTy 120

DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTCTGCTGCTGCAATGTCATTAACTAC 360

QY 121 AsnSerleuTyxProThrmecGluIyAlaGluValAsnserArgAsnIngIyAla 140

DB 361 AATAGCTTATATCCGACCAATGAAAGCAAGTAATCAATAATCAAGTCCAA 420

QY 141 LeuGlyIleGlnIleleuSerSerAspIleGlyIyIleSer 154

DB 421 TTGGGAATTCAAATACTCAGCAGTGCATGTAAGTAATCTCT 462

RESULT 3

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US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19
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Alignment Scores:

Pred. No.:	2,68-98	Length:	1092
Score:	793.00	Matches:	154
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-978-274A-6 (1-154) x US-09-978-274A-19 (1-1092)

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DB 1 ATGATTAATACGATCAGCTTGTGATGCTGGAATCCCATTAACAATATGCCACTTT 60
QY 21 MetGluserieuarganginalalyaspprolyleuIysCySTyrgIyIlePromet 40
DB 61 ATGGAATCTCTGCTATCAAGCGAAGATCCAAAATCTTAATGCGATGCCAATG 120
QY 41 LeuProaspThrAsnserThrProlyTyrlleuValIysleuIngIyAlaAsnleu 60
DB 121 CTACCTGATACATAATTCGACCCCTTAAGTACTTATGTAAGCTCCAAAGGCGAACTTA 180
```

QY 61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
DB 181 AAAACCATTAACATGCTGAGAGAAATTAATTATCGTAGGGCTATTCTGATCCC 240
QY 81 PheAsnGlyAsnLeuYsCyAsnGlyTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGCGCAATAGTGTCTTACCATATTAATGATTAATACAGACGCAAGCACT 300
QY 101 AspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyr 120
DB 301 GATGGAGAAATCTCTTGTCTCAAGTCTGATCTCTGTTGCAATGCTCAATTAACATC 360
QY 121 AsnSerLeuTyrProThrMetGluLeuYsValGluValAsnSerArgAsnGlnValGln 140
DB 361 AATGCTTATATCCGACCATGGAAGAAAGCAAGAACTCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerSerSerSerIleGlyIleSer 154
DB 421 TTGGGAATTCAAATATCTCAGCAGTCACTGGAAAAATCTCT 462

RESULT 4

US-09-978-274A-1
Sequence 1, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIORITY FILING DATE: 2001-10-15
PRIORITY FILING DATE: 20025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 945
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:

Pred. No.: 1.01e-97 Length: 945
Score: 788.00 Matches: 153
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.4% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-978-274A-1 (1-945)

QY 2 ILeAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyrAlaThrPheMet 21
DB 73 ATAAATACGATCACTTTGATGCTGGAATCCACCATTAACAATATGCACTTTATG 132
QY 22 GluSerLeuArgAsnGlnAlaLeuAspProLysLeuYsCyTyrGlyIleProMetLeu 41
DB 133 GAACTCTCTTCGTAATCAAGCGAAAGATCCAAATCAAAATGCTATGCGATCCATGCTA 192
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValIleAsnGlnGlyValAsnLeuYs 61
DB 193 CCGATATCAATATGACCCCTTAAGTACTTATTTAGTCCAGAGGTCGCAAACTTAA 252
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 253 ACCATTAACATTAATGCTGAGAGAAATTAATTATACGATGGGCTATTCGATCCCTTC 312
QY 82 AsnGlyAsnLeuYsCyAsnGlyTyrHisIlePheAsnAspIleThrSerThrGluArgThr 101
DB 313 AATGGCAATAGTGTCTTACCATATTAATGATTAATCAAGACCGAAGCACTGAT 372

QY 102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 373 GTGAGAAATCTCTTGTCTCAAGTCTGATCTCGTTCGCAATGCTCAATTAACAT 432
QY 122 SerLeuTyrProThrMetGluLeuYsValGluValAsnSerArgAsnGlnValGln 141
DB 433 AGCTTATATCCGACCATGGAAGAAAGCAAGATTAATCAAGAAATCAAGTCCAATG 492
QY 142 GlyIleGlnIleLeuSerSerSerSerSerIleGlyIleSer 154
DB 493 GGAATTCAAATATCTCAGCAGTCACTGGAAAAATCTCT 531

RESULT 5

US-09-978-274A-30
Sequence 30, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIORITY FILING DATE: 2001-10-15
PRIORITY FILING DATE: 20025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1379
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:

Pred. No.: 5.43e-71 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-978-274A-30 (1-1379)

QY 2 ILeAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyrAlaThrPheMet 21
DB 291 GTGAATACATCATCTCAATGTTGGAAGTACCACTTGAATACGACATTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLeuAspProLysLeuYsCyTyrGlyIleProMetLeu 41
DB 351 AATGATCTTGTATATGAGGAAAGATCCAAATTAAGTATGGAATCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValIleAsnGlnGlyValAsnLeuYs 61
DB 411 CCCAATCAAAATCAAAATCAAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATTA 470
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACATCACTAATATGCTGAGACCAAAATTTGATGATGATGATTTCTGATCCCTT 530
QY 82 AsnGlyAsnLeuYsCyAsnGlyTyrHisIlePheAsnAspIleThrSerThrGluArgThr 101
DB 531 GAAACCAATTAAGTGTCTTACCAATCTTAATGATTAATCAGATACGCAAGAT 590
QY 102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTGAGATCACTCTTTGTCGCAAAATGCAATTCGATTAATGATTAATCAAACTTGA 650
QY 122 SerLeuTyrProThrMetGluLeuYsValGluValAsnSerArgAsnGlnValGln 141
DB 651 AGTCATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAAATCAAGTCAAGTCACTG 710


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; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467,009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

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Alignment Scores:
Pred. No.: 2,08e-69 Length: 1376
Score: 584.50 Matches: 110
Percent Similarity: 86.3% Conservative: 22
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 73.7% Indels: 1
Gaps: 1

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US-09-978-274A-6 (1-154) x US-10-467-009-1 (1-1376)
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Oy 2 ILeaThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuYrAlaThrPheMet 21
Db 291 GGNAAATCAATCACTTACAAATGTTGAAAGTACCAACATTAACAAATGACCACTTTCTG 350
Oy 22 GluSerLeuArgAngInAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
Db 351 AATGATCTGCTGTAATGAAGCAAGAAATCAAGTTAAATCTAATGAAATCCAAATGCTG 410
Oy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAAAATACAAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATTAATAA 470
Oy 62 ThrIleThrLeuMetLeuArgAspAsnLeuYrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTTAAGCTGAAGCAAGAAATGTAATGATGAGGTATTCGATCCCTTT 530
Oy 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAACCAATTAATTCGTTACCAATATCTTAATGATATCTAGATCAAGTCAAGCAAGAT 590
Oy 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 591 GTACAGACTACTCTTTGCG---CCAGCCCAATTCGTTGTTAGTAAACATTAACCTTGAT 647
Oy 122 SerLeuYrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 648 AGTGAATATCCAAATGGAATCAAAAGCGGAATGAATGAATGAATGAATGAGTCAACTG 707
Oy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 708 GGAATTCAAATACCTGCACAGTAATATTCGAAGAATTTCT 746

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RESULT 9

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US-09-978-274A-32
; Sequence 32, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-32

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Alignment Scores:
Pred. No.: 4.51e-25 Length: 934
Score: 261.00 Matches: 63
Percent Similarity: 54.2% Conservative: 20
Best Local Similarity: 41.2% Mismatches: 60
Query Match: 32.9% Indels: 10
Gaps: 5

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US-09-978-274A-6 (1-154) x US-09-978-274A-32 (1-934)
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Oy 3 AsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuYrAlaThrPheMetGlu 22
Db 73 TCMAACATTAAGTCTTGAACGTTGAGAAATCCACACCAAACTTAAATTTCTACT 132
Oy 23 SerLeuArgAngInAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
Db 133 AGTTGGAGAGAGCTGTGAAGAACAAGAAATTCATGCAATGGAATGAATGAATGACCA 192
Oy 43 AspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuYrThr 62
Db 193 ACCCTCACTGAACCAACCAAGTATGTTGTTGACTCAAAATTCGATCT---GGAACA 249
Oy 63 ILeThrLeuMetLeuArgAspAsnLeuYrValMetGlyTyrSerAspProPheAsn 82
Db 250 TTCATTAATCAATCAAGAAAGGAAATTAATTTGAGGCTATTCGATTAATTAAT 309
Oy 83 GlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
Db 310 GGA---AAATGCTGTAATGCAATCTTCAAGAT-----TCGAATCCGATGCC 354
Oy 103 GluAsnThrLeuCysSerSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
Db 355 CAAGAGACCTTTGCCCCGGGGAACAAGCAAGCTGCACTGCAATTAATATCCCTAT 414
Oy 121 AsnSerLeuYrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
Db 415 GAAAAGATTAACAAGGATGGAATCAAAAGGT-----GGGCTGAATTAATTAAGG 468
Oy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIle 153
Db 469 TTAGAAAGATTAACACTCAAGATCGAATGCGTAAATC 507

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RESULT 10

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US-11-106-187-3
; Sequence 3, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: WANG, PINGER
; APPLICANT: NIEGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana

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FEATURE:	NAME/KEY:	mat_peptide
LOCATION:	(76)..(930)	
FEATURE:	NAME/KEY:	CDS
LOCATION:	(1)..(930)	
US-11-106-187-3		
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Prod. No.:	4,51e-25	Length: 934
Score:	261.00	Matches: 63
Percent Similarity:	54.2%	Conservative: 20
Best local Similarity:	41.2%	Mismatches: 60
Query Match:	32.9%	Indels: 10
DB:	10	Gaps: 5
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Db	133 AGTTGGGAGAACCTGTGAAGAACAAGAAATTGACATGCATGGATGATATATGCGCACA 192	
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Db	193 ACCCTCATCGAACACCCAAATGATGTGGTTGACCTCAATTCGATCT--GGAACA 249	
Qy	63 IleThrIleuMetLeuArgAsnAsnLeuTYRValMetGlyTYRserAspProPheAsn 82	
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Qy	83 GlyAsnLysCybArgTYRHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102	
Db	310 GGA---AAATGTGCTATCGATCTTCAAGGAT-----TCAGAAATCCGATGCC 354	
Qy	103 GluAsnThrIleuCybSerSerSerSerSerArg-----ValAlaMetSerIleAsnTYR 120	
Db	355 CAAGAGACCGTTGGCCCGGGGACAAAGCAAGCCCTGCATCAGATATATATCCCTAT 414	
Qy	121 AsnSerLeuTYRProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGln 140	
Db	415 GAAAGAGTTTACAAAGGATGGATCAAGGGGT-----GGGGCTAGAACTTAATTTAGGG 466	
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Sequence 20, Application US/11106187		
Publication No. US20050183162A1		
GENERAL INFORMATION:		
APPLICANT: TUNER, NILGUN E.		
APPLICANT: WANG, PINGER		
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN		
FILE REFERENCE: OCIRS 3.9-060 CONT		
CURRENT APPLICATION NUMBER: US/11/106,187		
CURRENT FILING DATE: 2005-04-14		
PRIOR APPLICATION NUMBER: US/09/721,047		
PRIOR FILING DATE: 2000-11-22		
PRIOR APPLICATION NUMBER: PCT/US99/11301		
PRIOR FILING DATE: 1999-05-21		
PRIOR APPLICATION NUMBER: 60/086,374		
PRIOR FILING DATE: 1998-05-22		
NUMBER OF SEQ ID NOS: 21		
SOFTWARE: PatentIn Ver. 3.3		
SEQ ID NO 20		

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1 LENGTH: 855
2 TYPE: DNA
3 ORGANISM: Phytolacca americana
4 FEATURE:
5 NAME/KEY: CDS
6 LOCATION: (1) .. (855)
7 US-11-106-187-20
8
9 Alignment Scores:
10 Pred. NO.: 5.39e-25 Length: 855
11 Score: 260.00 Matches: 63
12 Percent Similarity: 54.3% Conservative: 19
13 Best Local Similarity: 41.7% Mismatches: 59
14 Query Match: 32.8% Indels: 10
15 DB: 10 Gaps: 5
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17 US-09-978-274A-6 (1-154) x US-11-106-187-20 (1-855)
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22 QY 25 ArgAnGlnAlaIalYsApProlYsLeuYsCySTYGLYIIEPromeLLeuProAspThr 44
23 Db 64 CGAAGAGCTGTGAAGAACAAGAAATTCACATGCCAGATGATATATATGCGCACCAACCTTC 123
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25 QY 45 AsnSerThrProLYsTYrLeuLeuValLYsLeuGlnGlyAlaAsnLeuYsThrIIEthr 64
26 Db 124 ACGAACAACCCCAAGTATGTGTTGACTTCATAATTCGATCT---GGAACATTCA 180
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28 QY 65 LeuMeLLeuArgArGAnbnLeuTYrValMeGLYTYrSerAsPProPheAnGlyAen 84
29 Db 181 TTGACATTCAGAAAGGGGAAACTTATATTTGGAGGGCTATTCGACATTTACATGGA--- 237
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31 QY 85 LysCYsArGTyRhIstIIEPheAsnApIIEthrSerThrGluArgThrAspValGluAen 104
32 Db 238 AAATGTCTTATCGATCTTCAAGAT-----TCGAATTCGATGCCCAAGG 285
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34 QY 105 ThrLeuCYsSerSerSerSerSerArg-----ValAlaMetSerIIEAsnTYrAsnSer 122
35 Db 286 ACCGTTTGGCCCGGGACAAGCAAGCCTGGCACTCAGATAATATATCCCTATGAAAG 345
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37 QY 123 LeuTYrProthMetGluLYsIysAlaGluValAsnSerArgAnGlnValGlnLeuGly 142
38 Db 346 AGTTACAAAGGGATGGAATCAAGGGGT-----GGGGCTAGAACTTAATTAAGGTTAGGA 399
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40 QY 143 IIEGlnIIEuSerSerAspIIEGLYsIle 153
41 Db 400 AAGATAACACTCAAGAGTCGAATCGGTAAATC 432
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43 RESULT 12
44 US-09-792-793A-66
45 Sequence 66, Application US/09792793A
46 Patent No. US20020168370A1
47 GENERAL INFORMATION:
48 APPLICANT: McDonald, John R.
49 APPLICANT: Cogging, Philip
50 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
51 FILE REFERENCE: 25020-601D OTHER INFLAMMATORY CONDITIONS AND DISORDERS
52 CURRENT APPLICATION NUMBER: US/09/792, 793A
53 NUMBER OF SEQ ID NOS: 93
54 SOFTWARE: PatentIn Ver. 2.0
55 SEQ ID NO 66
56 LENGTH: 765
57 TYPE: DNA
58 ORGANISM: Artificial Sequence
59 FEATURE:
60 OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
61 OTHER INFORMATION: Methionine-Saporin fusion protein
62 NAME/KEY: CDS
63 LOCATION: (1) .. (765)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-09-978-274A-6

Perfect score: 793

Sequence: 1 MINTTFDAGNATINKATP.....SRNOVGCIQLISDGIKIS 154

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:
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2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	112	14.1	1855	8	US-10-893-584-5	Sequence 5, Appl
5	112	14.1	1855	8	US-10-893-584-7	Sequence 7, Appl
6	112	14.1	1855	8	US-10-893-584-9	Sequence 9, Appl
7	112	14.1	1855	8	US-10-893-584-13	Sequence 13, Appl
8	112	14.1	1855	8	US-10-893-584-15	Sequence 15, Appl
9	112	14.1	1855	8	US-10-893-584-17	Sequence 17, Appl
10	112	14.1	1855	8	US-10-893-584-19	Sequence 19, Appl
11	112	14.1	1855	8	US-10-893-584-21	Sequence 21, Appl
12	112	14.1	1855	8	US-10-893-584-23	Sequence 23, Appl
13	112	14.1	1855	8	US-10-893-584-25	Sequence 25, Appl
14	112	14.1	1855	8	US-10-893-584-27	Sequence 27, Appl
15	112	14.1	1855	8	US-10-893-584-29	Sequence 29, Appl
16	112	14.1	1855	8	US-10-893-584-31	Sequence 31, Appl
17	112	14.1	1855	8	US-10-893-584-33	Sequence 33, Appl
18	112	14.1	1855	8	US-10-893-584-35	Sequence 35, Appl
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20	112	14.1	1855	8	US-10-893-584-39	Sequence 39, Appl
21	112	14.1	1855	8	US-10-893-584-41	Sequence 41, Appl
22	112	14.1	1855	8	US-10-893-584-43	Sequence 43, Appl
23	112	14.1	1855	8	US-10-893-584-45	Sequence 45, Appl
24	112	14.1	1855	8	US-10-893-584-47	Sequence 47, Appl
25	112	14.1	1855	8	US-10-893-584-49	Sequence 49, Appl
26	112	14.1	1855	8	US-10-893-584-51	Sequence 51, Appl
27	112	14.1	1855	8	US-10-893-584-53	Sequence 53, Appl
28	112	14.1	1855	8	US-10-893-584-55	Sequence 55, Appl
29	112	14.1	1855	8	US-10-893-584-57	Sequence 57, Appl
30	112	14.1	1855	8	US-10-893-584-59	Sequence 59, Appl
31	112	14.1	1855	8	US-10-893-584-61	Sequence 61, Appl
32	112	14.1	1855	8	US-10-893-584-63	Sequence 63, Appl
33	112	14.1	1855	8	US-10-893-584-65	Sequence 65, Appl
34	112	14.1	1855	8	US-10-893-584-67	Sequence 67, Appl
35	112	14.1	1855	8	US-10-893-584-69	Sequence 69, Appl
36	112	14.1	1855	8	US-10-893-584-71	Sequence 71, Appl
37	112	14.1	1855	8	US-10-893-584-73	Sequence 73, Appl
38	112	14.1	1855	8	US-10-893-584-75	Sequence 75, Appl
39	112	14.1	1855	8	US-10-893-584-77	Sequence 77, Appl
40	112	14.1	1855	8	US-10-893-584-79	Sequence 79, Appl
41	112	14.1	1855	8	US-10-893-584-81	Sequence 81, Appl
42	112	14.1	1855	8	US-10-893-584-83	Sequence 83, Appl
43	112	14.1	1855	8	US-10-893-584-85	Sequence 85, Appl
44	112	14.1	1855	8	US-10-893-584-87	Sequence 87, Appl
45	112	14.1	1855	8	US-10-893-584-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NINGUN E.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OR INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
FILE REFERENCE: OCT93 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
PRIOR APPLICATION NUMBER: 2004-12-13
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 1360
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURE:
NAME/KEY: CDS
LOCATION: (207)..(1145)
US-11-010-795-19
Alignment Scores:

Pred. No.: 2,73e-61 Length: 1360
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 DB: 14 Gaps: 0

US-09-978-274A-6 (1-154) x US-11-010-795-19 (1-1360)

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QY 22 GluSerleuArgasnGlnAlaIysAspProlyseuLeuValylseuGlnGlyAlaMetleu 41
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Db 333 AATGATCTTGTAATGAAAGGAAAGATCAAGTTTAAAGCTATGGAATACCAATGCTG 392
QY 42 ProAspThrAsnSerThrProlystryleuLeuValylseuGlnGlyAlaMetleu 61
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Db 393 CCCAATACAAATCAAAATCCAAAGTACGTGTGAGCTCCAAAGTTCAAAATAAAAA 452
QY 62 ThrIleuMetleuArgAsnAsnleuValylseuGlnGlyTyrSerAspProPhe 81
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Db 453 ACCATGACCTAATGCTGAACGAAACAAATTTGATGTGATGCTTATTCATCCCTTT 512
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QY 122 SerleuTyrProThrMetGluYslyAlaGluValAsnSerArgasnGlnValGlnleu 141
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RESULT 2

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US-11-010-795-21
; Sequence 21, Application US/11010795
; Publication No. US2006005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NIGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: COINS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 21
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-11-010-795-21

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Alignment Scores:

Pred. No.: 3.15e-21 Length: 934
 Score: 261.00 Matches: 63
 Percent Similarity: 54.2% Conservative: 20
 Best Local Similarity: 41.2% Mismatches: 60
 Query Match: 32.9% Indels: 10
 DB: 14 Gaps: 5

US-09-978-274A-6 (1-154) x US-11-010-795-21 (1-934)

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QY 43 AspThrAsnSerThrProlystryleuLeuValylseuGlnGlyAlaMetleuTyr 62
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Db 193 ACCCTCACTGAACAAACCAAGTATGTTGTTGACCTCAAAATTCGAATCT--GGAACA 249
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Db 250 TTCACATTTAGCAATCAAGAGGGAACCTTATTTGAGGCTTATTTCACTTACAT 309
QY 83 GlyAsnlyscYsaRgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
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Db 310 GGA--AAATGCTTATCGATCTTCAAGAT-----TCAGATCCGATGCC 354
QY 103 GluAsnThrleuCyseSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
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Db 355 CAAGAGACCGTTTGCCCGGAGCAAAAGCAAGCTGCGACTCAGAAATATATCCCTTAT 414
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RESULT 3

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US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adamir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cathepsin B linker regions of pAB-214
US-10-893-584-3

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Alignment Scores:

Pred. No.: 0.00613 Length: 1855
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 Best Local Similarity: 26.0% Mismatches: 53
 Query Match: 14.1% Indels: 38
 DB: 8 Gaps: 7

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US-09-978-274A-6 (1-154) x US-10-893-584-7 (1-1855)

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 QY 45 AanserThrPro-----LysTyrLeuLeuValLysLeuGlnGlyValAasnLeuLys 61
 Db 256 GTTGGTTGGCCATATAACCAACGCTTATTTAGTTAGTGAACCTCAAAATCATGACAGACTT 315
 QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
 Db 316 TCTGTACATTAAGCCCTGAGTGTCAACAAATGATATGTGTGGCTACCGT----- 366
 QY 82 AangLYAsnLysCysArgTyr----- 88
 Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTGACATCAGAAAGATGCAAGACATCACT 426
 QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAasnThrLeuCysSer 108
 Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
 QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
 Db 451 -----CGATATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGA 492
 QY 129 LysLYsAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
 Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531

RESULT 8
 US-10-893-584-15
 ; Sequence 15, Application US/10893584
 ; Publication No. US20050272048A1

GENERAL INFORMATION:
 APPLICANT: Borgford, Thor
 APPLICANT: Braun, Curtis
 APPLICANT: Purac, Admr
 APPLICANT: Stoll, Dominik
 TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer.
 TITLE OF INVENTION: Viral or Parasitic Infections
 FILE REFERENCE: 10447-025
 CURRENT APPLICATION NUMBER: US/10/893,584
 PRIOR FILING DATE: 2004-07-19
 PRIOR APPLICATION NUMBER: US 09/551,151
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: US 09/403,752
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: US 10/089,058
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 274
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 15
 LENGTH: 1855
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pAP-226 insert
 US-10-893-584-15

Alignment Scores:
 Pred. No.: 0.00613 Length: 1855
 Score: 112.00 Matches: 40
 Percent Similarity: 40.9% Conservative: 23
 Best Local Similarity: 26.0% Mismatches: 53
 Query Match: 14.1% Indels: 38
 DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-15 (1-1855)

QY 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
 Db 136 ATAACTTTACCAACAGCGGCTGCTGACATGTCAGAAAGCTTATCATAGAGCTGTT 195

QY 25 ArgAanglnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
 Db 196 CGCGGTCGTTTAAACAACGTGAGCTGATGTGAGACATGATATACAGTGTGGCCAAACAGA 255
 QY 45 AanserThrPro-----LysTyrLeuLeuValLysLeuGlnGlyValAasnLeuLys 61
 Db 256 GTTGGTTGGCCATATAACCAACGCTTATTTAGTTAGTGAACCTCAAAATCATGACAGACTT 315
 QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
 Db 316 TCTGTACATTAAGCCCTGAGTGTCAACAAATGATATGTGTGGCTACCGT----- 366
 QY 82 AangLYAsnLysCysArgTyr----- 88
 Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTGACATCAGAAAGATGCAAGACATCACT 426
 QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAasnThrLeuCysSer 108
 Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
 QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
 Db 451 -----CGATATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGA 492
 QY 129 LysLYsAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
 Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531

RESULT 9
 US-10-893-584-17
 ; Sequence 17, Application US/10893584
 ; Publication No. US20050272048A1

GENERAL INFORMATION:
 APPLICANT: Borgford, Thor
 APPLICANT: Braun, Curtis
 APPLICANT: Purac, Admr
 APPLICANT: Stoll, Dominik
 TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer.
 TITLE OF INVENTION: Viral or Parasitic Infections
 FILE REFERENCE: 10447-025
 CURRENT APPLICATION NUMBER: US/10/893,584
 PRIOR FILING DATE: 2004-07-19
 PRIOR APPLICATION NUMBER: US 09/551,151
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: US 09/403,752
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: US 10/089,058
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 274
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 17
 LENGTH: 1855
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pAP-228 insert
 US-10-893-584-17

Alignment Scores:
 Pred. No.: 0.00613 Length: 1855
 Score: 112.00 Matches: 40
 Percent Similarity: 40.9% Conservative: 23
 Best Local Similarity: 26.0% Mismatches: 53
 Query Match: 14.1% Indels: 38
 DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-17 (1-1855)

QY 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
 Db 136 ATAACTTTACCAACAGCGGCTGCTGACATGTCAGAAAGCTTATCATAGAGCTGTT 195

```
QY 25 ArgAsnGlnAlaIaIysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
|||
|||
|||
Db 196 CGGGGTCGTTTAAACAAGTGAAGTGAAGATATACCATGTTGCCAAGACGA 255
|||
|||
|||
QY 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
|||
|||
|||
Db 256 GTTGGTTGGCTTAAACCAACGAGTTATTTAGTTAACTTCMAATCATGCAAGACTT 315
|||
|||
|||
QY 62 ThrIleThreuleMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
|||
|||
|||
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGCATATGTGTGGCTACCGT----- 366
|||
|||
|||
QY 82 AsnGlyAsnLysCysArgTyr----- 88
|||
|||
|||
Db 367 GCTGGAATAGCGCATATTTCTTTCATCTGACATCAGAAAGATGCAAGCAATCACT 426
|||
|||
|||
QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySer 108
|||
|||
|||
Db 427 CATCTTTTC-----ACTGATTTCAAAAT----- 450
|||
|||
|||
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
|||
|||
|||
Db 451 -----CGATATACATTGCGCTTGGTGTAAT-----TATGATAGACTTGAA 492
|||
|||
|||
QY 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
|||
|||
|||
Db 493 CAACTTGCTGCT---AATCTGAGAGAAATATCGAGTTGGGA 531
|||
|||
|||

RESULT 10
US-10-893-584-19
; Sequence 19, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-230 insert
US-10-893-584-19

Alignment Scores:
Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-19 (1-1855)
QY 5 IleThPheAspAlaGluValAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
|||
|||
|||
Db 136 ATAACTTTACCAACAGGGGTGCACTGTGCAAAAGCTACCAAACTTTATCAGAGCTGTT 195
|||
|||
|||
QY 25 ArgAsnGlnAlaIaIysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
|||
|||
|||
```

```
Db 196 CGGGGTCGTTTAAACAAGTGAAGTGAAGATATACCATGTTGCCAAGACGA 255
|||
|||
|||
QY 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
|||
|||
|||
Db 256 GTTGGTTGGCTTAAACCAACGAGTTATTTAGTTAACTTCMAATCATGCAAGACTT 315
|||
|||
|||
QY 62 ThrIleThreuleMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
|||
|||
|||
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGCATATGTGTGGCTACCGT----- 366
|||
|||
|||
QY 82 AsnGlyAsnLysCysArgTyr----- 88
|||
|||
|||
Db 367 GCTGGAATAGCGCATATTTCTTTCATCTGACATCAGAAAGATGCAAGCAATCACT 426
|||
|||
|||
QY 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySer 108
|||
|||
|||
Db 427 CATCTTTTC-----ACTGATTTCAAAAT----- 450
|||
|||
|||
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
|||
|||
|||
Db 451 -----CGATATACATTGCGCTTGGTGTAAT-----TATGATAGACTTGAA 492
|||
|||
|||
QY 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
|||
|||
|||
Db 493 CAACTTGCTGCT---AATCTGAGAGAAATATCGAGTTGGGA 531
|||
|||
|||

RESULT 11
US-10-893-584-21
; Sequence 21, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-232 insert
US-10-893-584-21

Alignment Scores:
Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-21 (1-1855)
QY 5 IleThPheAspAlaGluValAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
|||
|||
|||
Db 136 ATAACTTTACCAACAGGGGTGCACTGTGCAAAAGCTACCAAACTTTATCAGAGCTGTT 195
|||
|||
|||
QY 25 ArgAsnGlnAlaIaIysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
|||
|||
|||
```



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Db 196 CCGCGTCTTAAACAACGAGCTGATGTGACATGATATACAGTGTTCGCAACAGA 255
Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAenLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGAGGTTATTTAGTTGAAGCTCTCAATCATGCAGAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAenAenLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AenGlyAenLysCysArgTyr----- 88
Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTCGACAAATCAGAAAGATCAGAAACATCACT 426
Qy 89 HisIlePheAenAspIleThrSerThrGluArgThrAspValGluAenThrLeuCySer 108
Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAenTyrAenSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGTGTGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysIysAlaGluValAenSerArgAenGlnValGlnLeuGly 142
Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531
```

RESULT 12

```
US-10-893-584-23
/ Sequence 23, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Admitr
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ PRIOR FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 23
/ LENGTH: 1855
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: PAP-234 insert
US-10-893-584-23
```

Alignment Scores:

```
Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7
```

US-09-978-274a-6 (1-154) x US-10-893-584-23 (1-1855)

```
Qy 5 IlleThrPheAspAlaGlyAenAlaThrIleAenLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACCTTACCAACAGCGGTCACCTGTGCAAAAGCTACAAACTTATATCAGAGCTGT 195
Qy 25 ArgAenGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGTGTGTTAAACAACCTGAGCTGATGTGACATGATATATACAGAGTTGCCAAACAGA 255
```

```
Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAenLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGAGGTTATTTAGTTGAAGCTCTCAATCATGCAGAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAenAenLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AenGlyAenLysCysArgTyr----- 88
Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTCGACAAATCAGAAAGATCAGAAACATCACT 426
Qy 89 HisIlePheAenAspIleThrSerThrGluArgThrAspValGluAenThrLeuCySer 108
Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAenTyrAenSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGTGTGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysIysAlaGluValAenSerArgAenGlnValGlnLeuGly 142
Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531
```

RESULT 13

```
US-10-893-584-25
/ Sequence 25, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Admitr
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ PRIOR FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 25
/ LENGTH: 1855
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: PAP-236 insert
US-10-893-584-25
```

Alignment Scores:

```
Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7
```

US-09-978-274a-6 (1-154) x US-10-893-584-25 (1-1855)

```
Qy 5 IlleThrPheAspAlaGlyAenAlaThrIleAenLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACCTTACCAACAGCGGTCACCTGTGCAAAAGCTACAAACTTATATCAGAGCTGT 195
Qy 25 ArgAenGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGTGTGTTAAACAACCTGAGCTGATGTGACATGATATATACAGAGTTGCCAAACAGA 255
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Qy 45 AmsSerThirPro-----LySerThleuLeuVallybLeuGnglyAlaAmsLeuLys 61
Db 256 GTTGCTTTGCTATATAACCAACGGTTATTATTATTTAGTTGAACCTCAATCATGCAGAGCTT 315
Qy 62 ThirThleuMetLeuArgAmsLeuLysrVAlmetGlyrSerAspProche 81
Db 316 TCTGTTCATTACGCGCTGGATGTCCACCAATGCATATGTGTGGCTACCGT----- 366
Qy 82 AmsGlyAmsLysCybArgTyT----- 88
Db 367 GCTGGAAATACGCGCATATTCTTTTCATCTCGACATCAGAAATGACGAAGCATCACT 426
Qy 89 HisIlePheAmsApleThrSerThrGluArgThrAspValGluAmsThreucySer 108
Db 427 CATCTTTT-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerArgArgValAlaMetSerIleAenrVAnSerLeuTyProthrMetGlu 128
Db 451 -----CGATATACATTGCCCTTGGTGGTAAT-----TATGATGACTTGA 492
Qy 129 LysLysAlaGluValAmsSerArgAmsGluValGlnLeuGly 142
Db 493 CAATTGCTGCTG--AACTCGAGAGAAAATATCGACTTGGCA 531

RESULT 14
US-10-893-584-27
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgeford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Adamir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Rictin-like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 1855
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: pAP-238 insert
US-10-893-584-27

Alignment Scores:
Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-27 (1-1855)
Qy 5 IleThrPheAspAlaGlyAmsAlaThrIleAmsLysrVAlaThrPheMetGluSerLeu 24
Db 136 ATAAACTTTACCAACGCGGTGCACCTGTGCAGCAACAACTTATCAGAGCTGTT 195
Qy 25 ArgAmsGlnAlaLysAspProLysLeuLysCybTyrgIlePheMetLeuProAspThr 44
Db 196 CGCGCGTCGTTTAAACAATCGAGCTGATGTGAGACATGATATACCAAGCTTCCAAACGA 255
Qy 45 AmsSerThirPro-----LySerThleuLeuVallybLeuGnglyAlaAmsLeuLys 61

```

```

Db      256 GTTGTTGGCTTATTAACCAACGAGTTATTGTGAACCTTCATCATGCAGACTT   315
               |||                               ::::~::~|||:::~::~|||
Qy      62 ThrlleThrlwuetleuaAgaAganleuTyValmetglYrSerApProPhe    81
               ::::~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      316 TCGTTACATTAGCGCTGATGATCACCMAATGATNTGTGGCCGCCG-        366
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      82 AsnGlvanlyScysAgTyR-----                        88
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      367 GCTGAAATAGCCGATATTTCTTTCATCCGACATCAGAAAGATGCAGAAGCATCACT   426
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      89 HisllePheaAnbpilernserThrghuArgThrpAlguantHrleuCyser     108
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      427 CATCTTTT-----ACTGATGTTCAAAT-                    450
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      109 SerSerSerArqVAlAlameSerilleasntYrnseserleuYrProthrMetglu 128
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      451 -----CGATATACATTCGCTTTGGNGTAT-----TATGATAGACTGAA   492
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      129 LylsyalaglualanserArqAsnGlInvalGlnleugly 142
               :::~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      493 CAACCTGCTGCT--ANTCTAGAGAAAATATTCAGATTGGGA 531
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||

RESULT 15
US-10-893-584 -29
; Sequence 29, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borsford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Nadrie
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; CURRENT APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-240 Insert
US-10-893-584 -29

Alignment Scores:
Pred. No.:          0.00613           Length:          1855
Score:             112.00            Matches:         40
Percent Similarity: 40.9%            Conservative:    23
Best Local Similarity: 26.0%          Mismatches:     53
Query Match:       14.1%              Indels:        38
DB:                8                 Gaps:          7

US-09-978-274A-6 (1-154) x US-10-893-584-29 (1-1855)

Qy      5 IlleThrPheapAlagIyaenAlatrIlleaenlyTyRhlathrPhemetGluSerleu 24
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      136 ATAACTTTACACACACGGGTCCTGCTGCAAGCTAACCAACTTATACAGAGCTGT 199
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      25 ArgAsnGlnAlalayaAprprolysleuLyScetyGlylleprometleuProApThr 44
               ::::~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Db      196 CGCGGTCGTAAACAACCTGAGCTGATGTGACACATGATATACAGAGTTGCCAAACGA 255
               |||~::~|||~::~|||~::~|||~::~|||~::~|||~::~|||
Qy      45 AsnSerThrPro-----LysTryleuleuVallyleuGlnGlylaAleuLeuLy 61
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Db      256 GTTGGTTGGCTATAACCAACGCTTATTATTAGTTGAACCTCTCAATCATGCAGAGCTT 315
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Db      316 TCTGTTACATTAGCGCTGATGTCAACCATGATATGTGTGGCTACCGT----- 366
Qy      82 AsnGlyAsnLysCysArgTyr----- 88
Db      367 GCTGGAATAGCGCATATTCTTTTCATCCTGACAAATCAGAGATGACAGAACATCACT 426
Qy      89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db      427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy      109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db      451 -----CGATATACATTGCGCTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy      129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
Db      493 CAACTTGCTGGT---AATCTGAGAGAAATAATCGAGTTGGGA 531

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Search completed: April 9, 2006, 05:01:30
 Job time : 406.952 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:06:24 ; Search time 1958.59 Seconds
(without alignments)
9664.530 Million cell updates/sec

Title: US-09-978-274A-7

Perfect score: 333
Sequence: 1 atcgagagtcgattcattcc.....gaacctgcagacaactta 333

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank! :
1: gb_ba : *
2: gb_in : *
3: gb_env : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pr : *
9: gb_ro : *
10: gb_sfb : *
11: gb_sy : *
12: gb_un : *
13: gb_vl : *
14: gb_hcg : *
15: gb_pl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	6	AX427708 Sequence
2	329	98.8	945	6	AX427702 Sequence
3	328.4	98.6	792	6	AX427704 Sequence
4	325.8	97.8	1249	15	PAPAPSRIP
5	319	95.8	786	15	AB071855
6	302.4	90.8	1092	6	AX427720 Sequence
7	245.8	73.8	1052	15	AY137202
8	245.8	73.8	2472	6	E05033
9	245.8	73.8	2472	15	PTCAPAP
10	233	70.0	942	15	DI0600 P. american
11	233	70.0	942	15	AY547315 Phytolacc
12	233	70.0	1164	15	AY572976 Phytolacc
13	233	70.0	1195	6	PAPAP
14	233	70.0	1195	6	A42103 Sequence 1
15	233	70.0	1195	6	A42103 Sequence 1
16	233	70.0	1195	6	I43835 Sequence 1
17	233	70.0	1195	6	I55866 Sequence 1
18	233	70.0	1378	6	AX427732 Sequence
			1379	6	AR009535 Sequence

19	233	70.0	1379	6	AR136704
20	233	70.0	1379	6	AR136705
21	233	70.0	1379	6	AX427731
22	231.4	69.5	1114	15	AF533515
23	231.4	69.5	1179	6	AR141172
24	229.8	69.0	1164	15	AY049785
25	227.8	68.4	783	15	AB071854
26	225	67.6	951	6	A67185
27	225	67.6	2269	15	AR141331
28	223.4	67.1	882	6	A67183
29	221.8	66.6	918	6	A43003
30	221.8	66.6	918	6	A48150
31	221.8	66.6	918	6	I60482
32	221.8	66.6	918	6	I89987
33	215.4	64.7	939	15	AY327475
34	205.2	61.6	1113	15	AY071928
35	176.8	53.1	714	15	AY603352
36	176.8	53.1	714	15	AY603354
37	175.2	52.6	711	15	AF338910
38	175.2	52.6	714	15	AF603353
39	136.4	41.0	1226	15	CAANTIPR
40	136.4	41.0	1226	15	CAAV
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42	84.2	25.3	1080	15	BVBETAVUL
43	79.8	24.0	1137	15	AF228508
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45	78.8	23.7	1387	15	AP445416

ALIGNMENTS

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RESULT 1	AX427708	333 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427708	Sequence 7 from Patent WO0233107.			
DEFINITION	AX427708				
ACCESSION	AX427708				
VERSION	AX427708.1	GI:21537818			
KEYWORDS					
SOURCE					
ORGANISM	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE					
AUTHORS	Neelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 7 25-APR-2002;				
	CAMBRIDGE ADVANCED TECH (GB)				
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source	1..333	Location/Qualifiers			
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	/db_xref="taxon:3527"				
misc_feature	1..3				
misc_feature	/note="initiation codon added via PCR primer"				
misc_feature	331..333				
misc_feature	/note="stop codon added via PCR primer"				
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Query Match	100.0%; Score 333; DB 6; Length 333;				
Best Local Similarity	100.0%; Pred. No. 1.3e-79;				
Matches	333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ATGGAGTTGATTCTATCCCTGTAATAAATGAGGCTTTTCTACTAGTACCATCCAA	60			
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QY	61 ATGTTTCAAGGAGGAGGCGGATTCAGATCAATAGAAACCAAGTCAAGACTAATTTTAT	120			
DB	61 ATGTTTCAAGGAGGAGGCGGATTCAGATCAATAGAAACCAAGTCAAGACTAATTTTAT	120			
QY	121 AGAGCATTCACCTGATCCAAAGTATTAATTTGGAGGAAGTGGGCAAAATCTCT	180			

RESULT 4
PAPAPSRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS P.americana mRNA for pokeweed antiviral protein.
DEFINITION X98079.1 GI:1707648
ACCESSION PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating
VERSION protein.
KEYWORDS Phytolacca americana (American pokeweed)
SOURCE Phytolacca americana
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Poyet, J.L. and Hoeveler, A.
TITLE cDNA cloning and expression of pokeweed antiviral protein from
seeds in Escherichia coli and its inhibition of protein synthesis
in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet, J.L.
TITLE Direct Submision
DEFINITION Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16
route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES
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106..1050
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/protein_id="CA66702.1"
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/db_xref="GOA:P93444"
/db_xref="InterPro:IPR001574"
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1235
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polyA_signal
mat_peptide
sig_peptide
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Query Match 97.8%; Score 325.8; DB 15; Length 1249;
Best Local Similarity 99.4%; Pred. No. 9.4e-78;
Matches 327; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana pap2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855.1 GI:19570839
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 786)
REFERENCE Watanabe, K. and Honjo, E.
AUTHORS Direct Submision
TITLE Submitted (19-SEP-2001) Keiichi Watanabe, Saga University.
JOURNAL Department of Applied Biological Sciences; Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail:watakei@cc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)
FEATURES
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FIPDKVILBERWGISAIHNANRGAIPKPLVLDVAKGTWIVLVRDEINRDVALL
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Best Local Similarity 98.5%; Pred. No. 7.1e-76;
Matches 322; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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OY 64 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 123
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Db 520 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 579
OY 124 GCATTCTACCTTGATCCCAAGTAATTAATTGGAGAGAAATGGGGCAAAATCTTGAG 183
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Db 580 GCATTCTACCTTGATCCCAAGTAATTAATTGGAGAGAAATGGGGCAAAATCTTGAG 639
OY 184 GCATTTCACCAATGCCAAGATGGGGCTTACCCAAACCACTTGAGCTAGTGCACAA 243
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Db 640 GCATTTCACCAATGCCAAGATGGGGCTTACCCAAACCACTTGAGCTAGTGCACAA 699
OY 244 GGTACCAAGTGATAGTTCTTAGATGATGAATCAATCGTATGAGCACTCTTAAAG 303
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Db 700 GGTACCAAGTGATAGTTCTTAGATGATGAATCAATCGTATGAGCACTCTTAAAG 759
OY 304 TAGCTTAATGAACTGTGACAACT 330
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Db 760 TAGCTTAATGAACTGTGACAACT 786

RESULT 6
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.

REFERENCE
1 Neelam, A., Ackinson, H. J., Mcpherson, M. J. and Thomas, C. J. R.
  AUTHORS Plant cell death system
  TITLE Patent: WO 0233107-A 19 25-APR-2002;
  JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES
source 1..1092
    location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
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        /note="Binding site for primer p81BP"
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    misc_feature 766..806
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Best Local Similarity 99.7%; Pred. No. 2.2e-71;
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Db 463 GGAGTTGATTCATTCCTCTTAATAAAGGCTTTTCTACTGTAGCCATCCAAATG 522
OY 64 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 123
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Db 523 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 582
OY 523 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 582
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Db 124 GCATTCTACCTTGATCCCAAGTAATTAATTGGAGAGAAATGGGGCAAAATCTTGAG 183
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OY 583 GCATTCTACCTTGATCCCAAGTAATTAATTGGAGAGAAATGGGGCAAAATCTTGAG 642
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OY 244 GGTACCAAGTGATAGTTCTTAGATGATGAATCAATCGTATGAGCACTCTTAAAG 303
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Db 703 GGTACCAAGTGATAGTTCTTAGATGATGAATCAATCGTATGAGCACTCTTAAAG 762
OY 304 TACG 307
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Db 763 TACG 766

RESULT 7
AY137202 1052 bp DNA linear PLN 28-SEP-2002
LOCUS PhytoIaccia americana anti-virus protein (papn) gene, complete cds.
DEFINITION AY137202
ACCESSION AY137202
VERSION AY137202.1 GI:23343924
KEYWORDS
SOURCE PhytoIaccia americana (red stem pokeweed)
ORGANISM PhytoIaccia americana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    Caryophyllales; PhytoIaccaceae; PhytoIaccia.
    1 (bases 1 to 1052)
    Geo, B.
    Pokeweed anti-virus protein
    Unpublished
    2 (bases 1 to 1052)
    Direct Submission
    Submitted (29-JUN-2002) Department of Plant Pathology, Hunan
    Agricultural University, Fuzong District, Changsha, Hunan 410128,
    China

FEATURES
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    /gene="papn"
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Best Local Similarity 84.2%; Pred. No. 5.4e-56;
Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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OY 64 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 123
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Db 664 GTTTCAGAGGACGGGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTAATAGA 723
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QY 124 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 183
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 DB 784 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 843
 QY 244 GGTACCAAGTGAATAGTCTTAGAGTGAATGAATCAATGATGTCGACTCTTAAG 303
 DB 844 GGTACCAAGTGAATAGTCTTAGAGTGAATGAATCAATGATGTCGACTCTTAAG 903
 QY 304 TACGTTAATGGAACCTGTCAGCAACTTA 332
 DB 904 TATGTTAATGGAGCTGCAGCAACTTA 932

RESULT 8
 LOCUS B05033 2472 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding antiviral protein.
 ACCESSION B05033.1 GI:2173227
 VERSION JP 1993137580-A/1.
 KEYWORDS Phytolacca americana (American pokeweed)
 SOURCE Phytolacca americana
 ORGANISM Phytolacca americana (American pokeweed)
 BUKARYOTA; VIRIDIPLANTAE; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; 1 (bases 1 to 2472)
 Katakoka, U., Habuka, N., Masuda, O., Miyano, M. and Koiwai, A.
 NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
 Patent: JP 1993137580-A 1 01-JUN-1993;
 JAPAN TOBACCO INC
 OS Phytolacca americana
 PN JP 1993137580-A/1
 PD 01-JUN-1993
 PF 20-NOV-1991 JP 1991329672
 PI KATAOKA JIRO, HABUKA NORIYUKI, MASUDA OSAMU, MIYANO MASASHI, KOIWA AKIRA
 PC C12N15/29, C12N15/73, C12P21/02//C12N1/21, C12P21/02, C12R1.19), C12N1/21,
 PC C12R1.19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC feature is identified by similarity;
 FH Key Location/Qualifiers
 FT CAAT_signal 549..552
 FT TATA_signal 627..630
 FT sig_peptide 845..850
 FT mat_peptide 1014..1085
 FT /product:'antiviral protein'
 FT CDS 1014..1898
 FT polyA_site 2130..2135.
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 /organism="Phytolacca americana"
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ORIGIN
 Query Match 73.8%; Score 245.8; DB 6; Length 2472;
 Best Local Similarity 84.2%; Pred. No. 4.8e-56;
 Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 GGAGTTGATCTCCCTCTTAATAAAGTGGCTTTTCTTCTAGTGGTCAATCCCAATG 63
 DB 1542 GGAGTTGATCTCCCTCTTAATAAAGTGGCTTTTCTTCTAGTGGTCAATCCCAATG 1601

QY 64 GTTTCAGAGGACGCGGATTCAGATGATAGAGACCAATCAAGCTAATTTTATAGA 123
 DB 1602 GTTTCAGAGGACGCGGATTCAGATGATAGAGACCAATCAAGCTAATTTTATAGA 1661
 QY 124 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 183
 DB 1662 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 1721
 QY 184 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 243
 DB 1722 GCATTCTACCTGATCCCAAGTAATTATTGGAGAGAGTGGGCAAAATCTCGAG 1781
 QY 244 GGTACCAAGTGAATAGTCTTAGAGTGAATGAATCAATGATGTCGACTCTTAAG 303
 DB 1782 GGTACCAAGTGAATAGTCTTAGAGTGAATGAATCAATGATGTCGACTCTTAAG 1841
 QY 304 TACGTTAATGGAACCTGTCAGCAACTTA 332
 DB 1842 TATGTTAATGGAGCTGCAGCAACTTA 1870

RESULT 9
 LOCUS PTCAPAP 2472 bp DNA linear PLN 01-FEB-2000
 DEFINITION P. americana DNA for alpha-PAP (pokeweed antiviral protein), complete cds.
 ACCESSION D10600.D90537
 VERSION D10600.1 GI:218010
 KEYWORDS alpha-PAP; antiviral protein; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
 SOURCE Phytolacca americana (American pokeweed)
 ORGANISM Phytolacca americana (American pokeweed)
 BUKARYOTA; VIRIDIPLANTAE; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
 1 (bases 1 to 2472)
 Katakoka, U., Habuka, N., Masuda, O., Miyano, M. and Koiwai, A.
 Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein
 Plant Mol. Biol. 20 (5), 879-886 (1992)
 JOURNAL 1281438
 PUBMED 2 (bases 1 to 2472)
 Katakoka, J.
 DIRECT SUBMISSION
 REFERENCES Submitted (23-OCT-1991) Jiro Katakoka, Japan Tobacco Inc., Life Science Research Laboratory; 6-2 Umesaoka, Midori-ku, Yokohama, Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)
 Submitted (23-Oct-1991) to DDBJ by:
 Jiro Katakoka
 Life Science Research Laboratory
 Japan Tobacco Inc.
 6-2 Umesaoka, Midori-ku
 Yokohama 227
 Japan
 Phone: 045-972-5901
 Fax: 045-972-6205
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 source Location/Qualifiers
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2130 .2135

ORIGIN

Query Match 73.8%; Score 245.8; DB 15; Length 2472;
Best Local Similarity 84.2%; Pred. No. 4.8e-56;
Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTTTTCTTCTAGCTGATCCAAATG 63
DB 1542 GGAGTGGATTCATTCCTGTAATAAAGCTTTTCTTCTAGCTGATCCAAATG 1601
QY 64 GTTTCAGAGGAGCGGATTCAGATCATAGAGAACCAAGTCAAGCTAATTTAATGA 123
DB 1602 GTTTCAGAGGAGCGGATTCAGATCATAGAGAACCAAGTCAAGCTAATTTAATGA 1661
QY 124 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 183
DB 1662 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 1721
QY 184 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 243
DB 1722 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 1781
QY 244 GTACCAAGTGAATGTTCTTAGAGTGAATCAATCGATGAGCTCTTAAG 303
DB 1782 GTACCAAGTGAATGTTCTTAGAGTGAATCAATCGATGAGCTCTTAAG 1841
QY 304 TACGTTAATGGAACCTGTCAGCAACTTA 332
DB 1842 TACGTTAATGGAACCTGTCAGCAACTTA 1870

RESULT 10
AY547315 942 bp DNA linear PIN 13-JUL-2005
LOCUS Phytolectra americana antiviral protein gene, complete cds.
DEFINITION AY547315
ACCESSION AY547315
VERSION AY547315.1 GI:44889055
KEYWORDS
SOURCE
ORGANISM

Phytolectra americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 942)
2 (bases 1 to 942)

REFERENCE
AUTHORS Zhao, Y., Wang, X., Zhou, G. and Li, H.
TITLE A pokeweed antiviral protein gene in roots of *Phytolectra americana*
JOURNAL Acta Virol. 48 (2), 131-132 (2004)
PUBMED 15462289
REFERENCE
AUTHORS Zhao, Y., Wang, X. and Li, H.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-2004) Plant Virology, Institute of Plant
Protection, CARS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
China

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source Location/Qualifiers
1..942
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mRNA
CDS

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ORIGIN

Query Match 70.0%; Score 233; DB 15; Length 942;
Best Local Similarity 81.8%; Pred. No. 1.7e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTTTTCTTCTAGCTGATCCAAATG 63
DB 526 GGAGTGGATTCATTCCTGTAATAAAGCTTTTCTTCTAGCTGATCCAAATG 585
QY 64 GTTTCAGAGGAGCGGATTCAGATCATAGAGAACCAAGTCAAGCTAATTTAATGA 123
DB 586 GTTTCAGAGGAGCGGATTCAGATCATAGAGAACCAAGTCAAGCTAATTTAATGA 645
QY 124 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 183
DB 646 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 705
QY 184 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 243
DB 706 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCAAAATCTCTAG 765
QY 244 GTACCAAGTGAATGTTCTTAGAGTGAATCAATCGATGAGCTCTTAAG 303
DB 766 GTACCAAGTGAATGTTCTTAGAGTGAATCAATCGATGAGCTCTTAAG 825
QY 304 TACGTTAATGGAACCTGTCAGCAACTTA 332
DB 826 TACGTTAATGGAACCTGTCAGCAACTTA 854

RESULT 11
AY572976 942 bp mRNA linear PIN 05-APR-2004
LOCUS Phytolectra americana antiviral protein (PAP) mRNA, complete cds.
DEFINITION AY572976
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE
ORGANISM

Phytolectra americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 942)
2 (bases 1 to 942)

REFERENCE
AUTHORS Xiao, Z.A. and Jiang, Y.
TITLE A gene encoding the pokeweed antiviral protein in the leaf of
JOURNAL Phytolectra americana
PUBMED Unpublished
REFERENCE
AUTHORS Xiao, Z.A.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
University, No. 19 Xijiekouwai Street, Haidian District, Beijing
100875, China

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source Location/Qualifiers
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1..942
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gene
CDS

ORIGIN

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Query Match 70.0%; Score 233; DB 15; Length 942;
Best Local Similarity 81.8%; Pred. No. 1.7e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTTAAACTGAGGCTTTTCTTCTAGTGTAGCCATCAATG 63
DB 526 GGAGTGAATGTCATTCCTGTTAAACTGAGGCTTTTCTTCTAGTGTAGCCATCAATG 585
QY 64 GTTTCAGAGGCGGCGATTCAGTACATGAGAACCAAGCTCAAGCTAATTTTAATGA 123
DB 586 GTATCAGAGGCGGCGATTCAGTACATGAGAACCAAGCTCAAGCTAATTTTAATGA 645
QY 124 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGTGGGCAAAATCTGAG 183
DB 646 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGTGGGCAAAATCTGAG 705
QY 184 GCATTCACATGCGCAAGATGGGCTTTTACCACCACTTGAAGTGTAGTCCAAA 243
DB 706 GCATTCACATGCGCAAGATGGGCTTTTACCACCACTTGAAGTGTAGTCCAAA 765
QY 244 GGATCCAGTGAATGTTCTTAGAGTGAAGAAATCATGTGTGTGGCACTGCTTAAG 303
DB 766 GGATCCAGTGAATGTTCTTAGAGTGAAGAAATCATGTGTGTGGCACTGCTTAAG 825
QY 304 TACGTTAATGAACTGTGACAACTTA 332
DB 826 TACGTTGTTGGAGCTGTGACAACTTA 854

RESULT 12

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
LOCUS P.americana PAP gene for anti-viral protein.
DEFINITION X55383
ACCESSION X55383
VERSION X55383.1 GI:20421

KEYWORDS antiviral protein; cell wall protein; PAP gene; ribosome
inactivating protein.

SOURCE Phytophthora americana (American pokeweed)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE 1 (bases 1 to 1164)
Lin, Q., Chen, Z.C., Antoniw, J.F. and White, R.F.

AUTHORS Antoniw, J.F.

TITLE Direct Submision

JOURNAL Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops
Research, Dept. of Plant Pathology, Rothamsted Experimental
Station, Harpenden, Hert, AL5 2JQ, UK

FEATURES location/Qualifiers

source

1..1164 /organism="Phytolacca americana"

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2..943 /gene="PAP"

CDS /gene="PAP"

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ORIGIN

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Query Match 70.0%; Score 233; DB 15; Length 1164;
Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTTAAACTGAGGCTTTTCTTCTAGTGTAGCCATCAATG 63
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QY 64 GTTTCAGAGGCGGCGATTCAGTACATGAGAACCAAGCTCAAGCTAATTTTAATGA 123
DB 587 GTATCAGAGGCGGCGATTCAGTACATGAGAACCAAGCTCAAGCTAATTTTAATGA 646
QY 124 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGTGGGCAAAATCTGAG 183
DB 647 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGTGGGCAAAATCTGAG 706
QY 184 GCATTCACAAAGCCAAAGATGGGCTTTTACCACCACTTGAAGTGTAGTCCAAA 243
DB 707 GCATTCACAAAGCCAAAGATGGGCTTTTACCACCACTTGAAGTGTAGTCCAAA 766
QY 244 GGATCCAGTGAATGTTCTTAGAGTGAAGAAATCATGTGTGTGGCACTGCTTAAG 303
DB 767 GGATCCAGTGAATGTTCTTAGAGTGAAGAAATCATGTGTGTGGCACTGCTTAAG 826
QY 304 TACGTTAATGAACTGTGACAACTTA 332
DB 827 TACGTTGTTGGAGCTGTGACAACTTA 855

RESULT 13

A36639 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A36639
DEFINITION Sequence 1 from Patent EP0585554.
ACCESSION A36639
VERSION A36639.1 GI:2293943

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified sequences.

REFERENCE 1 (bases 1 to 1195)
Kim, M., Lee, K., Na, B., Jeong, H.S., Choi, K., Moon, Y. and Jeon, H.

AUTHORS Process for preparing a transgenic plant expressing phytophthora
antiviral protein

TITLE JINRO LIMITED (KR)

JOURNAL Other publication JP 6078775 940322
Other publication KR 9512900 951023.

COMMENT

FEATURES location/Qualifiers

source

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Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTTAAACTGAGGCTTTTCTTCTAGTGTAGCCATCAATG 63
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QY 304 TACGTTAATGAACTGTGCAAGCAACTTA 332
Db 858 TACGTTGTGGAGCTGTGCAAGCAACTTA 886

RESULT 14
A42103 1195 bp DNA linear PAT 05-MAY-1997
LOCUS
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 1195)
Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.
A novel expression vector for phytolacca antiviral protein
Patent: EP 0637591-A 1 08-FEB-1995;
JINRO LIMITED (KR)
Other publication AU 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
Location/Qualifiers
1..1195
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ORIGIN
Query Match 70.0%; Score 233; DB 6; Length 1195;
Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTTAAACCTGAGGCTTTTCTTACTGTGATCCATCCAAATG 63
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QY 64 GTTTCAGAGGACGCGCATTCAGATACATAGAGAACCAAGTCAAGCTTAATTTAATAGA 123
Db 618 GTATCAGAGGACGAGAAATTCAGTACATAGAGAAATCAGGTGAAGAACTTAATTTAACAG 677
QY 124 GCATTTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTGTAG 183
Db 678 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTTCAACA 737
QY 184 GCAATTCAATGCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGAGTCCAAA 243
Db 738 GCAATTCATGATGCCAAGATGAGATTTTACCAAACTCTCGAGCTAGTGAGTCCAGT 797
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Db 798 GGTGCCAAGTGAATGTTTCTTAGAGTGAATGAATCAATCGATGTAGCACTCTTAAC 857
QY 304 TACGTTAATGAACTGTGCAAGCAACTTA 332
Db 858 TACGTTGTGGAGCTGTGCAAGCAACTTA 886

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Job time : 1958.59 secs

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QY 304 TACGTTAATGAACTGTGCAAGCAACTTA 332
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RESULT 15
I43835 1195 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 1 from patent US 5633155.
ACCESSION I43835
VERSION I43835.1 GI:2468933
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 1195)
Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.
A novel expression vector for phytolacca antiviral protein and process for
preparing transgenic plant transformed therewith
Patent: US 5633155-A 1 27-MAY-1997;
Location/Qualifiers
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ORIGIN
Query Match 70.0%; Score 233; DB 6; Length 1195;
Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTTAAACCTGAGGCTTTTCTTACTGTGATCCATCCAAATG 63
Db 558 GGAGTGTGTCATTCAGTGAAGAAACCGAAGCCGAATTCCTATTGTGAGCCATACAAATG 617
QY 64 GTTTCAGAGGACGCGCATTCAGATACATAGAGAACCAAGTCAAGCTTAATTTAATAGA 123
Db 618 GTATCAGAGGACGAGAAATTCAGTACATAGAGAAATCAGGTGAAGAACTTAATTTAACAG 677
QY 124 GCATTTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTGTAG 183
Db 678 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTCAACA 737
QY 184 GCAATTCAATGCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGAGTCCAAA 243
Db 738 GCAATTCATGATGCCAAGATGAGATTTTACCAAACTCTCGAGCTAGTGAGTCCAGT 797
QY 244 GGTACCAAGTGAATGTTTCTTAGAGTGAATGAATCAATCGATGTGGCACTCCTTAG 303
Db 798 GGTGCCAAGTGAATGTTTCTTAGAGTGAATGAATCAAGCCGATGTAGCACTCTTAAC 857
QY 304 TACGTTAATGAACTGTGCAAGCAACTTA 332
Db 858 TACGTTGTGGAGCTGTGCAAGCAACTTA 886

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	245.8	73.8	2472	2	AAQ43967
6	233	70.0	1195	2	AAQ56672
7	233	70.0	1195	2	AAQ81457
8	233	70.0	1378	6	AAD42739
9	233	70.0	1378	12	ADG76061
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11	233	70.0	1379	3	AAZ59221
12	233	70.0	1379	3	AAZ59220
13	233	70.0	1379	6	AAD42738
14	233	70.0	1379	10	AD105787
15	231.4	69.5	1379	4	AAQ87929
16	229.8	69.0	1164	11	ADM74751
17	228.2	68.5	1164	11	ADM74765
18	225	67.6	2369	2	AAT95557
19	225	67.6	2369	2	ABA95543

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21	221.8	66.6	918	2	AAQ64893
22	221.8	65.6	918	2	AAT04782
23	86	25.8	774	2	AAQ22981
24	75.4	22.6	864	1	AAN91504
25	73.8	22.2	804	2	AAQ53895
26	73.8	22.2	804	2	AAQ53896
27	73.8	22.2	804	2	AAQ85385
28	73.8	22.2	804	2	AAQ85384
29	73.8	22.2	804	2	AAQ99041
30	73.8	22.2	804	2	AAQ99042
31	73.8	22.2	804	2	AAT17963
32	73.8	22.2	804	2	AAT17964
33	73.8	22.2	804	3	AAI12861
34	73.8	22.2	804	3	AAI12862
35	73.8	22.2	804	9	ACD67204
36	73.8	22.2	804	9	ACD67205
37	73.8	22.2	804	10	ADQ34588
38	73.8	22.2	804	10	ADQ34589
39	73.8	22.2	804	10	ADH92012
40	73.8	22.2	804	10	ADH92013
41	72.6	21.8	1233	2	AAT43997
42	72.6	21.8	1233	3	AAI12896
43	72.6	21.8	1233	9	ACD27613
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45	72.6	21.8	1233	10	ADH92070

ALIGNMENTS

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Aaq64893 Antiviral
Aat04782 DNA_PUMC2
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Aan91504 DNA of ri
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Aag53896 Saporin c
Aag85385 Saporin c
Aag85384 Saporin c
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Aag99042 M13mpl8-G
Aat17963 Saporin c
Aat17964 Saporin c
Aai12861 Saporin D
Aai12862 Saporin D
Acd67204 Common 80
Acd67205 Common 80
Adc34588 Common 80
Adc34589 Common 80
Adh92012 DNA encod
Aat43997 E. coli c
Aai12896 Escherich
Acd27613 Bacterial
Adc34646 E. coli c
Adh92070 Fibrobias

RESULT 1
AAD42718
ID AAD42718 standard; DNA; 333 BP.
AC AAD42718;
XX
DT 15-NOV-2002 (first entry)
XX
DE pokeweed PAP-Sbeta protein encoding DNA.
XX
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW PAP-Sbeta; ds.
XX
OS PhytoIacca americana.
XX
FH Key location/Qualifiers
FT 1..465
FT CDS /tag= a
FT /product= "PAP-Sbeta protein"
PN WO200233107-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-GE004593.
XX
PR 14-OCT-2000; 2000GB-00025217.
XX
PA (ADTS-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI Thomas CR, Mepherston MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX P-PSDB; AAR25921.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX Claim 4; Page 78; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in

specific cells of a plant. The method involves transforming the plant with chimeric gene(s) which encodes a pokeweed antiviral protein namely PAV', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts in response to the application of a specific stimulus to the plant so as to facilitate expression of the pokeweed antiviral protein in specific cells of the plant. The method is useful for inducing a necrotic effect in specific cells of a plant. The present sequence is pokeweed PAP-Sbeta protein encoding DNA

CC Sequence 333 BP; 106 A; 63 C; 76 G; 88 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 333; DB 6; Length 333;

XX Best Local Similarity 100.0%; Pred. No. 5.4e-95; Indels 0; Gaps 0;

XX Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTAGCCATCCAA 60

DB 1 ATGGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTAGCCATCCAA 60

QY 61 ATGGTTTCAGAGGAGCGCCATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAA 120

DB 61 ATGGTTTCAGAGGAGCGCCATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAA 120

QY 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

DB 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

QY 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

DB 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

QY 181 GAGGCATTCACAAATGCGCAAGATGGGCTTTACCAACCACTTGAAGTGGATGCC 240

DB 181 GAGGCATTCACAAATGCGCAAGATGGGCTTTACCAACCACTTGAAGTGGATGCC 240

QY 241 AAAGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTCT 300

DB 241 AAAGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTCT 300

QY 301 AAGTACGTTAATGAACTGTGACCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTGACCAACTTAA 333

RESULT 2
AAD42715 standard; DNA; 945 BP.

XX AAD42715;

XX 15-NOV-2002 (first entry)

DB Pokeweed pro-PAP-S protein encoding DNA.

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;

KW gene; ds.

XX Phytoacca americana.

XX Location/Qualifiers

XX Key 1..945

XX /tag= a

XX /product= "Pro-PAP-S protein"

XX /tag= b

XX /bound_molecy= "Primer PPS1BF"

XX /tag= c

XX /bound_molecy= "Primer PSXDR"

XX /tag= d

XX /bound_molecy= "Primer PSXDP"

XX /tag= e

XX /note= "Sequence replacing removed XbaI site"

XX /tag= f

PT /bound_molecy= "Primer PPS2BR"

PN WO200233107-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-GB004593.

XX 14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;

XX WPI, 2002-489891/52.

XX P-PADB; AAE25918.

PT Inducing necrotic effect in specific cells of plant by transforming plant with a chimeric gene encoding pokeweed antiviral protein and a promoter

PT which acts in response to application of specific stimulus to plant.

PS Claim 24; Page 73-74; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in

XX specific cells of a plant. The method involves transforming the plant

XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely

XX PAV', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts

XX in response to the application of a specific stimulus to the plant so as

XX to facilitate expression of the pokeweed antiviral protein in specific

XX cells of the plant. The method is useful for inducing a necrotic effect

XX in specific cells of a plant. The present sequence is pokeweed pro-PAP-S

XX protein encoding DNA

XX Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

XX Query Match 98.8%; Score 329; DB 6; Length 945;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-93; Indels 0; Gaps 0;

XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAATGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTAGCCATCCAAATG 63

DB 532 GGAATGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTAGCCATCCAAATG 63

QY 64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAAATG 123

DB 592 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAAATG 123

QY 124 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTCTGAG 183

DB 652 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTCTGAG 183

QY 184 GCAATTCACCAATGCGCAAGATGGGCTTTACCAACCACTTGAAGTGAATGAGCCAA 243

DB 712 GCAATTCACCAATGCGCAAGATGGGCTTTACCAACCACTTGAAGTGAATGAGCCAA 243

QY 244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGAGTGGCACTCTTAAG 303

DB 772 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGAGTGGCACTCTTAAG 303

QY 304 TACGTTAATGAACTGTGACCAACTTA 332

DB 832 TACGTTAATGAACTGTGACCAACTTA 860

RESULT 3
AAD42716 standard; DNA; 792 BP.

XX AAD42716;

XX 15-NOV-2002 (first entry)

DB Pokeweed mature PAP-S protein encoding DNA.

```

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM gene; ds.
XX
OS Phytolacca americana.
XX
PH Key Location/Qualifiers
FT 1..792
FT /tag= a
FT /product= "Mature PAP-S protein"
FT primer_bind
FT 1..29
FT /tag= b
FT /bound_moiety= "Primer PS1BP"
FT primer_bind
FT complement(436..462)
FT /tag= c
FT /bound_moiety= "Primer PS1SR"
FT primer_bind
FT 463..492
FT /tag= d
FT /bound_moiety= "Primer PS2BP"
FT misc_feature
FT 681..686
FT /tag= e
FT /note= "Sequence replacing removed XbaI site"
FT primer_bind
FT complement(765..792)
FT /tag= f
FT /bound_moiety= "Primer PS2SR"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25919.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 2; Page 76; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed mature PAP
XX -S protein encoding DNA
XX
XX Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;
XX
XX Query Match 98.6%; Score 328.4; DB 6; Length 792;
XX Best Local Similarity 99.7%; Pred. No. 2.2e-93;
XX Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 GGAGTTGATTCATTCCTGTAAGAGAGGCTTTTCTTACTGTAGCCATCAATG 63
XX |||||
XX 463 GGAGTTGATTCATTCCTGTAAGAGAGGCTTTTCTTACTGTAGCCATCAATG 522
XX |||||
XX 64 GTTTCAGAGCAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTATAG 123
XX |||||
XX 523 GTTTCAGAGCAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTATAG 582
XX |||||
XX 124 GCATTCTACCTGATCCCAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAG 183
XX |||||

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DB 583 GCATTCTACCTGATCCCAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAG 642
QY 184 GCAATTTCACATGCGCAAGATGGGCTTTACCCAACCACTTAGCTAGTGCACAA 243
DB 643 GCAATTTCACATGCGCAAGATGGGCTTTACCCAACCACTTAGCTAGTGCACAA 702
QY 244 GGTACCAAGTGAATAGTTCTTGAAGTGAATGAATCAATCGTAGTGGCACTCTTAAG 303
DB 703 GGTACCAAGTGAATAGTTCTTGAAGTGAATGAATCAATCGTAGTGGCACTCTTAAG 762
QY 304 TACGTTAATGGAACCTGTGACGCAACTTAA 333
DB 763 TACGTTAATGGAACCTGTGACGCAACTTAA 792

RESULT 4
AAD42729
ID AAD42729 standard; DNA; 1092 BP.
XX
XX AAD42729;
AC 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX chimeric; rice; cystatin delta D86; N1a protease cleavage site; PCS; ds.
XX
XX Phytolacca americana.
XX
XX Oryza sativa.
XX
XX Tobacco; Etch virus.
XX
XX Chimeric.
XX
XX Key Location/Qualifiers
XX primer_bind
XX 1..29
XX /tag= a
XX /bound_moiety= "Primer PS1BP"
XX misc_feature
XX 681..686
XX /tag= b
XX /note= "Modified XbaI site"
XX primer_bind
XX complement(742..786)
XX /tag= c
XX /bound_moiety= "Primer PCS-PAPSR"
XX primer_bind
XX 766..806
XX /tag= d
XX /bound_moiety= "Primer PCS-Delta86P"
XX misc_feature
XX 766..786
XX /tag= e
XX /note= "TEV N1a protease cleavage site"
XX primer_bind
XX complement(1066..1092)
XX /tag= f
XX /bound_moiety= "Primer SYNPOTdelta86P"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Disclosure; Page 83; 87pp; English.

```


XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-8, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pro-PAP-8 DNA, rice cytosolic delta D86 DNA
CC and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
CC on 29-AUG-2003 to standardise OS field)

SO Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Query Match 90.8%; Score 302.4; DB 6; Length 1092;
Best Local Similarity 99.7%; Pred. No. 4.2e-85;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGTGAGCATCCAAATG 63
DB 463 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGTGAGCATCCAAATG 522
QY 64 GTTTCAGAGGAGCGGCGATTCAGATGAGAAACCAAGTCAGACTAATTTTAATAGA 123
DB 523 GTTTCAGAGGAGCGGCGATTCAGATGAGAAACCAAGTCAGACTAATTTTAATAGA 582
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 583 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 642
QY 184 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAAACCACTGAGCTAGTATGCCAAA 243
DB 643 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAAACCACTGAGCTAGTATGCCAAA 702
QY 244 GGATCCAAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTGCACTCTTTAAG 303
DB 703 GGATCCAAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTGCACTCTTTAAG 762

QY 304 TACG 307
DB 763 TACG 766

RESULT 5
AAQ43967 standard; DNA; 2472 BP.

XX AAQ43967;
XX 09-NOV-1993 (first entry)

XX Pokeweed antiviral protein.
XX Pokeweed; ricin; protein synthesis inhibitor; cancer;
XX polymerase chain reaction; PCR; ss.

XX Phytolacca americana.

XX Key Location/Qualifiers
XX CAAT_signal 549..552

XX CAAT_signal 627..630

XX TATA_signal 845..850

XX sig_peptide 1014..1085

XX mat_peptide 1086..1868

XX polyA_signal 2130..2135

XX /tag= f

XX JP05137580-A.

XX 01-JUN-1993.

XX 20-NOV-1991; 91JP-00329672.

XX 20-NOV-1991; 91JP-00329672.

XX (N1SB) JAPAN TOBACCO INC.

XX WPI; 1993-211306/26.

XX F-PSDB; AAR37345.

XX New pokeweed antiviral protein (PAP) with similar activity to ricin -
XX used to treat cancer and as an agricultural chemical.

XX Claim 2; Page 11-13; 14pp; Japanese.

CC PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The
CC protein may be obtained all year round by recombinant DNA techniques. PAP
CC can be used partic. against cancer and as an agricultural chemical. Total
CC mRNA, is extracted from the seeds, leaves and roots of pokeweed and used
CC to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA
CC fractions, which are introduced into a cloning vector EMBL3 and then into
CC host R.coli PLK-17 (P2) to produce PAP

XX Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;

Query Match 73.8%; Score 245.8; DB 2; Length 2472;
Best Local Similarity 84.2%; Pred. No. 4.9e-67;
Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGTGAGCATCCAAATG 63
DB 1542 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGTGAGCATCCAAATG 1601

QY 64 GTTTCAGAGGAGCGGCGATTCAGATGAGAAACCAAGTCAGACTAATTTTAATAGA 123
DB 1602 GTTTCAGAGGAGCGGCGATTCAGATGAGAAACCAAGTCAGACTAATTTTAATAGA 1661

QY 124 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 1662 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 1721

QY 184 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAAACCACTGAGCTAGTATGCCAAA 243
DB 1722 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAAACCACTGAGCTAGTATGCCAAA 1781

QY 244 GGATCCAAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTGCACTCTTTAAG 303
DB 1782 GGATCCAAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTGCACTCTTTAAG 1841

QY 304 TACGTTAATGGAACCTGTGAGCAACTTA 332
DB 1842 TACGTTAATGGAACCTGTGAGCAACTTA 1870

RESULT 6
AAQ56672 standard; cDNA; 1195 BP.

XX AAQ56672;
XX 16-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 04-SEP-1994 (first entry)

XX Sequence of Phytolacca antiviral protein (PAP) cDNA.

XX Antiviral protein; PAP; virus-resistance; transgenic plant; ss.

XX Phytolacca americana; L.

XX

XX

XX

XX

XX


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XX 15-NOV-2002 (first entry)
DT
XX pokeweed PAP' DNA #2.
DE
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
KM
XX Phytolacca americana.
OS
XX Key Location/Qualifiers
FH misc_feature 290..1076
FT /tag= a
FT /note= "Mature PAP' sequence"
XX
XX MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86-87; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with a chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
XX Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 233; DB 6; Length 1378;
Best Local Similarity 81.8%; Pred. No. 4,4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
4 GAGATTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGAGCCATCCCAATG 63
750 GAGGTGATGTCATTCACCTGAGAAAACCAAGCCCAATTCCTATTGTTAGCATCAATG 809
64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGA 123
810 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGTGAATAAATTTTAAACGA 869
124 GCATTCTACCTGATCCCAAGATTAATTAATTTGAGAGAAAGTGGGGGAAATCTCTAG 183
870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 929
184 GCATTTCACATGCGCAAGATGGGCTTAACCAACCACTGAGCTAGTGATGCCAAA 243
930 GCAATTCAATGATGCCAAGATGAGATTTTAACTTAACTTGAAGTATGATGCAATG 989
244 GGTACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGATGCACTCTTAAAG 303
990 GGTGCCAAGTGAATGTTGTTGAGATGATGAATCAAGCTGATGATGCACTCTTAAAC 1049
304 TACGTTAATGAACCTGTGCAACAACTTA 332
1050 TACGTTGTTGGAGCTGTGCAACAACTTA 1078

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RESULT 9
ADG76061 standard: DNA; 1378 BP.
ID
XX ADG76061;
XX
XX ADG76061;
AC
XX 11-MAR-2004 (first entry)
DT
XX
XX American pokeweed antiviral protein (PAP) DNA Seqid 1.
DE
XX
XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
XX nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX American pokeweed; retroviral.
XX
XX Phytolacca americana.
OS
XX MO2003106479-A2.
XX
XX 24-DEC-2003.
XX
XX 17-JUN-2003; 2003MO-US019141.
XX
XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
XX replication, for inducing depurination of viral RNA, or for treating
XX viral infection in subject.
XX
XX Example 2; SEQ ID NO 1; 62pp; English.
XX
XX This invention relates to novel modified pokeweed antiviral proteins
XX (PAPs). Specifically, it refers to modifications relative to wild-type
XX PAP that confer increased activity towards viral RNA, particularly
XX retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
XX modified PAP also exhibits decreased activity towards ribosomal RNA
XX relative to wild-type PAP. The present invention describes a molecular
XX model of PAP-HIV RNA interactions that have been used for the rational
XX redesign of PAP mutants with potent anti-HIV activity, where
XX modifications have been introduced in regions other than the active site.
XX Accordingly, these mutants represent antiviral agents that can work as
XX nucleoside analogue inhibitors of reverse transcriptase, as well as viral
XX protease inhibitors that can be used for treating viral infections. As
XX such, they are useful for inhibiting viral replication and for
XX depurinating viral RNA. This polynucleotide sequence is the DNA encoding
XX the wild type American pokeweed antiviral protein (PAP) of the invention.
XX
XX Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 233; DB 12; Length 1378;
Best Local Similarity 81.8%; Pred. No. 4,4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
4 GAGATTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGAGCCATCCCAATG 63
749 GAGGTGATGTCATTCACCTGAGAAAACCAAGCCCAATTCCTATTGTTAGCATCAATG 808
64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGA 123
809 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGTGAATAAATTTTAAACGA 868
124 GCAATTCTACCTGATCCCAAGATTAATTAATTTGAGAGAAAGTGGGGGAAATCTCTAG 183
869 GCAATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 928
184 GCAATTCAATGCGCAAGATGGGCTTAACCAACCACTGAGCTAGTGATGCCAAA 243

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DB 929 GCAATTCATGATCCAGATGAGTTTACCCAACTCTGAGCTAGTGATGCGAGT 988
QY 244 GGTACCAAGTGGATGTTCTTGAAGTGAATCAATCGGATGTGCACTCTTAAAG 303
DB 989 GGTGCAAGTGGATGTTCTTGAAGTGAATCAATCGGATGTGCACTCTTAAAC 1048
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1049 TACGTTGCTGGAGCTGTGACCAACTTA 1077

RESULT 10
ID AA245197 standard; DNA; 1379 BP.
AC AA245197;
XX
XX 29-FEB-2000 (first entry)
DB
XX Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
XX Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
XX ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
XX potato virus X; cucumber mosaic virus; CMV; ss;
XX tomato yellow leaf curl virus.
XX
XX Phytophthora americana.
XX
XX Key Location/Qualifiers
XX CDS 225..1166
XX /*tag= a
XX /product= "PAP"
XX /note= "pokeweed antiviral protein"
XX
XX MO9960843-A1.
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-US011301.
XX
XX 22-MAY-1998; 98US-0086374P.
XX
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Turner NE, Wang P;
XX
XX WPI; 2000-062555/05.
XX P-PDB; AAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43pp; English.
XX
XX This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX Phytophthora americana (pokeweed). It is a single polypeptide chain that
XX catalytically removes a specific adenine residue from a highly conserved
XX stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX activities to plants. A DNA molecule encoding a PAP II protein with an
XX intact catalytic active site amino acid residue (E172) is useful for
XX generating transgenic plants. PAP II DNA is useful for generating
XX transgenic plants (especially cereal crops) through transforming a
XX protoplast or introducing the DNA directly into a plant part prior to
XX regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
XX activity thus have increased resistance to viruses and/or fungi. Viruses
XX include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
XX yellow leaf curl virus, and fungi include Pythium, Phytophthora,
XX Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
XX other plants pests including insects, bacteria and nematodes. PAP II DNA
XX is also useful for identifying a PAP II protein having reduced

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CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC unlike PAP transgenic plants which are stunted and sterile, PAP II
CC transgenic plants have a normal and fertile phenotype
XX
XX SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX Query Match 70 0%; Score 233; DB 3; Length 1379;
XX Beat Local Similarity 81.8%; Pred. No. 4.4e-63;
XX Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
XX
QY 4 GGAATTCATGATCCCTGTAATAAACTGAGGCTTTTCTTACTGTGATCCATCAATG 63
DB 750 GGAATTCATGATCCCTGTAATAAACTGAGGCTTTTCTTACTGTGATCCATCAATG 809
QY 64 GTTTCAGAGGAGCGCGATTCAGATGAGAGCAAGTCAAGATCAATATTTTAATGA 123
DB 810 GTATCAGAGGAGCGCGATTCAGATGAGAGCAAGTCAAGATCAATATTTTAATGA 869
QY 124 GCATTCTACCCCTGATCCCAAGTAAATTAATTTGAGAGGAAGTGGGCAAAATCTTGAG 183
DB 870 GCATTCTACCCCTGATCCCAAGTAAATTAATTTGAGAGGAAGTGGGCAAAATCTTGAG 929
QY 184 GCAATTCAGATGCGCAAGATGAGGCTTTTACCAACCACTTGAGTGTGATGCCAA 243
DB 930 GCAATTCAGATGCGCAAGATGAGGCTTTTACCAACCACTTGAGTGTGATGCCAGT 989
QY 244 GGTACCAAGTGGATGTTCTTGAAGTGAATCAATCGGATGTGCACTCTTAAAG 303
DB 990 GGTGCAAGTGGATGTTCTTGAAGTGAATCAATCGGATGTGCACTCTTAAAC 1049
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1050 TACGTTGCTGGAGCTGTGACCAACTTA 1078

RESULT 11
ID AA259221 standard; cDNA; 1379 BP.
AC AA259221;
XX
XX 20-APR-2000 (first entry)
DB
XX Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX Phytophthora americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS ) MONSANTO CO.
XX
XX Kaniowski WK, Turner NE, Lodge JK;
XX
XX WPI; 2000-126326/11.
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 7; Fig 5; 30pp; English.
XX
XX This is the coding sequence for a variant spring leaf form of the
XX pokeweed antiviral protein (PAP') which is used to generate transgenic
XX potato plants. PAP' is able to confer resistance to infection by potato

```

virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
CC the potato plant or tuber expressing PAP'. PAP' varies from PAP
CC (AA259220) by mutations L20R and Y49H
CC XX
SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
OY 4 GGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGTAGCCATCCAAATG 63
DB 750 GGAGTGATGTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGTAGCCATCCAAATG 809
OY 64 GTTTCAGAGCGCAGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTAATAGA 123
DB 810 GTATCAGAGCGCAGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTAATAGA 869
OY 124 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGATGGGCAAAATCTGTAG 183
DB 870 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGATGGGCAAAATCTGTAG 929
OY 184 GCATTCACCAATGCCAAGATGGGGCTTTACCAACCACTTGAAGTATGCCAA 243
DB 930 GCATTCATGATGCGCAAGATGGAGTTTACCAACCTCTCGAGCTAGTGAGTCCAGT 989
OY 244 GGTACCAAGTGATAGTCTTAGAGTGATGAATCAATCGTATGTGGCATCTCTTAAG 303
DB 990 GGTGCGAAGTGATAGTCTTAGAGTGATGAATCAATCGTATGTGGCATCTCTTAAG 1049
OY 304 TACGTTAATGGAACCTGTGACAACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGACAACTTA 1078
RESULT 12
AA259220
ID AA259220 standard; cDNA; 1379 BP.
XX
AC AA259220;
XX
DT 20-APR-2000 (first entry)
XX
DE Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; BB.
XX
OS Phytolacca americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS) MONSANTO CO.
XX
XX PA Kaniewski WK, Turner NB, Lodge JK;
XX
XX PI WPI; 2000-126326/11.
XX
XX DR Production of transgenic potato plants or tubers expressing pokeweed
XX PT antiviral protein which are resistant to potato virus X or Y.
XX
XX PS Claim 6; Fig 4; 30pp; English.
XX
XX This is the coding sequence for the spring leaf form of the pokeweed
XX antiviral protein (PAP) which is used to generate transgenic potato
XX plants. PAP is able to confer resistance to infection by potato virus X
CC

(PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC potato plant or tuber expressing PAP
CC XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
OY 4 GGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGTAGCCATCCAAATG 63
DB 750 GGAGTGATGTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGTAGCCATCCAAATG 809
OY 64 GTTTCAGAGCGCAGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTAATAGA 123
DB 810 GTATCAGAGCGCAGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTAATAGA 869
OY 124 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGATGGGCAAAATCTGTAG 183
DB 870 GCATTCACCTGATCCCAAGTAAATTTTGAAGAGAGATGGGCAAAATCTGTAG 929
OY 184 GCATTCACCAATGCCAAGATGGGGCTTTACCAACCACTTGAAGTATGCCAA 243
DB 930 GCATTCATGATGCGCAAGATGGAGTTTACCAACCTCTCGAGCTAGTGAGTCCAGT 989
OY 244 GGTACCAAGTGATAGTCTTAGAGTGATGAATCAATCGTATGTGGCATCTCTTAAG 303
DB 990 GGTGCGAAGTGATAGTCTTAGAGTGATGAATCAATCGTATGTGGCATCTCTTAAG 1049
OY 304 TACGTTAATGGAACCTGTGACAACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGACAACTTA 1078
RESULT 13
AAD2738
ID AAD2738 standard; DNA; 1379 BP.
XX
AC AAD2738;
XX
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP' DNA #1.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; db.
XX
XX Phytolacca americana.
XX
XX OS
XX FT Key location/qualifiers
XX FT m18c_feature 290..1076
XX FT /tag= a
XX FT /note= "Mature PAP' sequence"
XX
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX PA Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
XX PI Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
XX DR WPI; 2002-489891/52.
XX
XX XX Inducing necrotic effect in specific cells of plant by transforming plant
XX PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX PS Claim 5; Page 86; 87pp; English.
XX

CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 6; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTGAGGCAATCCAAATG 63
DB 750 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTGAGGCAATCCAAATG 809
QY 64 GTTTCAGAGGCGCGGATTCATGATAGAGAACCAAGTCAAGTAAATTTAATAGA 123
DB 810 GTATCAGAGGCGCGGATTCATGATAGAGAACCAAGTCAAGTAAATTTAATAGA 869
QY 124 GGATTCATCCCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 183
DB 870 GGATTCATCCCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 929
QY 184 GCAATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAA 243
DB 930 GCAATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 989
QY 244 GGATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 303
DB 990 GGATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 1049
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1050 TACGTTAATGGAACCTGTGACCAACTTA 1078

RESULT 14

AD105787
ID AD105787 standard; DNA; 1379 BP.

XX AD105787;

AC 15-APR-2004 (first entry)

XX DNA encoding the wild-type pokeweed antiviral protein.

XX ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
XX cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
XX medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX de.

XX Phytolacca americana.

XX Key Location/Qualifiers

XX CDS 225..1166

XX /tag= a

XX /product= "wild-type pokeweed antiviral protein"

XX WO200262952-A2.

XX 15-AUG-2002.

XX 01-FEB-2002; 2002WO-US002792.

XX 02-FEB-2001; 2001US-0266396P.

XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NR, Hudak KA, Parikh B;
XX
XX MPI; 2003-156656/15.
DR P-PSDB; AD105788.

XX
XX New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT type PAP, useful in agricultural biotechnology or in the fields of
PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
PT or autoimmune disease.

XX Disclosure; SEQ ID NO 1; S1BP; English.

XX
XX The invention relates to a novel pokeweed Antiviral Protein (PAP) mutant
CC that is less toxic than wild-type PAP and exhibits ribosome depurination
CC activity, where the mutant is a central domain mutant or N-terminal
CC domain mutant. The PAP mutants have the following activities: antifungal,
CC antiviral, virucide, anti-HIV, cytoskeletal and immunosuppressive. The PAP
CC mutants are useful in agricultural biotechnology as well as in the fields
CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
CC treating mammals with cancer, AIDS, viral infection or autoimmune
CC diseases associated with proliferations of unwanted T-cells or B-cells.
CC The transgenic plants are useful in exhibiting resistance to a broad
CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC sequence represents the DNA encoding the wild-type pokeweed antiviral
CC protein of the invention.

SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 10; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTGAGGCAATCCAAATG 63
DB 750 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTGAGGCAATCCAAATG 809
QY 64 GTTTCAGAGGCGCGGATTCATGATAGAGAACCAAGTCAAGTAAATTTAATAGA 123
DB 810 GTATCAGAGGCGCGGATTCATGATAGAGAACCAAGTCAAGTAAATTTAATAGA 869
QY 124 GGATTCATCCCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 183
DB 870 GGATTCATCCCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 929
QY 184 GCAATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAA 243
DB 930 GCAATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 989
QY 244 GGATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 303
DB 990 GGATTCGAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGTATGATGCCAGT 1049
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1050 TACGTTAATGGAACCTGTGACCAACTTA 1078

RESULT 15

AAC87929
ID AAC87929 standard; DNA; 1379 BP.

XX AAC87929;

XX 06-MAR-2001 (first entry)

XX P. americana pokeweed antiviral protein encoding DNA SEQ ID NO.1.

XX Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
XX bioreproductive; fusion protein; immunosuppressive; mutant; cytoskeletal;
XX anti-HIV; human immunodeficiency virus; AIDS; leukaemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; SB.
XX
XX Phytolacca americana.

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 1577.51 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-7

Perfect score: 333

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	73.8	22.2	816	2	BR035038 MM02A01 M
C 2	73.8	22.2	993	2	BR035039 MM02A03 M
C 3	58.2	17.5	1033	2	BR036541 MP01B07 M
C 4	56.6	17.0	639	6	CA835855 MCS004G12
C 5	56.6	17.0	649	6	CA838757 MCT020B02
C 6	56.6	17.0	649	6	CA839330 MCT020B02
C 7	56.6	17.0	661	6	CA835532 MCS038A11
C 8	56.6	17.0	671	6	CA839511 MCT020B04
C 9	56.6	17.0	689	6	CA833333 MCS021A09
C 10	56.6	17.0	689	6	CA833383 MCS021A04
C 11	52.4	15.7	405	8	T24255 CRE1345 1am
C 12	49.6	14.9	1038	2	BR033546 MP03A09 M
C 13	48.6	14.6	639	2	BR037217 MP18B02 M
C 14	46.4	13.9	829	2	CN782289 EST00385
C 15	44.6	13.4	1021	2	BR036639 MP03B03 M
C 16	43	12.9	267	1	AA856221 L30-242T3
C 17	41.6	12.5	571	7	CO298356 EK172829
C 18	40	12.0	700	3	BM634714 170006875
C 19	40	12.0	715	3	BM654071 170006875
C 20	39.8	12.0	837	1	AM053634 L30-1401T
C 21	39.6	11.9	614	7	CN845658 PG07003F0
C 22	38.6	11.6	593	3	BM610967 170006591

C 23	38.6	11.6	669	7	CN848288 PG07019B0
C 24	38.6	11.6	721	3	BM574953 170006589
C 25	38.2	11.5	791	7	CP998461 AGENCOURT
C 26	38	11.4	671	7	CN848973 PG07022B0
C 27	37.8	11.4	627	8	CK043173 1356846 N
C 28	37.8	11.4	676	3	BM585966 170006873
C 29	37.8	11.4	1012	6	CA125924 SCRUIR102
C 30	37	11.1	749	7	CR530626 CR530626
C 31	36.8	11.1	498	1	AJ281693 4A3A-P9D02
C 32	36.6	11.0	723	8	DR659480 ZM_BFB002
C 33	36.6	11.0	841	8	DR803998 ZM_BFB002
C 34	36.4	10.9	420	6	CP227009 IH149 sub
C 35	36.4	10.9	557	2	BG450283 NF014C03D
C 36	36.4	10.9	898	9	AZ676415 ENTKA15TP
C 37	36	10.8	472	2	BG042437 sv07h1.Y
C 38	36	10.8	612	9	AQ341401 RPTC11-11
C 39	36	10.8	670	9	AQ343493 RPTC11-12
C 40	35.8	10.8	889	10	C2951885 267847 TO
C 41	35.6	10.7	154	10	CR81274 L1gr-988
C 42	35.6	10.7	595	5	BU549020 GM880016A
C 43	35.4	10.6	1465	10	CI643815 CH213-56D
C 44	35	10.5	298	2	BM521963 BM521963
C 45	35	10.5	391	6	CA148398 SCUPRZ100

ALIGNMENTS

RESULT 1
BE035038/c 816 bp mRNA linear EST 07-JUN-2000
LOCUS MM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION
antiviral protein, mRNA sequence.

ACCESSION
BE035038
VERSION
BE035038.1 GI:8330047
KEYWORDS
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE
1 (bases 1 to 816)
Bohner, H., J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu.

TITLE
JOURNAL
COMMENT

FEATURES
source
1. 816
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"
/clone_id="MM"
/note="Vector: Bluescript SK+, site 1: EcoRI, site 2:
XhoI, Plants stressed 6 weeks in 500mM NaCl"

ORIGIN
Query Match 22.2%; Score 73.8; DB 2; Length 816;
Best Local Similarity 66.9%; Pred. No. 8.2e-11;
Matches 121; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

QY 17 TCCTGTAAACACGAGGCTTTTCTTACTGAGCATTCCAAATGTTTCAGAGCAG 76
DB 590 TCGATGGAAACACGAGGCTTTTCTTACTGAGCATTCCAAATGTTTCAGAGCAG 531

QY	77	CGGATTCGAAGTACTATAGAACCAAGT---	CAAGACTAATTTTAATAGACATTCTAC	133
Db	530	CAGGGTTCATTATATCGAGACTAAGGCGCCGAAAGTGGGTCACATGGTTGTTCAAC		471
QY	134	CTGATCCCAAGTAAATTAATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCCAATTACA	193	
Db	470	CCGATCCGAAAGTGAATTAACTTTGGAGAACCAACTGGGAAAGTTTCCGATGAGATTCTATA	411	
QY	194	A 194		
Db	410	A 410		
RESULT 2				
LOCUS	BE035039/c			
DEFINITION	BE035039	993 bp	mRNA	linear
ACCESSION	MM02A03	MM Mesembryanthemum crystallinum	CDNA 5'	similar to
VERSION	BE035039	antiviral protein, mRNA sequence.		
KEYWORDS	BE035039.1	GI:8330048		
SOURCE	EST.			
ORGANISM	Mesembryanthemum crystallinum	(common iceplant)		
REFERENCE	Mesembryanthemum crystallinum			
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.			
JOURNAL	1 (bases 1 to 993)			
COMMENT	Bohnert,H.,J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McColloough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R. Functional Genomics of Plant Strees Tolerance Unpublished (2000)			
FEATURES	Contact: Michalowski,C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: chm@u.arizona.edu Insert Length: 1 Std Error: 0.00. Location/Qualifiers			
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	/cell_type="epidermal bladder cells"			
	/dev_stage="12 weeks old"			
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Best Local Similarity	66.9%;	Pred. No. 8.7e-11;		
Matches	121;	Conservative	0;	Mismatches 57; Indels 3; Gaps 1;
QY	17	TCCCTGTAAAACTGAGGCTTTTTCCTACTGCTGTCATCCAAATGGTTTCAGAGCGAG	76	
Db	591	TGGAATGGGAAACTCGAGGCCCAAAATCTTAAGTATGCCATCCAGATGGTTTCAGAAAGC	532	
QY	77	CGCGATTCGAAGTACATAGAACCAAGT---	CAAGACTAATTTTAATGAGCATTTCTAC	133
Db	531	CAGGGTTCATTATATCGAGACTAAGGTCACCGAAAGTGGTCACATGGTTGTTCAAC	472	
QY	134	CTGATCCCAAGTAAATTAATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCCAATTACA	193	
Db	471	CCGATCCGAAAGTGAATTAACTTTGGAGAACCAACTGGGAAAGTTTCCGATGAGATTCTATA	412	
QY	194	A 194		
Db	411	A 411		
RESULT 3				

LOCUS	BE036541	1033 bp	mRNA	linear	EST 07-JUN-2000
DEFINITION	M01B07 MF Mesembryanthemum crystallinum cDNA 5' similar to				
ACCESSION	BE036541				
VERSION	BE036541.1 GI:9331550				
KEYWORDS	EST.				
SOURCE	Mesembryanthemum crystallinum (common iceplant)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.				
REFERENCE	1 (bases 1 to 1033)				
AUTHORS	Bohner, H.J., Borchert, C., Brazille, S., Brooke, J., Eaton, M., Ferreira, H., Kawabaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.				
TITLE	Functional Genomics of Plant Stress Tolerance				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Michalowski, C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: chm@u.arizona.edu An open reading frame exists.				
FEATURES	location/qualifiers				
source	1..1033				
ORIGIN	/organism="Mesembryanthemum crystallinum" /mol_type="mRNA" /db_xref="taxon:3544" /tissue_type="apical meristem and leaf primordia" /der_stage="6 weeks" /clone_id="MP" /note="3 d 500mM NaCl"				
Query Match	17.5%; Score 58.2; DB 2; Length 1033;				
Best Local Similarity	63.5%; Pred. No. 4.1e-06;				
Matches	106; Conservative 0; Mismatches 58; Indels 3; Gaps 1;				
QY	30 TGAGGCTTTTCTTACTGTAGCCATCCAAATGTTTCAGAGGACGCGCATTCAGTA 89				
DB	298 TGAGGCCAAATCTTCTGCGATTCGTATACATGTTTCTGAAACAGACGGTTTAAGTA 357				
QY	90 CATAGAGAACCAAGTCA--AGACTAAATTTAATPAGACATTCTACCTGTATCCAAAGT 146				
DB	358 TATTGAAGTGAAGTGACCCCAAAATGGGGTTCATGCGCTTCATPACCGACCCGAAGT 417				
QY	147 AATTAAATTTGAGAGAGAGTGGGGCAAAATCTCGAGCGCAATTACCA 193				
DB	418 GCTGAGTTTGAGAACCAATTTGGGGGAGATTTCGCAAGAGATTCAATA 464				
RESULT 4					
CA835855					
LOCUS	CA835855	639 bp	mRNA	linear	EST 12-DEC-2002
DEFINITION	MC5004612.161218 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MC5004612 5, mRNA sequence.				
ACCESSION	CA835855				
VERSION	CA835855.1 GI:26563620				
KEYWORDS	EST.				
SOURCE	Mesembryanthemum crystallinum (common iceplant)				
ORGANISM	Mesembryanthemum crystallinum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.				
AUTHORS	1 (bases 1 to 639)				
TITLE	Cushman, J.C.				
JOURNAL	An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum				
Unpublished (1997)					

High quality sequence stop: 649.

FEATURES

source

Location/Qualifiers

1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT026C11"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 649;

Best Local Similarity 62.4%; Pred. No. 1.1e-05; Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

25 AAAAAGAGGCTTTTCTACTGTAAGCCATCAAAATGTTTCAGAGCGCGCATTC 84
187 AGAAATGAGCCAAATCTTGCTATTCATACAGATGTTTCTGAAGCAGAGTTTC 246
85 AAGTACATAGAGAACCAAGTCAGACTTAATTT-----TAATGAGCATTCCTACCTGAT 138
247 AAGTATTTGAGAGTAAGTGAACCAAGTCGTAGATTATGATCGTTCTTACCGGAC 306
139 CCCAAATTAATTTTGAAGAGAGAGTGGGCGAAATCTCTGAGCGCATTC 191
307 CCGAAATGCTGCTTTTGAGAGCACAATTTGGGGAAGATTTGCGAGAGATTCA 359

RESULT 7

LOCUS

DEFINITION

CA835532 661 bp mRNA linear EST 12-DEC-2002
MCS038A11.160572 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS038A11 5, mRNA sequence.

ACCESSION CA835532
VERSION CA835532.1
KEYWORDS GI:26563297
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 661)
Cushman, J.C.

AUTORS An expressed sequence tag database for the common ice plant,
TITLE Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.

FEATURES

source

Location/Qualifiers

1..661
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 661;

Best Local Similarity 62.4%; Pred. No. 1.1e-05; Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

25 AAAAAGAGGCTTTTCTACTGTAAGCCATCAAAATGTTTCAGAGCGCGCATTC 84
198 AGAAATGAGCCAAATCTTGCTATTCATACAGATGTTTCTGAAGCAGAGTTTC 257
85 AAGTACATAGAGAACCAAGTCAGACTTAATTT-----TAATGAGCATTCCTACCTGAT 138
258 AAGTATTTGAGAGTAAGTGAACCAAGTCGTAGATTATGATCGTTCTTACCGGAC 317
139 CCCAAATTAATTTTGAAGAGAGAGTGGGCGAAATCTCTGAGCGCATTC 191
318 CCGAAATGCTGCTTTTGAGAGCACAATTTGGGGAAGATTTGCGAGAGATTCA 370

RESULT 8

LOCUS

DEFINITION

CA839511 671 bp mRNA linear EST 12-DEC-2002
MCT028D04.172117 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5, mRNA sequence.

ACCESSION CA839511
VERSION CA839511.1
KEYWORDS GI:26567276
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 671)
Cushman, J.C.

AUTORS An expressed sequence tag database for the common ice plant,
TITLE Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.

FEATURES

source

Location/Qualifiers

1..671
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

Query Match 17.0%; Score 56.6; DB 6; Length 671;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

25 AAAAAGTGGCTTTTCTACTGTGAGCCATCCAAATGGTTTCAGAGCGCGGATTC 84
187 AGAATAGAGCCAAATCTTCTGATTCGCAATGAGTGTTCGAAAGCAAGGTTTC 246
85 AAGTACATAGAGAACCAAGTCAAGCTAATTT-----TAATAGACATTCACCTGAT 138
247 AAGTATTTAGAGATTAAGTGAACCAAGTCCGTTAGTTATGATTCGTTTACCCGAC 306
139 CCCAAAGTAAATTTTGGAGAGAGAGTGGGCAAAATCTCTAGGCAATTC 191
307 CCGAAATGCTGCTTTTGGAGACCAATGGGGGAAGATTTGCGAGGAGATTC 359

RESULT 9
LOCUS CA833333
DEFINITION CA833333 689 bp mRNA linear EST 12-DEC-2002
MCS021A09 151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.

ACCESSION CA833333
VERSION CA833333.1 GI:26561098
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C.
AUTHORS An expressed sequence tag database for the common ice plant.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7 20mer
BACKWARD: T7 21mer
Plate: 021 row: A column: 09
Seq primer: T3 20mer
High quality sequence stop: 689.
Location/Qualifiers
1. 689

FEATURES
source
1. 689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021A09"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 689;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

25 AAAAAGTGGCTTTTCTACTGTGAGCCATCCAAATGGTTTCAGAGCGCGGATTC 84
198 AGAATAGAGCCAAATCTTCTGATTCGCAATGAGTGTTCGAAAGCAAGGTTTC 257
85 AAGTACATAGAGAACCAAGTCAAGCTAATTT-----TAATAGACATTCACCTGAT 138
258 AAGTATTTAGAGATTAAGTGAACCAAGTCCGTTAGATTATGATTCGTTTACCCGAC 317
139 CCCAAAGTAAATTTTGGAGAGAGAGTGGGCAAAATCTCTAGGCAATTC 191
318 CCGAAATGCTGCTTTTGGAGACCAATTTGGGGGAAGATTTGCGAGGAGATTC 370

RESULT 10
LOCUS CA833383
DEFINITION CA833383 689 bp mRNA linear EST 12-DEC-2002
MCS021P04 152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021P04 5, mRNA sequence.

ACCESSION CA833383
VERSION CA833383.1 GI:26561148
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C.
AUTHORS An expressed sequence tag database for the common ice plant.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7 20mer
BACKWARD: T7 21mer
Plate: 021 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 689.
Location/Qualifiers
1. 689

FEATURES
source
1. 689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021P04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 689;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;
25 AAAAAGTGGCTTTTCTACTGTGAGCCATCCAAATGGTTTCAGAGCGCGGATTC 84

Db 198 AGAATGAGCCAAATTTCTTGCTGATTCGATACAGATGGTTCTTGAGCAGCAGAGGTTTC 257

Qy 85 AAGTACATGAGAGCAACAGTCAAGACTAATTT-----TATAGAGCATTTCTACCTGAT 138
|||||
Db 258 AAGTATATTGAGAGTGAAGTGAACCAAGGCGTTAGATATATGATTCGTTTACCGGAC 317

Qy 139 CCCAAGTATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGCAATTCA 191
|||||
Db 318 CCGAATAATGCTGCTTTGGAGACCATTGGGGGAAGATTTCGAGGAGATTCA 370

RESULT 11
T24255 405 bp mRNA linear EST 28-JUN-1995
LOCUS crs1345 lambdaZAPST Ricinus communis cDNA clone pcrl345, mRNA
DEFINITION
T24255
T24255
T24255.1 GI:689074
KEYWORDS
EST:
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoidae;
COMMENT Acalyphese; Ricinus.
1 (bases 1 to 405)
vandeloo,F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers
1..405
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrl345"
/cclone_lib="lambdaZAPST"
/note="Vector: lambdaZAPIT; Site_1: EcoRI; Site_2: XhoI;
poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPIT according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN
Query Match 15.7%; Score 52.4; DB 8; Length 405;
Best Local Similarity 59.2%; Freq. No. 0.00018;
Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

Qy 27 AACTGAGGCTTTTCTTACTGCTGAGCCATCAATGTTTCAGAGCAGGCGCATTCAA 86
|||||
Db 82 AACTCTGCGCTGCTTCTTATGTTGATTCATCAATGATTTTCAGAGCAGCAGATTTC 141
|||||

Qy 87 GTACATGAGAACCAAGTCAAGACTAATTT-----AATGAGCATTTCTACCTGATTC 140
|||||
Db 142 GTACATTGAGGAGAAATGCGCAGAGAAATTAGTACCAACGNAATCTGCACCGATTC 201
|||||

Qy 141 CAAGTAAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGCAATTTCAC-ATGCCA 199
|||||
Db 202 TAGCTAATTAACACTTNAAGATAGTTGGGGGAGACTTTCACCTGCAATTCAAAGGTCTA 261
|||||

Qy 200 AGAATGGGCTTTACCAACACACTTGAGCT 230
|||||

Db 262 ACCAAGAGCCTTTGCTAGTCCANTTCAACT 292

RESULT 12
BE033546 1038 bp mRNA linear EST 07-JUN-2000
LOCUS MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein, mRNA sequence.
BE033546
ACCESSION BE033546.1 GI:8328555
VERSION
KEYWORDS
EST:
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL Caryophyllales; Alzooceae; Mesembryanthemum.
COMMENT 1 (bases 1 to 1038)
Bohner,H.J., Borchert,C., Brazille,S., Brooks,J., Baton,M.,
Ferreira,H., Kawasaki,S., McColough,A., Michalowski,C.B.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional genomes of plant stress tolerance
Unpublished (2000)
Contact: Michalowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu
An open reading frame exists.
Location/Qualifiers
1..1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="Root"
/dev_stage="5-6 weeks old"
/cclone_lib="MF"
/note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2:
xhoI"

ORIGIN
Query Match 14.9%; Score 49.6; DB 2; Length 1038;
Best Local Similarity 60.1%; Freq. No. 0.0016;
Matches 101; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

Qy 30 TGAGCCTTTTCTTACTGCTGATGCCATCCAAAGTTTCGAGCAGCGGATTCAGTA 89
|||||
Db 391 TGAGGCCAAATTTCTGCTGATGCTATACAGATGTTCTGAGCAGCAGCGTTTAGTT 450
|||||

Qy 90 CATGAGAACCAAGTCA---AGACTAATTTAATAGAGCAATTCACCTGATCCCAAGT 146
|||||
Db 451 TATTGAAGTAAAGTATGACCCAAAGTGTATACATGCTGTTCACCAACCGACCGAAAGT 510
|||||

Qy 147 AATTAATTTGGAGAGAGTGGGCAAAATCTCTGAGCAATTTCACA 194
|||||
Db 511 GCTGAGTTCGGGTATCAATTGGGTGAACATTTTCATGAGACTCATTA 558
|||||

RESULT 13
BE037217 639 bp mRNA linear EST 07-JUN-2000
LOCUS MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein/antiviral protein, mRNA sequence.
ACCESSION BE037217.1 GI:8332233
VERSION
KEYWORDS
EST:
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL Caryophyllales; Alzooceae; Mesembryanthemum.
COMMENT 1 (bases 1 to 639)
Bohner,H.J., Borchert,C., Brazille,S., Brooks,J., Baton,M.,

Retrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu.

FEATURES

source
1. 639
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN

Query Match 14.6%; Score 48.6; DB 2; Length 639;
Best Local Similarity 69.5%; Pred. No. 0.0027;
Matches 66; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 10 GATTGATCCCTGTAATAAGTGGCTTTTCTTCTAGTGGATCCATCAATGTTTCA 69
DB 374 GATTAATGATGAAAGAGCTGAGGCTACATTTCTTCTAGTGGATCCATCAATGTTTGT 433
QY 70 GAGGACGGCGATTCAAGTACATGAGAACCACT 104
DB 434 GAGGCTGACGCTTCTTCTACATGACGAGAGAGT 468

RESULT 14
CN782289
LOCUS
DEFINITION
CN782289 829 bp mRNA linear EST 21-MAY-2004
EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CN782289.1 GI:47561753
EST.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)

REFERENCE
AUTHORS
Colles, N.D., Coleman, C.E., Christensen, S.A., Jellen, E.N.,
Stevens, M.R., Bonifacio, A., Rojas-Beltran, J.A., Fairbanks, D.J. and
Maughan, P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms

TITLE
JOURNAL
COMMENT
Plant Sci. 168 (2), 439-447 (2005)
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.
Location/Qualifiers
1. 829

FEATURES

source
/organism="Chenopodium quinoa"
/mol_type="mRNA"
/cultivar="Real"
/db_xref="taxon:63459"
/clone="S02J22"

/tissue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_lib="cgsed"
/note="Vector: pRipLEX2; Site 1: Sfil; Site 2: Sfil;
Developing Seed cDNA library from Chenopodium quinoa"

ORIGIN

Query Match 13.9%; Score 46.4; DB 7; Length 829;
Best Local Similarity 67.7%; Pred. No. 0.013; Length 829;
Matches 65; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 25 AAAATGAGGCTTTTCTTCTAGTGGATCCATCCAAATGGTTTCAGAGCGCGATTC 84
DB 572 AAAATGAGGCTGGTTCTTCTAGTGGATCCATCCAAATGGTTTCAGAGCGCGATTC 631
QY 85 AAGTACATGAGAACCAAGTCAAGTCAATTTAT 120
DB 632 AAGTACATGAGAACCAAGTCAAGTCAATTTAT 667

RESULT 15

BE036639
LOCUS
DEFINITION
BE036639 1021 bp mRNA linear EST 07-JUN-2000
MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BE036639.1 GI:8331648
EST.
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astaceae; Mesembryanthemum.
1 (bases 1 to 1021)

REFERENCE
AUTHORS
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Retrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu
An open reading frame exists.
Insert length: 1 Std Error: 0.00.
Location/Qualifiers
1. 1021

FEATURES

source
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
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/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

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Best Local Similarity 58.9%; Pred. No. 0.049;
Matches 96; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

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DB 664 TGAAGCTTTTCTTCTAGTGGATCCATCCAAATGGTTTCAGAGCGCGATTCAGTA 723
QY 90 CATGAGAACCA--AGTCAAGCTAATTTATATAGAGATTCACCCGATCCCAAGT 146
DB 724 TATTGAAGTAGTACCCAAAGTGTGACATGCTCTTAACCCGACCCGAAAGT 783
QY 147 AATTATTTGAGAGAGAGTGGGCGCAATCTCTGAGGCAATT 189
DB 784 GCTGAGTTTGGGAGAACATGGGGAGAGTTTCGCAAGAAATT 826

Mon Apr 10 07:26:52 2006

us-09-978-274a-7.rst

Page 8

Search completed: April 9, 2006, 04:10:56
Job time : 1581.51 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 115.598 Seconds
(without alignments)
5120.590 Million cell updates/sec

Title: US-09-978-274A-7

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	233	70.0	1195	2	US-08-342-786B-1
3	233	70.0	1379	2	US-08-500-611-1
4	233	70.0	1379	2	US-08-500-694-1
5	233	70.0	1379	3	US-07-865-169-1
6	233	70.0	1379	3	US-07-865-169-2
7	233	70.0	1379	3	US-07-865-169-1
8	233	70.0	1379	3	US-09-005-273-1
9	233	70.0	1379	6	PCT-US96-11546-1
10	233	70.0	1379	3	US-08-501-253A-1
11	233	70.0	1379	3	US-08-138-636-1
12	233	70.0	1379	2	US-08-319-622A-1
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28	72.4	21.7	813	2	US-07-901-707-57	Sequence 57, Appl
29	72.4	21.7	813	2	US-07-988-430-11	Sequence 11, Appl
30	72.4	21.7	813	2	US-07-988-430-57	Sequence 57, Appl
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32	72.4	21.7	813	2	US-08-488-113B-11	Sequence 11, Appl
33	72.4	21.7	813	2	US-08-477-484B-11	Sequence 11, Appl
34	72.4	21.7	813	2	US-08-646-360-11	Sequence 11, Appl
35	72.4	21.7	813	2	US-08-621-803-246	Sequence 246, Appl
36	72.4	21.7	813	3	US-08-839-765-11	Sequence 11, Appl
37	72.4	21.7	813	3	US-09-136-389-11	Sequence 11, Appl
38	72.4	21.7	813	3	US-09-217-352-246	Sequence 246, Appl
39	72.4	21.7	813	3	US-09-610-838-11	Sequence 11, Appl
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41	72.4	21.7	813	6	PCT-US92-09487-11	Sequence 11, Appl
42	72.4	21.7	813	6	PCT-US92-09487-57	Sequence 57, Appl
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ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoleuca
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
TITLE OF INVENTION: Plant Transformed Thereof.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/117986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA

REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1

Query Match 70.0%; Score 233; DB 2; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;

Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 64 GTTTCAGAGGACGAGGATTCATGATGAGAACCAAGTCAAGTCAATTTTAAATGA 123
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DB 870 GCAATTCACCTGATCCCAAGTAAATTTTGGAGGAGAGTGGGGCAAAATCTGAG 929
QY 184 GCAATTCACATGCCAAGATGGGGCTTTAACCCAAACCACTTGAAGTGAATGCCAA 243
DB 930 GCAATTCACATGCCAAGATGGGGCTTTAACCCAAACCACTTGAAGTGAATGCCAA 989
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RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329

GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 70.0%; Score 233; DB 2; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTTCATTCATTCCTGTTAAACTGAGGCTTTTCTTACTGTAGCCATCAATG 63
DB 750 GAGTTCATTCATTCCTGTTAAACTGAGGCTTTTCTTACTGTAGCCATCAATG 809
QY 64 GTTTCAGAGGACGAGGATTCATGATGAGAACCAAGTCAAGTCAATTTTAAATGA 123
DB 810 GTTTCAGAGGACGAGGATTCATGATGAGAACCAAGTCAAGTCAATTTTAAATGA 869
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DB 930 GCAATTCACATGCCAAGATGGGGCTTTAACCCAAACCACTTGAAGTGAATGCCAA 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATGATGATGCACTCTTAAG 303
DB 990 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATGATGATGCACTCTTAAG 1049
QY 304 TACGTTAATGAACCTGTCAACAACCTTA 332
DB 1050 TACGTTGATGAGGCTGTCAACAACCTTA 1078

RESULT 5
US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940

GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:

ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-1

Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9,4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 123
810 GTATCAGAGGAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAACTAATTTTAACGA 869
124 GCAATTCACCTGATCCCAAGTAAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
870 GCAATTCACCTGATCCCAAGTAAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
184 GCAATTCACCAATGCCAAGATGGGCTTTACCCAAACCACTTGAAGTATGATGCCAA 243
930 GCAATTCATGATGCCAAGATGGAGTTTACCCAAACCTCTCGAGTATGATGCCAGT 989
244 GGTACCAAGTGAATGATTTCTTGAAGTGAATGAATCAATGATGATGGCACTCTTAAG 303
990 GGTGCCAAGTGAATGATTTCTTGAAGTGAATGAATCAAGCTGATGATGCACTTTAAC 1049
304 TACGTTAATGGAACCTGTCAACAACCTTA 332
1050 TACGTTGATGGAGCTGTCAACAACCTTA 1078

RESULT 6
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th

CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9,4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

4 GAGTTGATTCATTCCTCCGTAAACCTGAGGCTTTTCTACTGCTGATCCATCCAAATG 63
750 GAGTGATGTCATTCATCTGAGAAACCGAAGCGAATTCCTATTGCTAGCCATACAAATG 809
64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 123
810 GTATCAGAGGAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAACTAATTTTAACGA 869
124 GCAATTCACCTGATCCCAAGTAAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
870 GCAATTCACCTGATCCCAAGTAAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
184 GCAATTCACCAATGCCAAGATGGGCTTTACCCAAACCACTTGAAGTATGATGCCAA 243
930 GCAATTCATGATGCCAAGATGGAGTTTACCCAAACCTCTCGAGTATGATGCCAGT 989
244 GGTACCAAGTGAATGATTTCTTGAAGTGAATGAATCAATGATGATGGCACTCTTAAG 303
990 GGTGCCAAGTGAATGATTTCTTGAAGTGAATGAATCAAGCTGATGATGCACTTTAAC 1049
304 TACGTTAATGGAACCTGTCAACAACCTTA 332
1050 TACGTTGATGGAGCTGTCAACAACCTTA 1078

RESULT 7
US-09-005-273-1
Sequence 1, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAB MUTANTS THAT EXHIBIT ANTI-VIRAL
AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEHNER, DAVID, LITTEMBERG, KRUMHOLZ &
ADDRESSEE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey

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: COUNTRY: USA
: ZIP: 07090
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/005,273
: FILING DATE: 09-JAN-1998
: CLASSIFICATION: 800
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/500,611
: FILING DATE: 11-JUL-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/500,694
: FILING DATE: 11-JUL-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/11546
: FILING DATE: 11-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Foley, Shawn P.
: REGISTRATION NUMBER: 33,071
: REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-654-5000
: TELEFAX: 908-654-7866
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1379 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 225..1163
: FRATURE:
: NAME/KEY: sig_peptide
: LOCATION: 225..290
: US-09-005-273-1

Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTTACTGTGTAAGCCATCCAAATG 63
DB 750 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTTACTGTGTAAGCCATCCAAATG 809
QY 64 GTTTCAGAGCAGCGGATTCAGATCATAGAGAACCAAGTCAGACTAATTTTAATGA 123
DB 810 GTATCAGAGCAGCAAGATTCAGATCATAGAGAACCAAGTCAGACTAATTTTAATGA 869
QY 124 GCATTTACCTGATCCCAAGTAATTATTGGAGAGAGAGTGGGCAAAATCTCTAG 183
DB 870 GCATTTACCTGATCCCAAGTAATTATTGGAGAGAGAGTGGGCAAAATCTCTAG 929
QY 184 GCAATTCAGATCCCAAGTAATTATTGGAGAGAGAGTGGGCAAAATCTCTAG 243
DB 930 GCAATTCAGATCCCAAGTAATTATTGGAGAGAGAGTGGGCAAAATCTCTAG 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATGTAAGTGGCACTCTTAAG 303
DB 990 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATGTAAGTGGCACTCTTAAG 1049
QY 304 TACGTTATGGAACCTCTCAGACACTTA 332
DB 1050 TACGTTATGGAACCTCTCAGACACTTA 1078
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RESULT 8
US-09-005-273-3

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: Sequence 3, Application us/09005273
: Patent No. 6337030
: GENERAL INFORMATION:
: APPLICANT: Tumer, Nilgun E.
: TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
: TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESS: LERNER, DAVID, LITTENBERG, KRUMHOLTZ &
: ADDRESS: MENTILIK
: STREET: 600 South, Avenue West
: CITY: Westfield
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07090
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/005,273
: FILING DATE: 09-JAN-1998
: CLASSIFICATION: 800
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/500,611
: FILING DATE: 11-JUL-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/500,694
: FILING DATE: 11-JUL-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/11546
: FILING DATE: 11-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Foley, Shawn P.
: REGISTRATION NUMBER: 33,071
: REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-654-5000
: TELEFAX: 908-654-7866
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1379 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 225..1163
: FRATURE:
: NAME/KEY: sig_peptide
: LOCATION: 225..290
: US-09-005-273-3

Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTTACTGTGTAAGCCATCCAAATG 63
DB 750 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTTACTGTGTAAGCCATCCAAATG 809
QY 64 GTTTCAGAGCAGCGGATTCAGATCATAGAGAACCAAGTCAGACTAATTTTAATGA 123
DB 810 GTATCAGAGCAGCAAGATTCAGATCATAGAGAACCAAGTCAGACTAATTTTAATGA 869
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Qy 304 TACGTTAATGAACTGTCAACAACCTTA 332
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RESULT 9
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSES: Lerner, David, Littleberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Query Match 70.0%; Score 233; DB 6; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 4 GGAGTGAATTCATTCCTGTAATAAAGCTTTTCTACTGTAGCCATCCAAATG 63
Db 750 GGAGTGAATTCATTCCTGTAATAAAGCTTTTCTACTGTAGCCATCCAAATG 809

Qy 64 GTTTCAGAGCGCGCATTCATGATACATAGAGAACCAAGTCAATTTTAAATAGA 123
Db 810 GTATCAGAGCGCGCATTCATGATACATAGAGAACCAAGTCAATTTTAAAGAG 869
Qy 124 GCATTCATCCTGATCCCAAGTAAATTAATTTGGAGAGAAATGGGCAAAATCTGTAG 183
Db 870 GCATTCATCCTGATCCCAAGTAAATTAATTTGGAGAGAAATGGGCAAAATCTGTAG 929
Qy 184 GCAATTCATGATGCCAAGATGAGGCTTTACCCAAACCACTTGACTAGTGCAGTCCAGT 243
Db 930 GCAATTCATGATGCCAAGATGAGGCTTTACCCAAACCTTGACTAGTGCAGTCCAGT 989
Qy 244 GGTACCAAGTGTAGTCTTGTAGTGTGAATGATCGATGTCGACCTCCCTAG 303
Db 990 GGTGCCAAGTGTAGTGTGAGAGATGAATCAACCTGATGTACACTTTAAAC 1049
Qy 304 TACGTTAATGAACTGTCAACAACCTTA 332
Db 1050 TACGTTGTGGAGCTGTCAACAACCTTA 1078

RESULT 10
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
APPLICANT: Turner, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSES: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 69.5%; Score 231.4; DB 3; Length 1379;
Best Local Similarity 81.5%; Pred. No. 3.2e-66;
Matches 268; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 4 GGAGTGAATTCATTCCTGTAATAAAGCTTTTCTACTGTAGCCATCCAAATG 63
Db 750 GGAGTGAATTCATTCCTGTAATAAAGCTTTTCTACTGTAGCCATCCAAATG 809

QY 64 GTTTCAGAGCGCAGCGGATTCAAGTACATAGAGAACCAAGTCAAGCTAATTTTATAGA 123
DB 810 GTATCAGAGGAGCAGAGATTCAAGTACATAGAGAAATCAGTGAAACTAATTTTAAACAA 869
QY 124 GAATCTACCCCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGGCAAAATCTGTGAG 183
DB 870 GCATTCACCCCTTAATCCCAAGTACTTAATTTTGCAAGAACATGGGGTAAGATTTCAACA 929
QY 184 GCAATTCACCAATGCCAAGAAATGGGGCTTTACCCAAACCACTTGAGCTAGTGAATGCCAA 243
DB 930 GCAATTCATGATGCCAAGAAATGAGATTTTACCCAAACCTCTGAGCTAGTGAATGCCAA 989
QY 244 GTTACCAAGTGATAGTCTTGAAGTGAATCAATCGATGTGCACTCCTTAAG 303
DB 990 GGTGCAAGTGATAGTGTGAGAGTGAATCAAGCTGATGTGCACTCCTTAAC 1049
QY 304 TACGTTATGGAACCTGTCAAGCACTTA 332
DB 1050 TACGTTGTTGGAGCTGTCAAGCACTTA 1078

RESULT 11

US-08-138-636-1
Sequence 1, Application US/08138636

Patent No. 534865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 534865e1 Genome Coding PhytoIacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PhytoIacca Insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3,9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GAGATTGATTCATTCCTCTGTAATAAACTGAGGCTTTTCTTCTACTGTAGCCATCAATG 63
DB 517 GAGAGAGCTGATTCATCTAGAGAAACGAGCTGAATTCCTACTGTAGCCATCAATG 576
QY 64 GTTTCAGAGCGCAGCGGATTCAAGTACATAGAGAACCAAGTCAAGCTAATTTTATAGA 123
DB 577 GTATCAGAGGAGCAGCAAGATTCAGTACATAGAGAAATCAGTGAAACTAATTTTAAACGA 636
QY 124 GAATCTACCCCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGGCAAAATCTGTGAG 183
DB 637 CCATTCACCCCTTAATCCCAAGTACTTAATTTTGCAAGAACATGGGGTAAGATTTCTTCA 696
QY 184 GCAATTCACCAATGCCAAGAAATGGGGCTTTACCCAAACCACTTGAGCTAGTGAATGCCAA 243
DB 697 GCAATTCATGATGCCAAGAAATGAGATTTTACCCAAACCTCTGAGCTAGTGAATGCCAA 756
QY 244 GTTACCAAGTGATAGTCTTGAAGTGAATCAATCGATGTGCACTCCTTAAG 303
DB 757 GGTGCAAGTGATAGTGTGAGAGTGAATCAAGCTGATGTGCACTCCTTAAC 816
QY 304 TACGTTATGGAACCTGTCAAGCACTTA 332
DB 817 TACGTTGTTGGAGCTGTCAAGCACTTA 845

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A

Patent No. 565646

GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/04445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622a-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3.9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GGAGTGAATCATCCCTGTAACTGAGGCTTTTCTACTGTAGCCATCCAAATG 63
DB 517 GGAGTGAATCATCCCTGTAACTGAGGCTTTTCTACTGTAGCCATCCAAATG 576
QY 64 GTTCAGAGGAGCGCCATTCAGTACATAGAGAACCAAGTCAAGCTTAATTTAATGA 123
DB 577 GTATCAGAGGAGCGCAAGTTCAGTACATAGAGTCAAGTCAAGTCAATTTTAACGA 636
QY 124 GCATTCACCTGATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 637 CCATTCACCTGATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
QY 184 GCAATTCAGTATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 697 GCAATTCAGTATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
QY 244 GTTACCAAGTATGATTTCTTAGAGTGAATGAATCATCGATGTCATCTTAG 303
DB 757 GGTGCAAAATGATGATTTCTTAGAGTGAATGAATCATCGATGTCATCTTAG 303
QY 304 TACGTTAATGGAACCTGTCAAGCACTTA 332
DB 817 TACGTTAATGGAACCTGTCAAGCACTTA 332

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326e1 Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3.9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GGAGTGAATCATCCCTGTAACTGAGGCTTTTCTACTGTAGCCATCCAAATG 63
DB 517 GGAGTGAATCATCCCTGTAACTGAGGCTTTTCTACTGTAGCCATCCAAATG 576
QY 64 GTTACAGAGGAGCGCCATTCAGTACATAGAGAACCAAGTCAAGCTTAATTTAATGA 123
DB 577 GTATCAGAGGAGCGCAAGTTCAGTACATAGAGTCAAGTCAAGTCAATTTTAACGA 636
QY 124 GCATTCACCTGATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 637 CCATTCACCTGATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
QY 184 GCAATTCAGTATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 697 GCAATTCAGTATCCCAAGTATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
QY 244 GTTACCAAGTATGATTTCTTAGAGTGAATGAATCATCGATGTCATCTTAG 303
DB 757 GGTGCAAAATGATGATTTCTTAGAGTGAATGAATCATCGATGTCATCTTAG 303
QY 304 TACGTTAATGGAACCTGTCAAGCACTTA 332
DB 817 TACGTTAATGGAACCTGTCAAGCACTTA 332

RESULT 14
PCT-US91-05766-1
Sequence 1, Application PC/TUS9105766
GENERAL INFORMATION:
APPLICANT: Rosenblum, Michael
APPLICANT: Kohr, William Jack
APPLICANT: Agarwal, Bharat
TITLE OF INVENTION: Protein Structure of the Plant Toxin
TITLE OF INVENTION: Gelonin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney #5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Search completed: April 8, 2006, 09:48:55
Job time : 116.598 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 384.756 Seconds
(without alignments)
7157.007 Million cell updates/sec

Title: US-09-978-274A-7

Perfect score: 333
Sequence: 1 atggagagtgatcattcc.....gaacctgcagacaactta 333

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	US-09-978-274A-7	Sequence 7, Appl1
2	329	98.8	945	US-09-978-274A-1	Sequence 1, Appl1
3	328.4	98.6	792	US-09-978-274A-3	Sequence 3, Appl1
4	302.4	90.8	1092	US-09-978-274A-19	Sequence 19, Appl1
5	233	70.0	1368	US-09-978-274A-31	Sequence 31, Appl1
6	233	70.0	1376	US-10-467-009-1	Sequence 1, Appl1
7	233	70.0	1379	US-09-978-274A-30	Sequence 30, Appl1
8	233	70.0	1379	US-11-106-187-1	Sequence 1, Appl1
9	78.8	23.7	2404	US-11-084-080-15	Sequence 15, Appl1
10	78.8	23.7	2404	US-11-084-080-19	Sequence 19, Appl1
11	78.8	23.7	2404	US-11-084-080-21	Sequence 21, Appl1
12	78.8	23.7	2404	US-11-084-080-23	Sequence 23, Appl1
13	78.8	23.7	2431	US-11-084-080-27	Sequence 27, Appl1
14	75.4	22.6	935	US-10-919-750-4	Sequence 4, Appl1
15	73.8	22.2	804	US-09-861-257-37	Sequence 37, Appl1
16	73.8	22.2	804	US-09-861-257-38	Sequence 38, Appl1
17	73.8	22.2	804	US-10-189-360-22	Sequence 22, Appl1
18	73.8	22.2	804	US-10-189-360-23	Sequence 23, Appl1
19	72.6	21.8	1233	US-09-861-257-24	Sequence 24, Appl1
20	72.6	21.8	1233	US-10-189-360-80	Sequence 80, Appl1
21	72.4	21.7	813	US-09-765-527-246	Sequence 246, Appl1
22	72.4	21.7	813	US-10-127-890-11	Sequence 11, Appl1
23	72.4	21.7	813	US-10-717-243-11	Sequence 11, Appl1

24	72.4	21.7	955	US-09-765-527-258	Sequence 258, App
25	72.4	21.7	1003	US-09-765-527-252	Sequence 252, App
26	72.4	21.7	1072	US-09-765-527-250	Sequence 250, App
27	72.4	21.7	1176	US-10-074-596-2	Sequence 2, Appl1
28	72.4	21.7	1500	US-10-964-195-12	Sequence 12, Appl1
29	72.4	21.7	1527	US-10-074-596-10	Sequence 10, Appl1
30	72.4	21.7	2407	US-11-084-080-25	Sequence 25, Appl1
31	70.6	21.2	855	US-11-106-187-20	Sequence 20, Appl1
32	70.6	21.2	934	US-09-978-274A-32	Sequence 32, Appl1
33	70.6	21.2	934	US-11-106-187-3	Sequence 3, Appl1
34	69	20.7	804	US-09-861-257-22	Sequence 22, Appl1
35	69	20.7	804	US-09-861-257-36	Sequence 36, Appl1
36	69	20.7	804	US-10-189-360-19	Sequence 19, Appl1
37	69	20.7	804	US-10-189-360-21	Sequence 21, Appl1
38	69	20.7	1230	US-10-189-360-53	Sequence 53, Appl1
39	69	20.7	1251	US-09-861-257-77	Sequence 77, Appl1
40	69	20.7	1251	US-10-189-360-74	Sequence 74, Appl1
41	69	20.7	1260	US-10-189-360-75	Sequence 75, Appl1
42	69	20.7	1260	US-10-189-360-72	Sequence 72, Appl1
43	69	20.7	1266	US-09-861-257-78	Sequence 78, Appl1
44	69	20.7	1266	US-10-189-360-75	Sequence 75, Appl1
45	69	20.7	1269	US-09-861-257-81	Sequence 81, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-7
Sequence 7, Application US/0978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225-4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7
LENGTH: 333
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-7

Query Match	100.0%	Score 333;	DB 3;	Length 333;
Best Local Similarity	100.0%;	Pred. No. 4.6e-94;		
Matches 333;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGTTGATTCATTCCTGTAATAAAGAGGCTTTTCTTCTAGTGGATTCGAA	60	
DB	1	ATGGAGTTGATTCATTCCTGTAATAAAGAGGCTTTTCTTCTAGTGGATTCGAA	60	
QY	61	ATGGAGTTGAGGAGGAGGATTCAGATCATAGAGCAAGCACTTAAGTGAATTTTAAAT	120	
DB	61	ATGGAGTTGAGGAGGAGGATTCAGATCATAGAGCAAGCACTTAAGTGAATTTTAAAT	120	
QY	121	AGAGCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGGAGCAAAATCTCT	180	
DB	121	AGAGCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGGAGCAAAATCTCT	180	
QY	181	GAGGCAATTCAGAAATGCAAGAAATGGGGCTTAAACCAACCTTAAGTGAATGCGC	240	
DB	181	GAGGCAATTCAGAAATGCAAGAAATGGGGCTTAAACCAACCTTAAGTGAATGCGC	240	
QY	241	AAAGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATCGATGAGCACTCTT	300	
DB	241	AAAGTACCAAGTGAATGTTCTTAGAGTGAATGAATCAATCGATGAGCACTCTT	300	

QY 301 AAGTACGTTAATGGAACCTGTGACAACTTAA 333
DB 301 AAGTACGTTAATGGAACCTGTGACAACTTAA 333

RESULT 2
US-09-978-274A-1
Sequence 1, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 945
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-1

Query Match 98.8%; Score 329; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 63
DB 532 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 591
QY 64 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 123
DB 592 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 651
QY 124 GCATTTACCTGTATCCCAAGTAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
DB 652 GCATTTACCTGTATCCCAAGTAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 711
QY 184 GCAATTCACAATGCCAAGATGGGGCTTTAACCACCACTTGAGCTAGTGAGTGCAGAA 243
DB 712 GCAATTCACAATGCCAAGATGGGGCTTTAACCACCACTTGAGCTAGTGAGTGCAGAA 771
QY 244 GGTAACAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGATGCACTCTCTTAA 303
DB 772 GGTAACAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGATGCACTCTCTTAA 831
QY 304 TACGTTAATGGAACCTGTGACAACTTAA 332
DB 832 TACGTTAATGGAACCTGTGACAACTTAA 860

RESULT 3
US-09-978-274A-3
Sequence 3, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
PRIORITY FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 792
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-3

Query Match 98.6%; Score 328.4; DB 3; Length 792;
Best Local Similarity 99.7%; Pred. No. 1.9e-92;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 63
DB 463 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 522
QY 64 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 123
DB 523 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 582
QY 124 GCATTTACCTGTATCCCAAGTAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 183
DB 583 GCATTTACCTGTATCCCAAGTAATTTTGAAGAGAGAGTGGGCAAAATCTCTGAG 642
QY 184 GCAATTCACAATGCCAAGATGGGGCTTTAACCACCACTTGAGCTAGTGAGTGCAGAA 243
DB 643 GCAATTCACAATGCCAAGATGGGGCTTTAACCACCACTTGAGCTAGTGAGTGCAGAA 702
QY 244 GGTAACAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGATGCACTCTCTTAA 303
DB 703 GGTAACAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGATGCACTCTCTTAA 762
QY 304 TACGTTAATGGAACCTGTGACAACTTAA 333
DB 763 TACGTTAATGGAACCTGTGACAACTTAA 792

RESULT 4
US-09-978-274A-19
Sequence 19, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 1092
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PAP-S/Cybotatin fusion
US-09-978-274A-19

Query Match 90.8%; Score 302.4; DB 3; Length 1092;
Best Local Similarity 99.7%; Pred. No. 3.3e-84;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 63
DB 463 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 522
QY 64 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 123
DB 523 GTTTCAGAGGCGCGGATTCAGATCATTAGAGAACCAAGTCAAGCTAATTTAATAGA 582

RESULT 6
US-10-467-009-1
; Sequence 1, Application US/10467009

Query Match	70.0%;	Score 233;	DB 3;	length 1379;
-------------	--------	------------	-------	--------------

Best Local Similarity 81.8%; Pred. No. 2,5e-62;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTCTAGCTGATGCAATCCAAATG 63
DB 750 GGAGTGTATGCTACTGAGAAACCGAAGCCGAATTCCTATTTGGTAGCATTAACAATG 809
QY 64 GTTTCAGAGGACGGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAATAGA 123
DB 810 GTATCAGAGGACGACGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAACGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCATTCACATGCGAAGTAATGGGCTTTTACCACCACTTGAAGTGAATGCCAA 243
DB 930 GCATTCATGATCCAGAAATGAGTTTACCCAACTCTGAGCTAGTGAATGCCAGT 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGAGTGTGCACTCTTAA 303
DB 990 GGTGCGAAGTGAATGTTGTTGAGTGAATCAAGCTGATGATGAGTGTGCACTCTTAA 1049
QY 304 TACGTTAATGAACTGTGACACACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGACACACTTA 1078

RESULT 8

US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: *Physiolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 70.0%; Score 233; DB 10; Length 1379;
Best Local Similarity 81.8%; Pred. No. 2,5e-62;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTCTAGCTGATGCAATCCAAATG 63
DB 750 GGAGTGTATGCTACTGAGAAACCGAAGCCGAATTCCTATTTGGTAGCATTAACAATG 809
QY 64 GTTTCAGAGGACGGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAATAGA 123
DB 810 GTATCAGAGGACGACGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAACGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCATTCACATGCGAAGTAATGGGCTTTACCCAAACCACTTGAAGTGAATGCCAA 243

DB 930 GCATTCATGATCCCAAGTAATGAGTTTACCCAACTCTCAGCTAGTGAATGCCAGT 989

QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGAGTGGCACTCTTAA 303
DB 990 GGTGCGAAGTGAATGTTGTTGAGTGAATCAAGCTGATGATGAGTGTGCACTCTTAA 1049

QY 304 TACGTTAATGAACTGTGACACACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGACACACTTA 1078

RESULT 9

US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeanick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-15

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGTAGGCAATCCAAATGTTTCAGAGGACGGGATTCAGATGACATGAGAC 99
DB 1287 TTCTTCTTATGTCATCCAAATGTTTCAGAGGACGGGATTCAGATGACATGAGAC 1346
QY 100 CAAGTCAAGCTAAT---TTTAATAGAGCAATTCACCTGATCCCAAGTAATTAATTTG 156
DB 1347 GAGGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1406
QY 157 GAGGAGAAGTGGGCAAAATCTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 1407 GAGGAGAAGTGGGCAAAATCTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 1466
QY 213 ACCCAAC--CACTTGAAGTGAATGCCAAGTGAATGCCAAGTGAATGTTCTTGAAGT 270
DB 1467 ATTATCCGCACTTCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1526
QY 271 GATGAATCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
DB 1527 AGTCAATTAATGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560

RESULT 10

US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1

GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSCH, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGTTAGCCATCAATGGTTTCAAGGAGCGGCAATTCAGTACATAGAGAC 99
DB 2105 TTCTTTCTATGTCTATCCAAATGGTTTCAAGGAGCGCTCGTTCAAAATATATAGACT 2164
QY 100 CAAGTCAAGACTAAT--TTAATAGAGACTTCACTGATCCCAAGTAAATTAATTTG 156
DB 2165 GAGGTGTTGATAGAGATTAATGATCATTCAAACCTAATTTAAAGTATGAACTTG 2224
QY 157 GAGGAGAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 2225 GAGAACATTTGGGGGCAATCTTGATGCCATTCACAAATCAATCCCAATGTACCACT 2284
QY 213 ACCCAAC--CACTTGAGCTAGTGATGCCAAGGTACCAAGTATGTTCTTAGAGTG 270
DB 2285 ATTAATCCGCACTTCAGTTGATTAAGCCCTCAAAATGACCCATGGGTTGTAATTAAGTG 2344
QY 271 GATGAATCAATCGTATGATGGCACTCCTTAAGT 304
DB 2345 AGTCAAATTAAGTCCGATATGGGTATCCTTAAGT 2378

RESULT 11
US-11-084-080-21
Sequence 21, Application US/11084080
Publication No. US20050238642A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSCH, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-21

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGTTAGCCATCAATGGTTTCAAGGAGCGGCAATTCAGTACATAGAGAC 99
DB 594 TTCTTTCTATGTCTATCCAAATGGTTTCAAGGAGCGCTCGTTCAAAATATATAGACT 653
QY 100 CAAGTCAAGACTAAT--TTAATAGAGACTTCACTGATCCCAAGTAAATTAATTTG 156
DB 654 GAGGTGTTGATAGAGATTAATGATCATTCAAACCTAATTTAAAGTATGAACTTG 713
QY 157 GAGGAGAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 714 GAGAACATTTGGGGGCAATCTTGATGCCATTCACAAATCAATCCCAATGTACCACT 773
QY 213 ACCCAAC--CACTTGAGCTAGTGATGCCAAGGTACCAAGTATGTTCTTAGAGTG 270
DB 774 ATTAATCCGCACTTCAGTTGATTAAGCCCTCAAAATGACCCATGGGTTGTAATTAAGTG 833
QY 271 GATGAATCAATCGTATGATGGCACTCCTTAAGT 304
DB 834 AGTCAAATTAAGTCCGATATGGGTATCCTTAAGT 867

RESULT 12
US-11-084-080-23
Sequence 23, Application US/11084080
Publication No. US20050238642A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSCH, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTCTAGTGAAGCCATCCAAATGTTTCAGAGGCGAGCGCATTCAGATACATAGAGAC 99
DB 1412 TTCTTTCTTATTTGATCCAAATGTTTCAGAGGCGAGCGCATTCAGATACATAGAGAC 1471
QY 100 CAAGTCAAGACTAAT---TTTAATAGAGATTTCTACCTGATCCCAAGTAATTAATTTG 156
DB 1472 GAGGTGTTGATAGAGATTAATGATCATTCAACTTAATTTAAAGTATTAAGACTTG 1531
QY 157 GAGGAGAAAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 1532 GAGAACCAATTGGGGCGCATCTTGATGCGCATTCACAATCATCCCAATATGACACT 1591
QY 213 ACCCAAC--CACTGAGCTAGTGAATGCGCAAGGTACCAAGTGAATGTTCTTAGAGTG 270
DB 1592 ATTATCCGGCATTCAGTTGATTAAGCCCTTCAAATGACCATGGTGTGTAATTAAGTG 1651
QY 271 GATGAATCAATCGTGAATGTCGCACTCCTTAAGT 304
DB 1652 AGTCAATTAAGTCCCGAATATGGGTAATCCTTAAGT 1685

RESULT 13

US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeanick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGAINVILLE PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THERMOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 2431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-27

Query Match 23.7%; Score 78.8; DB 10; Length 2431;
Best Local Similarity 63.1%; Pred. No. 1e-13; Indels 9; Gaps 3;
Matches 173; Conservative 0; Mismatches 92;

QY 40 TTCTCTAGTGAAGCCATCCAAATGTTTCAGAGGCGAGCGCATTCAGATACATAGAGAC 99
DB 1314 TTCTTTCTTATTTGATCCAAATGTTTCAGAGGCGAGCGCATTCAGATACATAGAGACT 1373
QY 100 CAAGTCAAGACTAAT---TTTAATAGAGATTTCTACCTGATCCCAAGTAATTAATTTG 156
DB 1374 GAGGTGTTGATAGAGATTAATGATCATTCAACTTAATTTAAAGTATTAAGACTTG 1433
QY 157 GAGGAGAAAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 1434 GAGAACCAATTGGGGCGCATCTTGATGCGCATTCACAATCATCCCAATATGACACT 1493
QY 213 ACCCAAC--CACTGAGCTAGTGAATGCGCAAGGTACCAAGTGAATGTTCTTAGAGTG 270
DB 1494 ATTATCCGGCATTCAGTTGATTAAGCCCTTCAAATGACCATGGTGTGTAATTAAGTG 1553

QY 271 GATGAATCAATCGTGAATGTCGCACTCCTTAAGT 304
DB 1554 AGTCAATTAAGTCCCGAATATGGGTAATCCTTAAGT 1587

RESULT 14

US-10-919-750-4
; Sequence 4, Application US/10919750
; Publication No. US20050120414A1
; GENERAL INFORMATION:
; APPLICANT: Diamond, Paul
; TITLE OF INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
; FILE REFERENCE: P1100-4US
; CURRENT APPLICATION NUMBER: US/10/919,750
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US 10/644,288
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 10/354,903
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/352,705
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 4
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Saponaria officinalis
US-10-919-750-4

Query Match 22.6%; Score 75.4; DB 9; Length 935;
Best Local Similarity 58.9%; Pred. No. 7.9e-13;
Matches 149; Conservative 0; Mismatches 101; Indels 3; Gaps 1;

QY 22 GTAAAACTGAGCTTTTCTTCTAGTGTGAGCATCCAAATGTTTCAGAGGCGAGCGCA 81
DB 634 GTTAAAGCAAGAGTGAATTCCTTCTTATGCTAATGATGACGCGTGAGCGCGCA 693
QY 82 TTCAAGTACATAGAGCAAGCAAGTCAATTTTAATGAGCATCTACCTGATCCC 141
DB 694 TTATGATACATCAAACTTGATATCAAGAACTTCCCAAGTCAACTCGGAAAC 753
QY 142 AAATTAATTAATTTGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCA---ATAGCC 198
DB 754 AAATGATTCAGTTTGAAGTTTAATGAGAAATTTCTACGGCAATATACGGGATGCC 813
QY 199 AAGATGGGCTTTACCAACCACTTGAAGTGAATGCAAGGTACCAAGTGATA 258
DB 814 AAAACGCGCTTAAATTAAGATTATTCGTTGGAAAGTTAGGCAAGTGAG 873
QY 259 GTTCTTAGAGTGG 271
DB 874 GACTTGCAATGG 886

RESULT 15

US-09-861-257-37
; Sequence 37, Application US/09861257
; Publication No. US2003004096A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Fietze, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100.423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G7"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-09-861-257-37

Query Match 22.2%; Score 73.8; DB 3; Length 804;
Best Local Similarity 58.5%; Pred. No. 2.4e-12;
Matches 148; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

QY	22	GTAAAACTGAGGCTTTTCTCTGAGCAATCCAAATGTTTTCAGAGGCAAGCGGA	81
DB	523	GTAAAAACGAAAGCTAGATTCCTTATCGTATTCAGATGACGCTGAGGCAAGCA	582
QY	82	TTCAAGTACATAGAACCAAGTCAAGCTAATTTTATAGACATCTTACCTGATCC	141
DB	583	TTTAGTACATACAAACTTGTATCAAGAACTTCCCAACAAGTCAACTCGGAAAC	642
QY	142	AAAGTAATTAATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	198
DB	643	AAAGTATTCAGTTGAGGTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	702
QY	199	AAGATGAGGCTTACCAACCACTGAGCTAGTGAATGCAAGATACCAAGTGATA	258
DB	703	AAAAACGCGTGTTAATAAGATTATGATTCGGGTTTGAAAAAGTGAAGCAAGT	762
QY	259	GTTCTTAGAGTG 271	
DB	763	GACTTGCAATGG 775	

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Job time: 385.756 secs

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OM nucleic - nucleic search, using SW model

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(without alignments)
4595.111 Million cell updates/sec

Title: US-09-978-274A-7
Perfect score: 333
Sequence: 1 atggagagtgatcattcc.....gaacctgacagacactta 333

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications NA New:
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6: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233	70.0	1360	14 US-11-010-795-19	Sequence 19, Appl
2	70.6	21.2	934	14 US-11-010-795-21	Sequence 21, Appl
3	63	18.9	1623	8 US-10-893-584-273	Sequence 273, Appl
4	61.4	18.4	807	14 US-11-010-795-23	Sequence 23, Appl
5	61.4	18.4	1807	8 US-10-893-584-196	Sequence 196, Appl
6	61.4	18.4	1810	8 US-10-893-584-168	Sequence 168, Appl
7	61.4	18.4	1813	8 US-10-893-584-245	Sequence 245, Appl
8	61.4	18.4	1819	8 US-10-893-584-238	Sequence 238, Appl
9	61.4	18.4	1822	8 US-10-893-584-175	Sequence 175, Appl
10	61.4	18.4	1822	8 US-10-893-584-182	Sequence 182, Appl
11	61.4	18.4	1825	8 US-10-893-584-231	Sequence 231, Appl
12	61.4	18.4	1828	8 US-10-893-584-210	Sequence 210, Appl
13	61.4	18.4	1831	8 US-10-893-584-161	Sequence 161, Appl
14	61.4	18.4	1831	8 US-10-893-584-203	Sequence 203, Appl
15	61.4	18.4	1834	8 US-10-893-584-154	Sequence 154, Appl
16	61.4	18.4	1837	8 US-10-893-584-266	Sequence 266, Appl
17	61.4	18.4	1843	8 US-10-893-584-259	Sequence 259, Appl
18	61.4	18.4	1849	8 US-10-893-584-252	Sequence 252, Appl

19	61.4	18.4	1855	8 US-10-893-584-3	Sequence 3, Appl
20	61.4	18.4	1855	8 US-10-893-584-5	Sequence 5, Appl
21	61.4	18.4	1855	8 US-10-893-584-7	Sequence 7, Appl
22	61.4	18.4	1855	8 US-10-893-584-9	Sequence 9, Appl
23	61.4	18.4	1855	8 US-10-893-584-13	Sequence 13, Appl
24	61.4	18.4	1855	8 US-10-893-584-15	Sequence 15, Appl
25	61.4	18.4	1855	8 US-10-893-584-17	Sequence 17, Appl
26	61.4	18.4	1855	8 US-10-893-584-19	Sequence 19, Appl
27	61.4	18.4	1855	8 US-10-893-584-21	Sequence 21, Appl
28	61.4	18.4	1855	8 US-10-893-584-23	Sequence 23, Appl
29	61.4	18.4	1855	8 US-10-893-584-25	Sequence 25, Appl
30	61.4	18.4	1855	8 US-10-893-584-27	Sequence 27, Appl
31	61.4	18.4	1855	8 US-10-893-584-29	Sequence 29, Appl
32	61.4	18.4	1855	8 US-10-893-584-31	Sequence 31, Appl
33	61.4	18.4	1855	8 US-10-893-584-33	Sequence 33, Appl
34	61.4	18.4	1855	8 US-10-893-584-35	Sequence 35, Appl
35	61.4	18.4	1855	8 US-10-893-584-37	Sequence 37, Appl
36	61.4	18.4	1855	8 US-10-893-584-39	Sequence 39, Appl
37	61.4	18.4	1855	8 US-10-893-584-48	Sequence 48, Appl
38	61.4	18.4	1855	8 US-10-893-584-50	Sequence 50, Appl
39	61.4	18.4	1855	8 US-10-893-584-52	Sequence 52, Appl
40	61.4	18.4	1855	8 US-10-893-584-54	Sequence 54, Appl
41	61.4	18.4	1855	8 US-10-893-584-74	Sequence 74, Appl
42	61.4	18.4	1855	8 US-10-893-584-77	Sequence 77, Appl
43	61.4	18.4	1855	8 US-10-893-584-80	Sequence 80, Appl
44	61.4	18.4	1855	8 US-10-893-584-83	Sequence 83, Appl
45	61.4	18.4	1855	8 US-10-893-584-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILDUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOPTERIN FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 70.0%; Score 233; DB 14; Length 1360;
Best Local Similarity 81.8%; Pred. No. 2.1e-61;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 4 GGAATTATTCATCCCTGTTAAAGAGGCTTTTCTACTGTGAGCATCAATG 63
DB 732 GGAATTATTCATCCCTGTTAAAGAGGCTTTTCTACTGTGAGCATCAATG 791
QY 64 GTTTCAGAGGAGCGCATTCAGATCATAGAGCAAGTCAAGATTAATTAAGA 123
DB 792 GTATCAAGGAGGAGCAATTCAGATCATAGAGTGAAGTGAATTAATTAAGA 851
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGGAGGAGAGTGGGCAAAATCTGAG 183
DB 852 GCATTCACCTGATCCCAAGTAATTAATTGGAGGAGAGTGGGCAAAATCTGAG 911

QY	GCATTTACATGCGCAAGATGGGGCTTACCCAAACCACTTGAGCTAGTGAATGCCAA	243
QY		
Db	GCAATTCATGATGCGCAAGATGAGTTTACCCAAACCTTCGAGCTAGTGAATGCCAGT	971
QY	GGTACCAAGTGAATAGTCTTACAGATGGATGAATCAATCGTAGTGGCACTCCTTAAG	303
QY		
Db	GGTGGCCAGTGGATATAGTCTTACAGATGGATGAATCAAGCCTGATGTAGCACTTAAAC	1031
QY	TACGTTAATGAACTGTACAGCAACTTA	332
QY		
Db	TACGTTGGTGGAGATGTACAGCAACTTA	1060

```

RESULT 2
US-11-010-795-21
; Sequence 21, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-11-010-795-21

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	Query Match	Similarity	21.2%	Score	70.6	DB	14	Length	934
	Best Local	Similarity	66.5%	Pred	2.2e-11				
	Matches	119	Conservative	0	Mismatches	54	Indels	6	Gaps
QY	24	AAAACTAGGCTTTTCTACTGTGATCCAAATGGTTTCAGAGCGCCGAT	83						
Db	543	AAAAATGAGGTGAATTTCTTTATAGCGTTCAATGGTTACTGAGGATCAAGTT	602						
QY	84	CAAGTACATAGGAACCAAGTCAAGCTTAATTTAAT-----AAGCATTTACCTGA	137						
Db	603	CAAAATACATTGGAACCAAGTGAAGGTAAATTTATGATGTCCAATGGGTATCAACCGA	662						
QY	138	TCCCAAGTAATTAATTTGAGAGAAAGTGGGGCAAAATCTGTAGGCAATCAATG	196						
Db	663	TCCTAAGGTATTTCCCTTAGAGAAAATTTGGAGCAGTGTCTTAAGTTCATTCGAAAG	721						

```

RESULT 3
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
;
GENERAL INFORMATION:
;
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Adamir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893, 584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403, 752
PRIOR FILING DATE: 1999-10-29

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: PRIOR APPLICATION NUMBER: US 10/089,058
: PRIOR FILING DATE: 2000-10-04
: NUMBER OF SEQ ID NOS: 274
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 273
: LENGTH: 1623
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Ricin-like toxin (T
US-10-893-564-273

```

Query Match	18.9%;	Score 63;	DB 8;	Length 1623;
Best Local Similarity	54.0%;	Pred. No. 6.2e-09;		
Matches 154;	Conservative	0;	Mismatches 125;	Indels 6;
				Gaps 1;

Qy	27	AACGAGGCTTTT	TTTCTACGTGAGC	CATCAAAATGGTTT	CAGAGGAGCGC	GATTCAA	86
Db	486	AACCTGCGCTG	TCTCTTTATTT	TGATCCAAATGATTT	CAGAAGCAGCA	AAATTTCA	545
Qy	87	GTACATGAGAAC	CAAGTCAAGCTA	ATTTT-----	AATGAGCATTT	CTACCTGATCC	140
Db	546	ATATTTTGA	GAGAGAAATG	CGCAGAGAAAT	TAGTACCAACG	GAGATCTGAC	605
Qy	141	CAAGTAATTA	TTTGTGAGAGAA	GTGGGGCAAA	TCTCTGAGCAAT	TCAATGCCA	200
Db	606	TAGCGATTT	CACTTGAGAA	TAGTGGGGAG	ACTTTCCACTGCA	ATTTCAAGAGCTTA	665
Qy	201	GAATGGGCTT	YACCAACCA	CTTGAGCTG	ATGATGCCAA	AGGTACCAAGT	260
Db	666	CCAAAGAGC	CTTGTGATG	CCAAATTC	CACTCAGAGAG	ATGATGTTCC	725
Qy	261	TCTTAGATG	ATGAATCA	ATCGATG	ATGGCACTC	CTTAAAGTA	305
Db	726	GTACAGTGT	AGATTAATTA	TCCATCAT	ATAGCTTCA	ATGGTGTA	770

```

RESULT 4
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US2006000571A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGÜN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010.795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/5529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ. ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Ricinus communis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

```

Query Match	18.4%	Score 61.4	DB 14	Length 807
Best Local Similarity	53.7%	Pred. No. 1.4e-08		
Matches	153	Conservative 0	Mismatches 126	Indels 6
			Gaps 1	
QY	27	AACGTAGGCTTTTCTTACTGTAGTCATCAATGTTTCAGAGCGAGCGCATTTCAA	86	
DB	489	AACCTGGCTGTTCTTTATTAATTGTCATCCAAATGATTTTCAGAGCAGCAAGATTCCA	548	
QY	87	GTACATAGAGAACCAAGTCAGAGCTTAATTT-----AATAGAGCATTTCAACCCGATCC	140	
DB	549	ATATATTTAGAGGAATATGCCGACGAGATTTAGTACACCGGAGATTTGCACCCGATCC	608	

US-10-893-584-245

Query Match 18.4%; Score 61.4; DB 8; Length 1813;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCCCAATGTTTCAGAGGAGCGGCAATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCCAATATATTTTCAGAGGAGCGGCAATTCAA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAATTAGGTACACCGGAGATCTGACCAAGATCC 716
QY 141 CAAAGTAAATTATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 200
DB 717 TAGCGTAATTACACTTGAGAAATAGTTGGGGAGACTTTCCACTGCAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 260
DB 777 CCAAGGAGCCTTGTCTGATGTCATTAATTCAGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTGAATGTGGCACTCCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATTCCTTATCATATGCTCTCATGTGTGA 881

RESULT 8

US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-238

Query Match 18.4%; Score 61.4; DB 8; Length 1819;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCCCAATGTTTCAGAGGAGCGGCAATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCCAATATATTTTCAGAGGAGCGGCAATTCAA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAATTAGGTACACCGGAGATCTGACCAAGATCC 716
QY 141 CAAAGTAAATTATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 200
DB 717 TAGCGTAATTACACTTGAGAAATAGTTGGGGAGACTTTCCACTGCAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 260

DB 777 CCAAGAGCCTTGTCTAGTCCCAATTCACACTGCAAGAGCGTAATGTTCCAAATTCAGTGT 836

QY 261 TCTTAGAGTGAGTAATCAATCGTGAATGGGCACTCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATTCCTTATCATATGCTCTCATGTGTGA 881

RESULT 9

US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175

Query Match 18.4%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCCCAATGTTTCAGAGGAGCGGCAATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCCAATATATTTTCAGAGGAGCGGCAATTCAA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAATTAGGTACACCGGAGATCTGACCAAGATCC 716
QY 141 CAAAGTAAATTATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 200
DB 717 TAGCGTAATTACACTTGAGAAATAGTTGGGGAGACTTTCCACTGCAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 260
DB 777 CCAAGGAGCCTTGTCTGATGTCATTAATTCAGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTGAATGTGGCACTCCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATTCCTTATCATATGCTCTCATGTGTGA 881

RESULT 10

US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584

;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 182
;; LENGTH: 1822
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-182

Query Match 18.4%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 86
DB 597 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 656
QY 87 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCAGCAAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTAATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGCAATTCACATGCCAA 200
DB 717 TAGGTAATTACCTTGGAATAGTGGGGAGACTTTCACCTGAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGGCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTAGTGCGACCTCCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 11
US-10-893-584-231
;; Sequence 231, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 231
;; LENGTH: 1825
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-231

Query Match 18.4%; Score 61.4; DB 8; Length 1825;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
QY 27 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 86

DB 597 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 656
QY 87 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCAGCAAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTAATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGCAATTCACATGCCAA 200
DB 717 TAGGTAATTACCTTGGAATAGTGGGGAGACTTTCACCTGAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGGCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTAGTGCGACCTCCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 12
US-10-893-584-210
;; Sequence 210, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 210
;; LENGTH: 1828
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-210

Query Match 18.4%; Score 61.4; DB 8; Length 1828;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
QY 27 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 86
DB 597 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCGATTCAA 656
QY 87 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCAGCAAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTAATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGCAATTCACATGCCAA 200
DB 717 TAGGTAATTACCTTGGAATAGTGGGGAGACTTTCACCTGAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGGCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTAGTGCGACCTCCTTAAGTA 305
DB 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 13
US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 161
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-161

Query Match 18.4%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGCTGAGCATCCAAATGTTTCAGAGCGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTTGCAATCCAAATGTTTCAGAGCGAGATTCGA 656
QY 87 GTACATAGAGAACCAAGTCAAGTATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGATTAAGTACACCGAGATCTGACAGATCC 716
QY 141 CAAAGTATTAATTTTGGAGAGAAAGTGGGCAAAATCTGAGGCAATTCAGATGCCAA 200
DB 717 TAGCGTATTAATCACTGAGAAATAGTTGGGAGACTTTCACATGCAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTGAGCTAGTGAATGCCAAAGTCAAGTATAGT 260
DB 777 CCAAGAGCCTTTGCTGATGTCATTCATTCAGTCAAGACGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 14
US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 203
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-203

Query Match 18.4%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGCTGAGCATCCAAATGTTTCAGAGCGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTTGCAATCCAAATGTTTCAGAGCGAGATTCGA 656
QY 87 GTACATAGAGAACCAAGTCAAGTATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGATTAAGTACACCGAGATCTGACAGATCC 716
QY 141 CAAAGTATTAATTTTGGAGAGAAAGTGGGCAAAATCTGAGGCAATTCAGATGCCAA 200
DB 717 TAGCGTATTAATCACTGAGAAATAGTTGGGAGACTTTCACATGCAATTCAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTGAGCTAGTGAATGCCAAAGTCAAGTATAGT 260
DB 777 CCAAGAGCCTTTGCTGATGTCATTCATTCAGTCAAGACGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 15
US-10-893-584-154
; Sequence 154, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 154
; LENGTH: 1834
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-154

Query Match 18.4%; Score 61.4; DB 8; Length 1834;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGCTGAGCATCCAAATGTTTCAGAGCGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTTGCAATCCAAATGATTTTCAGAGCGAGATTCGA 656
QY 87 GTACATAGAGAACCAAGTCAAGTATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGATTAAGTACACCGAGATCTGACAGATCC 716

Qy	141	CAAGTAATTATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCATTCACATGCCAA	200
Db	717	TAGCTTAATTACACTGGAATAGTTGGGGGAGACTTTCACCTGCAATTCAGAGTCTTA	776
Qy	201	GAATGGGGCTTTACCCAAACCACTTGAGTGTGATGCAAGGTACCAAGTGATAGT	260
Db	777	CCAGGAGCCCTTGTCTAGTCCAAATTCAGCAAGAGCGTAATGGTTCCAAATTCAGTGT	836
Qy	261	TCTTAGAGTGATGAATCAATCGTATGAGCACTCCTTAAGTA	305
Db	837	GTACGATGTGAGTATATTATCCCTATCATAGCTCTCATGTGTA	881

Search completed: April 9, 2006, 04:47:48
 Job time : 289.914 secs

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GenCore version 5.1.7
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OM protein - nucleic search **using frame p2n model**

Run on: April 9, 2006, 01:20:32 ; Search time 2511.43 seconds
(without alignments)
2489.732 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPVKTAEPLVAIQ.....DEINRDVALLKYNGTCOTT 110

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abseq04
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6 -RGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_in:*
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4: gb_ov:*
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6: gb_pat:*
7: gb_ph:*
8: gb_dr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	100.0	333	6	AX427708 Sequence
2	564	99.1	792	6	AX427704 Sequence
3	564	99.1	945	6	AX427702 Sequence

4	564	99.1	1249	15	PAPASRIP	X98079 P.americana
5	559	98.2	786	15	AB071855	AB071855 PhytoIacc
6	519	91.2	1092	6	AX427720	AX427720 Sequence
7	457	80.3	2472	6	B05033	B05033 DNA encodin
8	457	80.3	2472	15	PTCAPAP	D10600 P. american
9	454	79.8	942	15	AY547315	AY547315 PhytoIacc
10	454	79.8	942	15	AY572976	AY572976 PhytoIacc
11	454	79.8	1114	15	AF53515	AF53515 PhytoIacc
12	454	79.8	1164	15	PAPAP	X55383 P.americana
13	454	79.8	1195	6	A36639	A36639 Sequence 1
14	454	79.8	1195	6	A42103	A42103 Sequence 1
15	454	79.8	1195	6	I43835	I43835 Sequence 1
16	454	79.8	1195	6	I58866	I58866 Sequence 1
17	454	79.8	1378	6	AX427732	AX427732 Sequence
18	454	79.8	1379	6	AR009535	AR009535 Sequence
19	454	79.8	1379	6	AR136704	AR136704 Sequence
20	454	79.8	1379	6	AR136705	AR136705 Sequence
21	454	79.8	1379	6	AX427731	AX427731 Sequence
22	451	79.3	1379	6	AR141172	AR141172 Sequence
23	449	78.9	1164	15	AY049785	AY049785 PhytoIacc
24	443	77.9	1052	15	AY137202	AY137202 PhytoIacc
25	440.5	77.4	939	15	AY327475	AY327475 PhytoIacc
26	439	77.2	882	6	A67183	A67183 Sequence 1
27	438	77.0	1113	15	AY071928	AY071928 PhytoIacc
28	437	76.8	951	6	A67185	A67185 Sequence 3
29	437	76.8	2369	15	AF141331	AF141331 PhytoIacc
30	429	75.4	783	15	AB071854	AB071854 PhytoIacc
31	399	70.1	918	6	A43003	A43003 Sequence 1
32	399	70.1	918	6	A48150	A48150 Sequence 1
33	399	70.1	918	6	I60482	I60482 Sequence 1
34	399	70.1	918	6	I89987	I89987 Sequence 1
35	356	62.6	714	15	AY603352	AY603352 PhytoIacc
36	355	62.4	711	15	AF38910	AF38910 PhytoIacc
37	353	62.0	711	15	AY603353	AY603353 PhytoIacc
38	352	61.9	714	15	AY603354	AY603354 PhytoIacc
39	302	53.1	1226	15	CAAT1PR	X96474 C.aculeatum
40	302	53.1	1226	15	CAAV	AY491967 Beta vulg
41	215	37.8	926	15	BVBTAVUL	X85867 B.vulgaris
42	215	37.8	1080	15	AR003721	AR003721 Sequence
43	213.5	37.5	813	6	AR010057	AR010057 Sequence
44	213.5	37.5	813	6	AR055263	AR055263 Sequence
45	213.5	37.5	813	6	AR055263	AR055263 Sequence

ALIGNMENTS

RESULT 1
AX427708 333 bp DNA
DEFINITION Sequence 7 from Patent WO0233107.
ACCESSION AX427708
VERSION AX427708.1 GI:21537818

KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

Phytolacca americana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
1
AUTHORS Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 7 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES
Location/Qualifiers

Source

misc_feature
1..333
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

misc_feature
331..333
/note="Initiation codon added via PCR primer"
misc_feature
/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-56 Length: 333
Score: 569.00 Matches: 110
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427708 (1-333)

QY 1 MetGlyValAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGln 20
DB 1 ATGGGAGTGTATTCATTCCTGTAAAACTGAAGCTTTTCTACTGAGGCAATCCAA 60
QY 21 MetValSerGluAlaIaArgPheIySTyIleGluAsnGlnValIySThrAsnPheAsn 40
DB 61 ATGGTTTCAGAGCAGCGCAATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAA 120
QY 41 ArgAlaPheTyPProAspProIySValIleAsnLeuGluGluIySTyPGLySileSer 60
DB 121 AGAGCATTTACCTGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCT 180
QY 61 GluAlaIleHisAsnAlaIySaenGlyAlaLeuProIySProLeuGluLeuValAspAla 80
DB 181 GAGGCAATTCAACAATGCCAAGAAATGGGCTTTTACCCAAACCACTTGAGTGAATGCC 240
QY 81 LyeGlyThrIySTyPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
DB 241 AAGGATCCAGTGAATGATGTTCTTAGAGTGAATCAATGATGATGAGCACTCTT 300
QY 101 LyeTyValAsnGlyThrCySGlnThrThr 110
DB 301 AAGTACGTATATGGAACCTGTCAACAACT 330

RESULT 2

AX427704 LOCUS AX427704 792 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from Patent WO0233107.
ACCESSION AX427704
VERSION AX427704.1 GI:21537816

KEYWORDS

SOURCE

Phytolacca americana (American pokeweed)
Phytolacca americana

ORGANISM

Phytolacca americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 3 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES

Location/Qualifiers

1..792

/organism="Phytolacca americana"

/mol_type="unassigned DNA"

/db_xref="taxon:3527"

1..792

/note="Binding site for primer PS1BF"

/note="Initiation codon added via PCR primer"

/complement(436..462)

/note="Binding site for primer PS1SR"

463..492

/note="Binding site for primer PS2BF"

/note="Binding site for primer PS2BP"

/note="Nucleotide change from published sequence"

681..686

/note="Sequence replacing removed XbaI site"

/complement(765..792)

/note="Binding site for primer PS2SR"

790..792

/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 2,13e-55 Length: 792
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427704 (1-792)

QY 2 GlyValAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 463 GAGGTGATTCAATTCCTGTAAAACTGAAGGCTTTTCTACTGATGCAATCCAAATG 522
QY 22 ValSerGluAlaIaArgPheIySTyIleGluAsnGlnValIySThrAsnPheAsnArg 41
DB 523 GTTCAGAGCGAGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAAGA 582
QY 42 AlaPheTyPProAspProIySValIleAsnLeuGluGluIySTyPGLySileSerGlu 61
DB 583 GCATTTCTACCTCGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTTGAG 642
QY 62 AlaIleHisAsnAlaIySaenGlyAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
DB 643 GCATTCACAAATCCCAAGAAATGGGCTTTTACCAACCACTTGAGTGAATGCCAA 702
QY 82 GlyThrIySTyPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
DB 703 GTTACCAAGGATGATGTTCTTAGAGTGAATCAATGATGATGAGCACTCTTAAAG 762
QY 102 TyrValAsnGlyThrCySGlnThrThr 110
DB 763 TACGTTAATGAACCTGTCAACAACT 789

RESULT 3

AX427702 LOCUS AX427702 945 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from Patent WO0233107.
ACCESSION AX427702
VERSION AX427702.1 GI:21537815

KEYWORDS

Phytolacca americana (American pokeweed)
Phytolacca americana

ORGANISM

Phytolacca americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 1 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES

Location/Qualifiers

1..945

/organism="Phytolacca americana"

/mol_type="unassigned DNA"

/db_xref="taxon:3527"

1..792

/note="Binding site for primer PS1BF"

/note="Initiation codon added via PCR primer"

/complement(735..776)

/note="Binding site for primer PSXDR"

736..777

/note="Binding site for primer PSXDP"

/note="Sequence replacing removed XbaI site"

750..759

/complement(922..945)

/note="Binding site for primer PS2SR"

ORIGIN

Alignment Scores: 2,58e-55 Length: 945
Pred. No.: 564.00 Matches: 109
Score: 564.00

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 99.1%
DB: 6
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-978-274a-8 (1-110) x AK427702 (1-945)

QY 2 GYVAlaAepSerPheProValIySThrgIuaIaPhePheLeuLeuValAlaIleGlnMet 21
DB 532 GGAAGTGAATTCATCCCTGTAATAAAGCTGAGGCTTTTCTTCTGTTAGCCATCCAAAG 591
QY 22 ValSerGIuaIaAlaArgPheIySTyriIleGIuaSngIuValIySThAsnPheAsnArg 41
DB 592 GTTACAGAGGAGCGCGGATTCAGATCAATAGAACCAAGTCAAGCTAATTTTATATAGA 651
QY 42 AlaPheTYrProAaPProLySValIleAsnLeuGIuGIuLySTyriIleSerGIu 61
DB 652 GCATTCACCTCGATCCCAAGATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAG 711
QY 62 AlaIleHisAaAlaIySaSngIyAlaLeuProLySProLeuGIuLeuValAlaAspAlaIyS 81
DB 712 GCAATTCACAAATGCGCAAGATGGGGCTTTACCCAAACGACTGAGTATGATGCCAA 771
QY 82 GlyThrIySTyriIleValLeuArgValaAspGIuIleAsnArgAspValAlaLeuLeuIyS 101
DB 772 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATCGATGAGGCACTCCTTAG 831
QY 102 TyrValaSngIyThrCySgIInThrThr 110
DB 832 TACGTTAATGCAACCTGTCAAGCAACT 858

RESULT 4
LOCUS PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
DEFINITION P.americana mRNA for pokeweed antiviral protein.
ACCESSION X98079.1 GI:1707648
VERSION X98079.1
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
REFERENCE 1 Poyet,J.L. and Hoeveler,A.
AUTHORS Poyet,J.L. and Hoeveler,A.
TITL E CDNA cloning and expression of pokeweed antiviral protein from seeds in Escherichia coli and its inhibition of protein synthesis in vitro
JOURNAL FBBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet,J.L.
TITL E Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES
source location/Qualifiers
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/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"
/cblseq_type="seeds"
1..1249
/gene="PAP-S"
106..1050
/gene="PAP-S"
/notes="ribosome-inactivating protein type I"
/codon_start=1
/product="pokeweed antiviral protein"
/protein_id="CAA66702.1"
/db_xref="GI:1707649"

/db_xref="GOA:P93444"
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/db_xref="UniProt/TREMBL:P93444"
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QVQIGIQLISDIDIKISGVDSFPVTEAFPLVLAIQWSEARFXYIENQVNTNRA
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106..117
/gene="PAP-S"
178..1047
/gene="PAP-S"
/product="unnamed"
1212..1217
/gene="PAP-S"
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/gene="PAP-S"
polyA_signal
polyA_site
ORIGIN

Alignment Scores:
Pred. No.: 3.5e-55 Length: 1249
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatch: 0
Query Match: 99.1% Indels: 0
DB: 15 Gaps: 0

US-09-978-274a-8 (1-110) x PAPASRIP (1-1249)

QY 2 GYVAlaAepSerPheProValIySThrgIuaIaPhePheLeuLeuValAlaIleGlnMet 21
DB 637 GGAAGTGAATTCATCCCTGTAATAAAGCTGAGGCTTTTCTTCTGTTAGCCATCCAAAG 696
QY 22 ValSerGIuaIaAlaArgPheIySTyriIleGIuaSngIuValIySThAsnPheAsnArg 41
DB 697 GTTACAGAGGAGCGCGATTCAGATCAATAGAACCAAGTCAAGCTAATTTTATATAGA 756
QY 42 AlaPheTYrProAaPProLySValIleAsnLeuGIuGIuLySTyriIleSerGIu 61
DB 757 GCATTCACCTCGATCCCAAGATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAG 816
QY 62 AlaIleHisAaAlaIySaSngIyAlaLeuProLySProLeuGIuLeuValAlaAspAlaIyS 81
DB 817 GCAATTCACAAATGCGCAAGATGGGGCTTTACCCAAACCTTAGAGCTAGTGAGGCCAA 876
QY 82 GlyThrIySTyriIleValLeuArgValaAspGIuIleAsnArgAspValAlaLeuLeuIyS 101
DB 877 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGTGATGTGGCACTCCTTAG 936
QY 102 TyrValaSngIyThrCySgIInThrThr 110
DB 937 TACGTTAATGCAACCTGTCAAGCAACT 963

RESULT 5
LOCUS AB071855 786 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paper2 gene for PAP-S2, partial cds.
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
REFERENCE 1 Honjo,B. and Watanabe,K.
AUTHORS Honjo,B. and Watanabe,K.
TITL E Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 786)

AUTHORS Watanabe, K. and Honjo, B.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watanake@cc.saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)

FEATURES

source Location/Qualifiers

gene 1..786
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/mol_type="genomic DNA"
/db_xref="taxon:3527"
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/gene="paps2"
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/codon_start=1
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/protein_id="BAB86350.1"
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/translation="INTPTDAGNSTINKYATMESLRNKAQPKLCYIGIPMLPTDN
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KTEAPPLIVAIOWVSEARPKYIENOVKTPNPAFYDPPVIMLEEKWKISPAIHNA
KNGALPPELVDPAKTKMIVLRVDEINRVALIKYNGTCQAT"

ORIGIN

Alignment Scores:

Pred. No.: 7,94e-55 Length: 786
Score: 559.00 Matches: 108
Percent Similarity: 99.1% Conservative: 0
Best Local Similarity: 99.1% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: 15 Gaps: 0

US-09-978-274A-8 (1-110) x AB071855 (1-786)

QY 2 G1YValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 460 GGAGTTGATTCATTCCTCGTAAAAAAGTGAAGGCTTTTCTTACCTGTAGCATCCAATG 519
QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIyThrAsnPheAsnArg 41
Db 520 GTTTCAGAGGAGCGCATTCAGACATAGAGAACCAAGTCACAGACTAATTTTATAGA 579
QY 42 AlaPheTyProAspProLyValIleAsnLeuGluGluTyrlleGlyIleSerGln 61
Db 580 GCATTTCACCTGATCCCAAGTAACTTGAAGAGAGAGTGGGCAAAATCTCTGAG 639
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProLyProLeuGluLeuValAspAlaIyS 81
Db 640 GCAATTCACAATGCGCAAGAAATGGGGCTTTACCCAAACCTTAGAGCTAGTGAGTCCAAA 699
QY 82 GlyThrLySTPILeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
Db 700 GGTACCAAGTGATAGTTCTTAGAGTGAATCAATCGTAGTGCGACTCTTAAAG 759
QY 102 TyrValaAsnGlyThrCyGlnThrThr 110
Db 760 TACGTTAATGGAACCTGTCAAGCCACT 786

RESULT 6
LOCUS AX427720 1092 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from Patent WO0233107.
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Neelam, A., Atkinson, H.J., Mephereson, M.J. and Thomas, C.J.R.

TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES

source Location/Qualifiers

misc_feature 1..1092
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/mol_type="unassigned DNA"
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1..29
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681..686
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/note="Binding site for primer PCS-PAPSR"
766..806
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766..786
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complement(1066..1092)
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ORIGIN

Alignment Scores:

Pred. No.: 4.6e-50 Length: 1092
Score: 519.00 Matches: 101
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 91.2% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427720 (1-1092)

QY 2 G1YValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 463 GGAGTTGATTCATTCCTCGTAAAAAAGTGAAGGCTTTTCTTACCTGTAGCATCCAATG 522
QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIyThrAsnPheAsnArg 41
Db 523 GTTTCAGAGGAGCGCATTCACATACATAGAGAACCAAGTCAAGACTAATTTTATAGA 582
QY 42 AlaPheTyProAspProLyValIleAsnLeuGluGluTyrlleGlyIleSerGln 61
Db 583 GCATTTCACCTGATCCCAAGTAACTTGAAGAGAGAGTGGGCAAAATCTCTGAG 642
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProLyProLeuGluLeuValAspAlaIyS 81
Db 643 GCAATTCACAATGCGCAAGAAATGGGGCTTTACCCAAACCACTTAGCTAGTGAGTCCAAA 702
QY 82 GlyThrLySTPILeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
Db 703 GGTACCAAGTGATAGTTCTTAGAGTGAATCAATCGTAGTGCGACTCTTAAAG 762
QY 102 Tyr 102
Db 763 TAC 765

RESULT 7
LOCUS E05033 2472 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding antiviral protein.
ACCESSION E05033
VERSION E05033.1 GI:2173227
KEYWORDS
SOURCE JP 1993137580-A/1.
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana (American pokeweed)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolacaceae; Phytolacca.
1 (bases 1 to 2472)
Katoaka, J., Habuka, N., Masuda, O., Miyano, M. and Koiwai, A.
NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
REFERENCE 1
JOURNAL Patent: JP 1993137580-A 1 01-JUN-1993;

QY 62 AAlaHhSaNa1a1aYsaNg1yAlaLeuProLySProLeuGluLeuValaAspAlaLys 81
Db 1722 GCGATTACCAATCCCAAGATGGGGCTTTAAACCAAGTCTCTTACAGCTAAATAATGCAAC 1781
QY 82 GLThLyETrPLeValLeuArGValaAspGluileAsnArGAspValAlaLeuLeuLys 101
Db 1782 GGAGCAAGGAGTAGTGGTGAAGTGGATGATTCGAACCTGATGTGGACCTCTTAAG 1841
QY 102 TYrValaAsnGlyThrCySgIntThr 110
Db 1842 TATGTTATGGAAGCTGCCAGGCAACT 1868
RESULT 9
AY547315 942 bp DNA linear PLN 13-JUN-2005
LOCUS PhytoIaccas americana antiviral protein gene, complete cds.
DEFINITION AY547315
VERSION AY547315.1 GI:44889055
KEYWORDS PhytoIaccas americana (American pokeweed)
SOURCE PhytoIaccas americana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; PhytoIaccaceae; PhytoIaccas.
REFERENCE 1 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X., Zhou, G. and Li, H.
TITLE A pokeweed antiviral protein gene in roots of PhytoIaccas americana
JOURNAL Acta Virol. 48 (2), 131-132 (2004)
PUBMED 15462289
REFERENCE 2 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X. and Li, H.
TITLE Direct Submission
REFERENCE Submitted (11-FEB-2004) Plant Virology, Institute of Plant
JOURNAL Protection, CAAS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
China
FEATURES
source Location/Qualifiers
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QLGIQILDSNIGKISGVMSFTEKTEAEFLVLAIQVSEAPKFIENQVKTNFRAFN
PNKRVLDQETWKGISTAIHDANKGVLPKLELVASGAKWIVLRVDEIKPDVLLNY
VGSGCQTTYNAMFPQIMSTIYNVNIADLDFEGF"
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-42 Length: 942
Score: 454.00 Matches: 90
Percent Similarity: 87.28 Conservative: 5
Best Local Similarity: 82.64 Mismatches: 14
Query Match: 79.84 Indels: 0
Gaps: 0
US-09-978-274A-8 (1-110) x AY547315 (1-942)
QY 2 GLyValaAspSerPheProValLyEThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 526 GGAAGAGTCACTTCACTGAGAAACCGAAGCCGAATTCCTATYTGTCATACCAATG 585
QY 22 ValSerGluAlaAlaArgPheLyETrIleGluAsnGlnValLyEThrAsnPheAsnArg 41
Db 586 GTATCAAGGCGAGCAAGATTCAAGTACATAGAGATCAAGTCAAGAAACTATTTTAAACGA 645

QY 42 AAlaPheTyProAspProLySValileAsnLeuGluGluLeuTrpGlyLySileSerGlu 61
Db 646 GCAATTACACCTTAATCCCAAGATGACTTAATTTCAGAGAGACATGGGTAAGATTTCACA 705
QY 62 AAlaHhSaNa1a1aYsaNg1yAlaLeuProLySProLeuGluLeuValaAspAlaLys 81
Db 706 GCAATTACATGATCCCAAGATGAGTTTAAACCAAGTCTCTCGAGCTAGTGATGCCAGT 765
QY 82 GLThLyETrPLeValLeuArGValaAspGluileAsnArGAspValAlaLeuLeuLys 101
Db 766 GGAGCAAGGAGTAGTGGTGAAGTGGATGAATCAAGCTGATGAGCACTTTAAAC 825
QY 102 TYrValaAsnGlyThrCySgIntThr 110
Db 826 TACGTTGGTGGAGCTGTCTGACAACT 852
RESULT 10
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS AY572976
DEFINITION PhytoIaccas americana antiviral protein (PAP) mRNA, complete cds.
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS PhytoIaccas americana (American pokeweed)
SOURCE PhytoIaccas americana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; PhytoIaccaceae; PhytoIaccas.
REFERENCE 1 (bases 1 to 942)
AUTHORS Xiao, Z.A. and Jiang, Y.
TITLE A gene encoding the pokeweed antiviral protein in the leaf of
JOURNAL PhytoIaccas americana
REFERENCE 2 (bases 1 to 942)
AUTHORS Xiao, Z.A.
TITLE Direct Submission
REFERENCE Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
JOURNAL University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
100875, China
FEATURES
source Location/Qualifiers
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QLGIQILDSNIGKISGVMSFTEKTEAEFLVLAIQVSEAPKFIENQVKTNFRAFN
PNKRVLDQETWKGISTAIHDANKGVLPKLELVASGAKWIVLRVDEIKPDVLLNY
VGSGCQTTYNAMFPQIMSTIYNVNIADLDFEGF"
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-42 Length: 942
Score: 454.00 Matches: 90
Percent Similarity: 87.28 Conservative: 5
Best Local Similarity: 82.64 Mismatches: 14
Query Match: 79.84 Indels: 0
Gaps: 0
US-09-978-274A-8 (1-110) x AY572976 (1-942)
QY 2 GLyValaAspSerPheProValLyEThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 586 GTATCAAGGCGAGCAAGATTCAAGTACATAGAGATCAAGTCAAGAAACTATTTTAAACGA 645

Db 526 GGAAGTATGTCATTCACTGAGAAAACCGAAGCCGAAATTCCTATTGGTAGCCATACAAATG 585
 Qy 22 ValSerGluAlaAlaArgPheIleTyrIleGluGlnValIleThrAspPheAsnArg 41
 Db 586 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGGTAAAACTAATTTTAAACGA 645
 Qy 42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
 Db 646 GCATTCAACCCCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTCAACA 705
 Qy 62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProIleProLeuGlnLeuValAspAlaIle 81
 Db 706 GCAATTCATGATGCGCAAGAAATGAGATTATTAACCAACCTCTCGAGCTAGTGGATCCAGT 765
 Qy 82 GlyThrIleTyrPleValIleLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
 Db 766 GTGCGAAGTGGATAGTGTGTGAGACTGATGAATCAAGCCGTGATGTGACTCTTAAAC 825
 Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
 Db 826 TACGTGTGGTGGAGCTGTACGCAACT 852

RESULT 11

AFS33515 1114 bp mRNA linear PLN 01-AUG-2005
 LOCUS PhytoIacca octandra anti-viral protein (pap) mRNA, partial cds.
 DEFINITION AFS33515
 ACCESSION AFS33515
 VERSION AFS33515.1 GI:33329822
 KEYWORDS
 SOURCE PhytoIacca octandra
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; PhytoIaccaceae; PhytoIacca.

REFERENCE

AUTHORS Lin, J.S. and McNally, K.P.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUL-2002) Reproductive Technologies, AgResearch
 Wallaseville, Ward Street, Upper Hut, Wellington, New Zealand
 FEATURES location/Qualifiers
 1..1114

FEATURES

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 SDIGKISGTVSFTKTEARPLVLAIVMSAARPYENQKTNPNRAFPNPNVNTL
 EETWGIKISTAIHDAKNGVLPKPLEIVDASGAKMIVSRVDEIKPDVALINTVSSCOTT
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gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-42 Length: 1114
 Score: 454.00 Matches: 90
 Percent Similarity: 87.2% Conservative: 5
 Best Local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 Gaps: 0

US-09-978-274A-8 (1-110) x AFS33515 (1-1114)

Qy 2 G|YVALAspSerPheProValIleTyrGluAlaPheIleLeuValAlaIleGlnMet 21

Db 504 GGAAGTATGTCATTCACTGAGAAAACCGAAGCCGAAATTCCTACTGTAGCCATACAAATG 563
 Qy 22 ValSerGluAlaAlaArgPheIleTyrIleGluGlnValIleThrAspPheAsnArg 41
 Db 584 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGGTAAAACTAATTTTAAACGA 623
 Qy 42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
 Db 624 GCATTCAACCCCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTCTACA 683
 Qy 62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProIleProLeuGlnLeuValAspAlaIle 81
 Db 684 GCAATTCATGATGCGCAAGAAATGAGATTATTAACCAACCTCTCGAGCTAGTGGATCCAGT 743
 Qy 82 GlyThrIleTyrPleValIleLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
 Db 744 GTGCGAAGTGGATAGTGTGTGAGACTGATGAATCAAGCCGTGATGTGACTCTTAAAC 803
 Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
 Db 804 TACGTGTGGTGGAGCTGTACGCAACT 830

RESULT 12

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
 LOCUS P.americana PAP gene for anti-viral protein.
 DEFINITION X53383
 ACCESSION X53383
 VERSION X53383.1 GI:20421
 KEYWORDS
 SOURCE PhytoIacca americana (American pokeweed)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; PhytoIaccaceae; PhytoIacca.

REFERENCE

AUTHORS Lin, J., Chen, Z.C., Antoniw, J.F. and White, R.F.
 TITLE Isolation and characterization of a cDNA clone encoding the
 JOURNAL anti-viral protein from PhytoIacca americana
 PUBMED 1912488
 REFERENCE 2 (bases 1 to 1164)
 AUTHORS Antoniw, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops
 Research, Dept. of Plant Pathology, Rothamsted Experimental
 Station, Harpenden, Hert, AL5 2JQ, UK
 FEATURES location/Qualifiers
 1..1164

FEATURES

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 /protein_id="CA39054.1"
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 QLGIOILDNIGKISGTVSFTKTEARPLVLAIVMSAARPYENQKTNPNRAFPNPNVNTL
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 VGSCTTTNQNAMPOLIMSTYTYNMANLGLDFEGP"

gene

CDS

ORIGIN

Alignment Scores:

Qy 2 G|YVALAspSerPheProValIleTyrGluAlaPheIleLeuValAlaIleGlnMet 21

Pred. No.: 1,51e-42 Length: 1164
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 15 Gaps: 0

US-09-978-274a-8 (1-110) x PABAP (1-1164)

QY 2 GlyValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 527 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 586
QY 22 ValSerGluAlaAlaArgPheIleYrTleGluGlnValIleYrThrAsnPhenArg 41
DB 587 GTATCAGAGGACCAAGATTCAAGTACATAGAGATCATGGTGAACCTAATTTTAACAGA 646
QY 42 AlaPheYrProAspProIysValIleAsnLeuGluGluYrTPGIYsIleSerGlu 61
DB 647 GCATTCACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAGATTTCACACA 706
QY 62 AlaIleHisAsnAlaIysAsnGlyAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 707 GCATTCATATGATGCCAAGATGAGATTTCACCAACCTCTCGAGCTAGTGCAGTCCAGT 766
QY 82 GlyThrIleYrTleValIleArgValAspGluIleAsnArgPheValAlaLeuLeuIys 101
DB 767 GGAGCCAAAGTGAATAGTGTGAGAGTGAATCAAGCTGATGACACTCTTAAC 826
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 827 TACGTTGGTGGAGCTGTGACACAACT 853

RESULT 13

A36639 A36639 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A36639
DEFINITION Sequence 1 from Patent EP0585554.
ACCESSION A36639
VERSION A36639.1 GI:2293943
KEYWORDS

SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 1195)

AUTHORS K.M., Lee, K., Na, B., Jeong, H.S., Choi, K., Moon, Y. and Jeon, H.
TITLE Process for preparing a transgenic plant expressing phytoacta
JOURNAL JINRO LIMITED (KR)
Patent: EP 0585554-A 1 09-MAR-1994;
Other publication JP 6078775 940322
Other publication KR 9512900 951023.
COMMENT Other publication KR 9512900 951023.
FEATURES location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1,55e-42 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 6 Gaps: 0

US-09-978-274a-8 (1-110) x A36639 (1-1195)

QY 2 GlyValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 558 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 617
QY 22 ValSerGluAlaAlaArgPheIleYrTleGluGlnValIleYrThrAsnPhenArg 41

DB 618 GTATCAGAGGACCAAGATTCAAGTACATAGGAATCAGGTGAAAACCTAATTTTACAGA 677
QY 42 AlaPheYrProAspProIysValIleAsnLeuGluGluYrTPGIYsIleSerGlu 61
DB 678 GCATTCACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAGATTTCACACA 737
QY 62 AlaIleHisAsnAlaIysAsnGlyAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 738 GCATTCATGATGCCAAGATGAGCTTTTACCAACCTCTCGAGCTAGTGCAGTCCAGT 797
QY 82 GlyThrIleYrTleValIleArgValAspGluIleAsnArgPheValAlaLeuLeuIys 101
DB 798 GGAGCCAAAGTGAATAGTGTGAGAGTGAATCAAGCTGATGACACTCTTAAC 857
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 858 TACGTTGGTGGAGCTGTGACACAACT 884

RESULT 14

A42103 A42103 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A42103
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS

SOURCE Phytoacta americana (American pokeweed)

ORGANISM Phytoacta americana (American pokeweed)
Phytolacca americana
Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 1195)

AUTHORS Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.
TITLE A novel expression vector for phytoacta antiviral protein
JOURNAL Patent: EP 0637591-A 1 08-FEB-1995;
JINRO LIMITED (KR)
Other publication AU 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
COMMENT Other publication AU 5064293 950119.
FEATURES location/Qualifiers
1..1195
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

ORIGIN

Alignment Scores:

Pred. No.: 1,55e-42 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 6 Gaps: 0

US-09-978-274a-8 (1-110) x A42103 (1-1195)

QY 2 GlyValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 558 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 617
QY 22 ValSerGluAlaAlaArgPheIleYrTleGluGlnValIleYrThrAsnPhenArg 41
DB 618 GTATCAGAGGACCAAGATTCAAGTACATAGAGATCATGGTGAACCTAATTTTAAACAGA 677
QY 42 AlaPheYrProAspProIysValIleAsnLeuGluGluYrTPGIYsIleSerGlu 61
DB 678 GCATTCACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAATTTTCAACA 737
QY 62 AlaIleHisAsnAlaIysAsnGlyAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 738 GCATTCATGATGAGCCAAAGTGAATTTTACCAACCTCTCGAGCTAGTGCAGTCCAGT 797

QY 82 GlyThrIySTPIleValIleuArgValAspGluIleAsnArgAspValAlaIleuLeuLys 101
 Db 798 GGTGCCAAGTGTAGTGTGTGAGTGTGATGAAATCAAGCTCGATGTAGCACTTTAAAC 857
 QY 102 TyrValaIeNGlyThrCysGlnThrThr 110
 Db 858 TACGTTGGTGGAGCTGTCAAGCAACT 884

RESULT 15

143835 1195 bp DNA linear PAT 07-OCT-1997
 LOCUS Sequence 1 from patent US 5633155.
 DEFINITION 143835
 ACCESSION 143835
 VERSION 143835.1 GI:2468933
 KEYWORDS
 SOURCE
 ORGANISM

Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1195)
 AUTHORS Kim,M.-K., Lee,K.-H., Na,B.-K., Jeong,H.-S., Choi,K.-W., Moon,Y.-H.
 and Jeon,H.-S.

TITLE Expression vector for phytolecta antiviral protein and process for
 preparing transgenic plant transformed therewith
 JOURNAL Patent: US 5633155-A 1 27-MAY-1997;
 FEATURES Location/Qualifiers
 source 1..1195
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.55e-42 Length: 1195
 Score: 454.00 Matches: 90
 Percent Similarity: 87.2% Conservative: 5
 Best local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x 143835 (1-1195)

QY 2 G|YValAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGlnMet 21
 Db 558 GGAAGTATGTCATTCACCTGAGAAACCGAACCCGAAATTCCTATTGTGTAGCCATCAAAATG 617
 QY 22 ValSerGluAlaAlaArgPheIySTyrIleGluAsnGluValIySThrAsnPheAsnArg 41
 Db 618 GTATCAGAAGCGACGAATTCAGATCACTAGAAATCGGTGAAACTAATTTTAACGA 677
 QY 42 AlaPheTyrProAspProIyValIleAsnLeuGluIySTyrIySTyrIleSerGlu 61
 Db 678 GCATTCAACCTTAATCCAAAGTACTAATTGCAAGAGACATGGGGTAAGATTTCACA 737
 QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProLeuGluLeuValAspAlaLys 81
 Db 738 GCATTTCATATGCAAGAAAGAGTTTACCAACCTCTCGAGCTAGTGATGCCAGT 797
 QY 82 GlyThrIySTPIleValIleuArgValAspGluIleAsnArgAspValAlaIleuLeuLys 101
 Db 798 GGTGCCAAGTGTAGTGTGTGAGTGTGATGAAATCAAGCTCGATGTAGCACTTTAAAC 857
 QY 102 TyrValaIeNGlyThrCysGlnThrThr 110
 Db 858 TACGTTGGTGGAGCTGTCAAGCAACT 884

Search completed: April 9, 2006, 07:31:30
 Job time : 2513.43 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 291.938 Seconds
(without alignments)
2511.204 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPFKTEAPFLVAIQ.....DEINRDVALLKYVNGTCQT 110

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/absas/ABSSMBR.spool/US09978274/rnat_07042006_173031_28376/app_query.fasta.1
-DB=N.Geneseq -QFMT=fastap -SURFIX=p2n.rng -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIT5=blis -START=1 -END=1 -MATRIX=blisum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=absas03h
-USER=US09978274 @CGN 1.1244 @rnatc 07042006 173031 28376 -NCPU=6 -ICPU=3
-NO MMP -NEG SCORES=0 -WAT -SPBLOCK=100 -LONLOG -DEV TIMEOUT=120
-MAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq 21:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	100.0	333	6	AAD42718 Pokeweed
2	564	99.1	792	6	AAD42716 Pokeweed
3	564	99.1	945	6	AAD42715 Pokeweed
4	519	91.2	1092	6	AAD42729 Pokeweed

5	457	80.3	2472	2	AAQ43967	Aag43967 Pokeweed
6	454	79.8	1195	2	AAQ56672	Aag56672 Sequence
7	454	79.8	1195	2	AAQ81457	Aag81457 Phytoleac
8	454	79.8	1378	6	AAD42739	Aad42739 Pokeweed
9	454	79.8	1379	3	AAZ45197	Aaz45197 Wild-type
10	454	79.8	1379	3	AAZ59221	Aaz59221 Variant p
11	454	79.8	1379	6	AAZ59220	Aaz59220 Pokeweed
12	454	79.8	1379	6	AAD42738	Aad42738 Pokeweed
13	452	79.8	1379	10	AD105787	Adi05787 DNA encod
14	452	79.3	1378	12	ADG76061	Adg76061 American
15	451	79.3	1379	4	AAQ87929	Aac87929 P. americ
16	449	78.9	1164	11	ADM74751	Adm74751 HIV-1 inh
17	449	78.9	1164	11	ADM74765	Adm74765 HIV-1 inh
18	439	77.2	882	2	AAT99556	Aat99556 Phytoleac
19	437	76.8	2369	2	AAT99557	Aat99557 Phytoleac
20	437	76.8	2369	2	ABA96543	AbA96543 Phytoleac
21	399	70.1	918	2	AAQ64893	Aaq64893 Antiviral
22	399	70.1	918	2	AAT04782	Aat04782 DNA pJMC2
23	213.5	37.5	813	2	AAQ48031	Aaq48031 Encodes p
24	213.5	37.5	813	2	AAQ42222	Aaq42222 Encodes p
25	213.5	37.5	813	2	AAQ75532	Aaq75532 Type I r1
26	213.5	37.5	813	2	AAQ75342	Aaq75342 Type I r1
27	213.5	37.5	1176	6	ABSS56021	Abss56021 CDNA enco
28	212.5	37.3	783	2	AAQ38041	Aaq38041 Synthetic
29	212.5	37.3	955	2	AAT86336	Aat86336 BPI pepti
30	212.5	37.3	1003	2	AAT86341	Aat86341 BPI pepti
31	212.5	37.3	1072	2	AAT86332	Aat86332 BPI pepti
32	212.5	37.3	1500	14	ABEB8721	AbEB8721 scFv23-ge
33	212.5	37.3	1527	6	ABSS56029	Abss56029 DNA encod
34	200	35.1	934	6	AAZ45198	Aaz45198 Wild-type
35	200	35.1	934	6	AAD42740	Aad42740 Pokeweed
36	200	35.1	1517	14	ABEB8719	AbEB8719 scFv23-ge
37	200	35.1	1518	14	ABEB8724	AbEB8724 scFv23-ge
38	196.5	34.5	1855	2	AAQ4224	Aaq4224 PAP-246 I
39	196.5	34.5	1855	13	ADT88532	Adt88532 Recombina
40	195.5	34.4	1813	5	AAI79929	Aai79929 Mutant pr
41	194	34.1	848	4	AAQ02363	Aaq02363 Castor be
42	194	34.1	1810	5	AAI79884	Aai79884 Mutant pr
43	193.5	34.0	1807	5	AAI79901	Aai79901 Mutant pr
44	192	33.7	807	2	AAQ46085	Aaq46085 Sequence
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ALIGNMENTS

RESULT 1	
ID	AAD42718 standard; DNA; 333 BP.
XX	
AC	AAD42718;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed PAP-Sbeta protein encoding DNA.
XX	
KW	Neurotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW	PAP-Sbeta; ds.
XX	
OS	Phytolacca americana.
XX	
PH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..465
FT	/*tag= a
FT	/product= "PAP-Sbeta protein"
XX	
PN	WO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001MO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.
XX	

(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PA Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25921.
PT Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 4; Page 78; 87pp; English.
CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP-Sbeta
CC protein encoding DNA
XX
XX
SQ Sequence 333 BP; 106 A; 63 C; 76 G; 88 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,41e-67 Length: 333
Score: 569.00 Matches: 110
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-09-978-274A-8 (1-110) x AAD42718 (1-333)
QY 1 MetGlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGln 20
DB 1 ATGGAGATTATTCATTCCTCGTAAATACTGAGGCTTTTTCACCTGATGCAATCCAA 60
QY 21 MetValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIyThrAsnPha 40
DB 61 ATGGTTTCAGAGGACGCGCATTCACATAGAGAACCAAGTCAAGACTAATTTTAAAT 120
QY 41 ArgAlaPheTyrrProAspProLyValIleAsnLeuGluGlySTPGLyIleSer 60
DB 121 AGAGCATTCACCTCGATCCCAAGTAATTAATTGAGAGGAGAGTGGGGCAAAATCTCT 180
QY 61 GluAlaIleHisAsnAlaLyAsnGlyValaLeuProLySProLeuGluLeuValAspAla 80
DB 181 GAGGCATTCACAAATGCCAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCC 240
QY 81 LySerIyThrIySTPILeValIleuArgValaSPGluIleAsnArgSPValAlaLeuLeu 100
DB 241 AAAGGTACCAAGTGATGATGTTCTTAGAGTGATGAATCATCGATGATGGCACTCCTT 300
QY 101 LySerIyValaAsnGlyIyThrCySglnThr 110
DB 301 AAATGACGTATATGAGAACCTGTGACAGCAACT 330

RESULT 2
AAD42716
ID AAD42716 standard; DNA; 792 BP.
XX
XX AAD42716;
AC
XX 15-NOV-2002 (first entry)
DT
XX
DB Pokeweed mature PAP-S protein encoding DNA.
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM gene; ds.
XX
OS Phytolacca americana.

XX
FH Key Location/Qualifiers
FT CDS 1..792
FT /tag= a
FT /product= "Mature PAP-S protein"
FT primer_bind 1..29
FT /tag= b
FT /bound_molecy= "Primer PS1BF"
FT primer_bind complement(436..462)
FT /tag= c
FT /bound_molecy= "Primer PS1SR"
FT primer_bind 463..492
FT /tag= d
FT /bound_molecy= "Primer PS2BF"
FT misc_feature 681..686
FT /tag= e
FT /note= "Sequence replacing removed XbaI site"
FT primer_bind complement(765..792)
FT /tag= f
FT /bound_molecy= "Primer PS2SR"
XX
XX W0200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25919.
DR
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 2; Page 76; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed mature PAP
XX -S protein encoding DNA
XX
XX
SQ Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.6e-66 Length: 792
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: Gaps: 0

US-09-978-274A-8 (1-110) x AAD42716 (1-792)
QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 463 GAGGTGATTCATTCCTCGTAAATACTGAGGCTTTTTCACCTGATGCAATCCAAATG 522
QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIySTPrrAsnPhaAsnArg 41
DB 523 GTTTCAGAGGACGCGCATTCACATAGAGAACCAAGTCAAGACTAATTTTAATAGA 582
QY 42 AlaPheTyrrProAspProLyValIleAsnLeuGluGlySTPGLyIleSerGlu 61

Db	583	GCATTCCTACCCGATCCCAAGATTAATTACTTGAGAGAGAGATGGGCGCAAAATCTCTGAG	642
Qy	62	AlaIleHisAsnAlaIysAsnGlyAlaIeuProIysProIeuGluIeuValAspAlaIys	81
Db	643	GCAATTCACAAATGCCAAGATGGGGCTTTATACCAACCACTGAGGCTAGTGATGCCAA	702
Qy	82	GlyThrIleValThrIleValIleuAlaGValAspGluIleAsnArgAspValAlaIleuLys	101
Db	703	GGTACCAAGATGGATGATGTTCTTAGAGAGATGGAATCAATCGTATGTGGCACTCCCTAAG	762
Qy	102	TyrValAsnGlyThrCysGlnThrThr	110
Db	763	TACGTTAATGGAACCTGTCTGACACACT	789
RESULT 3			
ID	AAD42715		
XX	AAD42715	standard; DNA; 945 BP.	
XX	AC		
XX	AAD42715;		
XX	DT	15-NOV-2002 (first entry)	
XX	DE	Pokeweed pro-PAP-S protein encoding DNA.	
XX	KM	Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;	
XX	gene; ds.		
XX	OS	Phytolacca americana.	
PH	Key	Location/Qualifiers	
FT	CDS	1..945	
FT		/*tag= a	
FT		/product= "Pro-PAP-S protein"	
FT	primer_bind	1..24	
FT		/*tag= b	
FT		/bound_moiety= "Primer PPS1BF"	
FT	primer_bind	complement(735..776)	
FT		/*tag= c	
FT		/bound_moiety= "Primer PSXDR"	
FT	primer_bind	736..777	
FT		/*tag= d	
FT		/bound_moiety= "Primer PSXDP"	
FT	misc_feature	750..759	
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FT		/note= "Sequence replacing removed XbaI site"	
FT	primer_bind	complement(922..945)	
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FT		/bound_moiety= "Primer PPS2BR"	
XX	WO200233107-A2.		
XX	25-APR-2002.		
XX	PD		
XX	15-OCT-2001; 2001WO-GB004593.		
XX	PP		
XX	14-OCT-2000; 2000GB-00025217.		
XX	PR		
XX	PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.	
XX	PI	Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;	
XX	XX		
XX	DR	WPI; 2002-489891/52.	
XX	XX	P-PSDB; AAE25918.	
PT	PT	Inducing necrotic effect in specific cells of plant by transforming plant	
PT	PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter	
PT	PT	which acts in response to application of specific stimulus to plant.	
PS	PS	Claim 24; Page 73-74; 87pp; English.	
CC	CC	The invention relates to a method of inducing a necrotic effect in	
CC	CC	specific cells of a plant. The method involves transforming the plant	

CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC	PAP', PAP11 and PAP-S, where the gene(s) comprises a promoter which acts
CC	in response to the application of a specific stimulus to the plant so as
CC	to facilitate expression of the pokeweed antiviral protein in specific
CC	cells of the plant. The method is useful for inducing a necrotic effect
CC	in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC	protein encoding DNA
XX	
SQ	Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	4.55e-66
Score:	564.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	99.1%
DB:	6
US-09-978-274A-8 (1-110) x AAD42715 (1-945)	
QY	2 GYValaPsserPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB	532 GGAGTTGATCACTTCCTGTAAAACTGAGGCTTTTCTACTGTAGCAATCCAAATG 591
QY	22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValIysThrAsnPheAsnArg 41
DB	592 GTTTCAGAGGCAAGCCCGATTCAGACACATAGCAACCAAGTCAAGACTAATTTAATAGA 651
QY	42 AlaPheTyrProAspProLysValIleAsnLeuGlnGluLysTyrGlyIleSerGlu 61
DB	652 GCATTCTACCCGATCCCAAGTAATTAATTGGAGGAGAAATGGGGCAAAATCTCTGAG 711
QY	62 AlaIleH1sAsnAlaIysAsnGlyAlaLeuPProLysProLeuGlnLeuValAspAlaIys 81
DB	712 GCAATTCACAAATGCCAAGAAATGGGCTTACCCAAACCACTTGAGCTAGTGATGCCAA 771
QY	82 GlyThrLysTyrPLeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB	772 GGATCCAGATGGATGATCTTAAGATGTGATGAATCAATCGATGATGSCATCTCCTTAAG 831
QY	102 TyrValaAsnGlyThrCysGlnThrThr 110
DB	832 TACGTTAAATGGAACTGTCAAGCAACT 858
RESULT 4	
ID	AAD42729 standard; DNA; 1092 BP.
XX	AAD42729;
XX	29-AUG-2003 (revised)
DT	15-NOV-2002 (first entry)
XX	Pokeweed PAP-S/REV PCS/rice cystatin delta D86 fusion DNA.
XX	
XX	Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW	chimeric; rice; cystatin delta D86; N1A protease cleavage site; PCS; ds.
XX	
OS	Phytolacca americana.
OS	Oryza sativa.
OS	Tobacco; Etch virus.
OS	Chimeric.
XX	
FT	Key
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FT	1..29
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FT	/bound moiety= "Primer PSIBP"
FT	misc_feature
FT	681..686
FT	/*tag= b
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FT	complement(742..786)
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FT	/bound moiety= "Primer PCS-PAPSR"

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FT mlec_feature 766..786
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PN MO20023107-A2.
XX 25-APR-2002.
XX 15-OCT-2001; 2001WO-GB004593.
XX 14-OCT-2000; 2000GB-00025217.
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX PS
XX Disclosure; Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC 'PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is a fusion DNA. This
XX CC sequence comprises pokeweed pro-PAP-S DNA, rice cytoatin delta D86 DNA
XX CC and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
XX CC on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 6.6e-60 Length: 1092
XX Score: 519.00 Matches: 101
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 91.2% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAD42729 (1-1092)
QY 2 GlyValAspSerPheProValIleThrGluAlaPheLeuLeuValAlaIleGlnMet 21
Db 463 GGAATTGATTCATTCCTCGTAAACCTAGAGCTTTTCTTACGCGTACCATTCCTAATG 522
QY 22 ValSerGluAlaAlaArgPheIleThrIleGluAsnGlnValIleThrAsnPheAsnArg 41
Db 523 GTTTCAGAGGCGCCGCAATTCAGTACATAGAGAACCAAGTCACAGCTAATTTTAATGA 582
QY 42 AlaPheTYRProAspProIleValIleAsnLeuGluIleValTYRGLYValIleSerGlu 61
Db 583 GCATTCATCCCTGCATCCCAAGTAATTAATTCGGAGAGAAAGTGGCGCAAAATCTCTAG 642
QY 62 AlaIleHisAsnAlaIleValAsnGlyAlaLeuProIleValIleValIleValAspAlaIle 81
Db 643 GCAATTTCACAAATGCGCAAAATGGGGCTTTACCCCAACCACTTGACCTAGTGATCCCAA 702
QY 82 GlyThrIleValTYRPIleValIleLeuArgValAspGluIleAsnArgAspValAlaLeuLeu 101
Db 703 GGTACCAAGTGGATGTTCTTGTAGAGTGAATGAAATCATGCTGTGAGCACTCTTAAG 762
```

```
QY 102 Tyr 102
Db 763 Trp 765
XX
XX RESULT 5
XX AAQ43967
XX ID AAQ43967 standard; DNA; 2472 BP.
XX AC AAQ43967;
XX
XX 09-NOV-1993 (first entry)
XX DB Pokeweed antiviral protein.
XX KW Pokeweed; ricin; protein synthesis inhibitor; cancer;
XX KM polymerase chain reaction; PCR; 88.
XX OS Phytolacca americana.
XX
XX Key Location/Qualifiers
XX FT CHAT_signal 549..552
XX FT /*tag= a
XX FT CHAT_signal 627..630
XX FT /*tag= b
XX FT TATA_signal 845..850
XX FT /*tag= c
XX FT sig_peptide 1014..1085
XX FT /*tag= d
XX FT mat_peptide 1086..1168
XX FT /*tag= e
XX FT /label= PAP
XX FT polyA_signal 2130..2135
XX FT /*tag= f
XX
XX JP05137580-A.
XX
XX 01-JUN-1993.
XX
XX 20-NOV-1991; 91JP-00329672.
XX
XX 20-NOV-1991; 91JP-00329672.
XX
XX (N1SB ) JAPAN TOBACCO INC.
XX
XX WPI; 1993-211306/26.
XX P-PSDB; AAR37345.
XX
XX New pokeweed antiviral protein (PAP) with similar activity to ricin -
XX used to treat cancer and as an agricultural chemical.
XX
XX Claim 2; Page 11-13; 14pp; Japanese.
XX
XX PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The
XX CC protein may be obtained all year round by recombinant DNA techniques. PAP
XX CC can be used partic. against cancer and as an agricultural chemical. Total
XX CC mRNA, is extracted from the seeds, leaves and roots of pokeweed and used
XX CC to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA
XX CC fractions, which are introduced into a cloning vector EMBL3 and then into
XX CC host E.coli PLK-17 (P2) to produce PAP
XX
XX Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 4.61e-51 Length: 2472
XX Score: 457.00 Matches: 50
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 80.3% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAQ43967 (1-2472)
```

```
QY      2 GlyValAspSerPheProValIleAsnLeuGluValAlaIleGlnMet 21
      1542 GGAGTGGATTCATTCACCTGAGAAAGCAATTCCTGTAGTCCATCCAAATG 1601
QY      22 ValSerGluAlaIleArgPheLeuTyrIleGluAsnGlnValIleThrAsnPheAsnArg 41
      1602 GTTTCAGAGGCGAGCGGTTCAGATACATAGAAAATCAGGTGAACCTAAATTTATATGA 1661
QY      42 AlaPheTyrProAspProValIleAsnLeuGluGluTyrGlyIleSerGlu 61
      1662 GCATTCTACCTTAAGCCAAAGTACTTAACCTTGAGGAGAGTGGGGTAAAGTCTCTACG 1721
QY      62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleProLeuGluLeuValAspAlaIle 81
      1722 GCGATTCAACATGCGCAAGATGGGGCTTTAACCACTCTAGAGCTAAAAAATGCAAAAC 1781
QY      82 GlyThrIleTyrPheIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
      1782 GGTGACAGGCGAGATGATGCTGAGAGTGAATATGCAACCTGATGTGGACTCCTTAAG 1841
QY      102 TyrValAsnGlyThrCysGlnThrThr 110
      1842 TATGTATATGGAGCTGCCAGCAACT 1868
Db
```

RESULT 6
AA056672
ID AA056672 standard; cDNA, 1195 BP.

XX AA056672;

DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)

XX Sequence of Phytolacca antiviral protein (PAP) cDNA.

XX Antiviral protein; PAP; virus-resistance; transgenic plant; ss.

XX Phytolacca americana; L.

XX Key Location/Qualifiers
FT 33..974
FT /*tag= a

XX EP585554-A1.

XX 09-MAR-1994.

XX 30-JUN-1993; 93EP-00110445.

XX 16-AUG-1992; 92KR-00014895.

XX (JINR-) JIN RO LTD.

XX Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;

XX WPI: 1994-076002/10.

XX P-PSDB; AAR48548.

XX Expression vector for phytolacca antiviral protein - used for producing

XX transgenic virus-resistant plants and for producing the antiviral agent.

XX Disclousure; Fig 1; 15pp; English.

XX To isolate PAP gene, total cellular mRNA was purified from leaves of

XX Phytolacca americana L. obd. in Korea. A cDNA library was constructed.

XX The PAP gene was selected by immunoscreening employing anti-PAP antibody.

XX A deletion mutant was prepd. from the isolated PAP gene, and the DNA

XX sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to

XX correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,47e-51 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-8 (1-110) x AA056672 (1-1195)

```
QY      2 GlyValAspSerPheProValIleAsnLeuGluValAlaIleGlnMet 21
      558 GGAGTGGATTCATTCACCTGAGAAAGCAATTCCTGTAGTCCATCCAAATG 617
QY      22 ValSerGluAlaIleArgPheLeuTyrIleGluAsnGlnValIleThrAsnPheAsnArg 41
      618 GTTTCAGAGGCGAGCGGTTCAGATACATAGAAAATCAGGTGAACCTAAATTTATATGA 677
QY      42 AlaPheTyrProAspProValIleAsnLeuGluGluTyrGlyIleSerGlu 61
      678 GCATTCTACCTTAAGCCAAAGTACTTAACCTTGAGGAGAGTGGGGTAAAGTCTCTACG 737
QY      62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleProLeuGluLeuValAspAlaIle 81
      738 GCAATTCATGATGCGCAAGATGGAGTGTAACTTAACTCGAGCTAGTGGATGCCAGT 797
QY      82 GlyThrIleTyrPheIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
      798 GGTGACAGGCGAGATGATGCTGAGAGTGAATATGCAACCTGATGTGGACTCCTTAAG 857
QY      102 TyrValAsnGlyThrCysGlnThrThr 110
      858 TACGTTGGTGGAGACTGTCAGCAACT 884
Db
```

RESULT 7
AA081457
ID AA081457 standard; cDNA, 1195 BP.

XX AA081457;

DT 16-OCT-2003 (revised)
DT 25-AUG-1995 (first entry)

XX Phytolacca antiviral protein (PAP) cDNA.

XX Antiviral protein; vector pMJ12; KCCM 10037; PAP; ss.

XX Phytolacca americana; L.

XX AU9350642-A.

XX 19-JAN-1995.

XX 11-NOV-1993; 93AU-00050642.

XX 02-JUL-1993; 93KR-00012360.

XX (JINR-) JIN RO LTD.

XX Lee K, Choi K, Jeon H, Kim M, Moon Y;

XX WPI: 1995-067516/10.

XX Recombinant vector for producing Phytolacca anti-viral protein - and

XX transformed E. coli useful for making immunconjugates for treatment of

XX AIDS.

XX Claim 1; Fig 1; 27pp; English.

XX Total cellular mRNA from leaves of P. americana was used to produce a

XX cDNA library and this screened with anti-PAP antibody raised in rabbits

XX against purified PAP. Inserts were isolated from 2 clones and sequenced

XX to identify a 1195 ORF (AA081457) that encodes a 313 AA PAP including a

CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
CC amplification using primers AAQ81458 and AAQ81459. The amplification
CC product was cut with Hind III and inserted into the commercial pGEMT (RTM)
CC vector cut with the same enzyme to form pGEMT. pGEMT is deposited with
CC the Korean Collection of Culture and Microorganism (KCCM), an
CC International Depository Authority, on June 30 1993, ad deposition No.
CC KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
XX

SO Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.47e-51	Length:	1195
Score:	454.00	Matches:	90
Percent Similarity:	87.2%	Conservative:	5
Best Local Similarity:	82.6%	Mismatches:	14
Query Match:	79.8%	Indels:	0
DB:	2	Gaps:	0

US-09-978-274A-8 (1-110) x AAQ81457 (1-1195)

QY 2 GIVVAlasPserPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 558 GGAAGTATGTCATTCCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATG 617
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 618 GTATCAGAGCGACGACCAAGATTCAAGTACATAGAGATCAGGTGAAGAACTAATTTTAAACA 677
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGlu 61
DB 678 GCATTCAACCTTAATCCCAAGTACCTTAATTTGCAAGACATGGGTAAAGATTTCACA 737
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 738 GCATTCAATATGCAAGAAATGAGATTTCACCAACCTCTCGAGCTAGTGCATGCCAGT 797
QY 82 GlyThrLysTrpIleValIleAsnArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 798 GGTGCCAAGTGATAGTGTGAGAGTGATGAAATCAAGCTGATGTAGCACTCTTAAC 857
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 858 TACGTTGTGGAGCTGTCAACAAC 884

RESULT 8

AAD42739 standard; DNA; 1378 BP.

AC AAD42739;

DT 15-NOV-2002 (first entry)

DE Pokeweed PAP' DNA #2.

KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.

XX Phytolacca americana.

OS Key Location/Qualifiers

FT misc_feature 290..1076

FT /tag= a

XX /note= "Mature PAP' sequence"

PN MO200233107-A2.

PD 25-APR-2002.

PF 15-OCT-2001; 2001MO-GB004593.

PR 14-OCT-2000; 2000GB-00025217.

PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

PI Thomas CR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.

PT Inducing necrotic effect in specific cells of plant by transforming plant

PT with a chimeric gene encoding pokeweed antiviral protein and a promoter

XX PT which acts in response to application of specific stimulus to plant.

XX PS Claim 5; Page 86-87; 87pp; English.

CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX

SO Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.4e-51	Length:	1378
Score:	454.00	Matches:	90
Percent Similarity:	87.2%	Conservative:	5
Best Local Similarity:	82.6%	Mismatches:	14
Query Match:	79.8%	Indels:	0
DB:	6	Gaps:	0

US-09-978-274A-8 (1-110) x AAD42739 (1-1378)

QY 2 GIVVAlasPserPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGTCATTCCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATG 809
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GTATCAGAGCGACCAAGATTCAAGTACATAGAGATCAGGTGAAGAACTAATTTTAAACA 869
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACCTTAATTTGCAAGACATGGGTAAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 930 GCATTCAATATGCAAGAAATGAGATTTCACCAACCTCTCGAGCTAGTGCATGCCAGT 989
QY 82 GlyThrLysTrpIleValIleAsnArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GGTGCCAAGTGATAGTGTGAGAGTGATGAAATCAAGCTGATGTAGCACTCTTAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGTGGAGCTGTCAACAAC 1076

RESULT 9

AAZ45197 standard; DNA; 1379 BP.

AC AAZ45197;

DT 29-FEB-2000 (first entry)

DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.

KW Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;

KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;

KW potato virus X; cucumber mosaic virus; CMV; ss;

XX tomato yellow leaf curl virus.

OS Phytolacca americana.

XX Key Location/Qualifiers

FT CDS 225..1166
FT /*tag= a
FT /product= "PAP"
FT /note= "Pokeweed antiviral protein"
PN W09960843-A1.
XX 02-DEC-1999.
XX 21-MAY-1999; 99WO-US011301.
XX 22-MAY-1998; 98US-0086374P.
XX (RUTE) UNIV RUTGERS STATE NEW JERSEY.
XX Turner NE, Wang P;
XX WPI: 2000-062555/05.
XX P-PSDB; MAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43pp; English.
XX
XX This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX Phytolacca americana (pokeweed). It is a single polypeptide chain that
XX catalytically removes a specific adenine residue from a highly conserved
XX stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX activities to plants. A DNA molecule encoding a PAP II protein with an
XX intact catalytic active site amino acid residue (R172) is useful for
XX generating transgenic plants. PAP II DNA is useful for generating
XX transgenic plants (especially cereal crops) through transforming a
XX protoplast or introducing the DNA directly into a plant part prior to
XX regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
XX activity thus have increased resistance to viruses and/or fungi. Viruses
XX include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
XX yellow leaf curl virus, and fungi include Pythium, Phytophthora,
XX Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
XX other plants pests including insects, bacteria and nematodes. PAP II DNA
XX is also useful for identifying a PAP II protein having reduced
XX cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
XX unlike PAP transgenic plants which are stunted and sterile, PAP II
XX transgenic plants have a normal and fertile phenotype
XX
XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5, 41e-51 Length: 1379
XX Score: 454.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.8% Indels: 0
XX Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAZ5197 (1-1379)
QY 2 G1yValAspSerPheProValIystrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGTCATTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheIystrIleGluAsnGlnValIystrPheAsnPheAsnArg 41
DB 810 GATTCAGAGGACAGCAATTCAGATCACTAGAGATCAGGTGAATACTTAATTTAAACAGA 869
QY 42 AlaPheTyProAspProLysValIleAsnLeuGluGlyLysTrpGlyLysIleSerGlu 61
DB 870 GCATTCACCTTAATCCCAAGTACTTAATTTCGAAGAGACATGGGTAAAGATTTCACACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81

DB 930 GCAATTCATGATGCCAAGATGAGTTTACCAACCTCTCGAGTACGATGCCAGT 989
QY 82 G1yThrIystrPileValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GTTCGCAAGTGGATGATGTTGATGATGAATAATCAAGCTGATGTAGCACTCTTAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGACTGTCAAGCAACT 1076
RESULT 10
AAZ59221
ID AAZ59221 standard; cDNA; 1379 BP.
AC AAZ59221;
XX
XX 20-APR-2000 (first entry)
XX
XX Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX Phytolacca americana.
XX
XX US6015940-A.
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS) MONSANTO CO.
XX
XX Kanielski WK, Turner NE, Lodge JK;
XX
XX WPI: 2000-126326/11.
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 7; Fig 5; 30pp; English.
XX
XX This is the coding sequence for a variant spring leaf form of the
XX pokeweed antiviral protein (PAP') which is used to generate transgenic
XX potato plants. PAP' is able to confer resistance to infection by potato
XX virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
XX the potato plant or tuber expressing PAP'. PAP' varies from PAP
XX (AAZ59220) by mutations L20R and Y49H
XX
XX Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5, 41e-51 Length: 1379
XX Score: 454.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.8% Indels: 0
XX Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAZ59221 (1-1379)
QY 2 G1yValAspSerPheProValIystrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGTCATTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheIystrIleGluAsnGlnValIystrPheAsnPheAsnArg 41
DB 810 GATTCAGAGGACAGCAATTCAGATCACTAGAGATCAGGTGAATACTTAATTTAAACAGA 869
QY 42 AlaPheTyProAspProLysValIleAsnLeuGluGlyLysTrpGlyLysIleSerGlu 61

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Db      870 GCATTACACCTTAATCCCAAGACTTAATTGTCAGAGACATGGGTTAGATTCAACA 929
Qy      62 AAlIhIshAaAlaIySaBngIyAlaLeuProLySProlengIuLeuValaPaAlaIyS 81
Db      930 GCATTACATGATGCCAAGATGAGATTTCACCAACCTCTCGAGCTAGTGCAGT 989
Qy      82 GLyThLySTrPlIeValleuArgValaSPgluIlIaShnArgaPaValaIaLeuLeuLyS 101
Db      990 GGTGCCAAGTGAGTAGTGTGAGATGGAATCAAGCCTGATGATGACACTTTAAAC 1049
Qy      102 TyrValaBngIyThrCySgInThrThr 110
Db      1050 TACGTTGGTGGAGCTGTCAACACT 1076

RESULT 11
AAZ59220
ID      AAZ59220 standard; cDNA; 1379 BP.
XX
AC      AAZ59220;
XX
DT      20-APR-2000 (first entry)
XX
DE      Pokeweed antiviral protein coding sequence spring leaf form.
XX
KW      Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KM      resistance; potato virus X; potato virus Y; potato leaf roll virus;
KW      tuber; 89.
XX
OS      Phytolacca americana.
XX
PN      US6015940-A.
XX
PD      18-JAN-2000.
XX
PF      07-APR-1992; 92US-00865169.
XX
PR      07-APR-1992; 92US-00865169.
XX
PA      (MONS ) MONSANTO CO.
XX
PI      Kaniewski WK, Turner NE, Lodge JK;
XX
DR      WPI; 2000-126326/11.
XX
PT      Production of transgenic potato plants or tubers expressing pokeweed
XX      antiviral protein which are resistant to potato virus X or Y.
XX
PS      Claim 6; Fig 4; 30pp; English.
XX
CC      This is the coding sequence for the spring leaf form of the pokeweed
CC      antiviral protein (PAP) which is used to generate transgenic potato
CC      plants. PAP is able to confer resistance to infection by potato virus X
CC      (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC      potato plant or tuber expressing PAP
XX
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,41e-51 Length: 1379
Score: 454.00 Matches: 90
Best Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274a-8 (1-110) x AAZ59220 (1-1379)
Qy      2 GLyValaSPSerPheProValaIySThrGluAlaPheLeuLeuValaIaIleGlnMet 21
Db      750 GGAGTGATGATCATTCATCGAAGAAACCGAAGCCGAATTCCTATTGTGTAGCCATCAAAATG 809
Qy      22 ValSerGluAlaAlaArgPheLeuTyrlIeGluBngInValLySThrAenPheAenArg 41

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Db      810 GTATGAGGCGACGAAGATTCAAGTACATAGAAATCAGGTGAATACTAATTTTAAACA 869
Qy      42 AlAphETrProaSPProLySaValIleAenIeGluLySTrPlLySIlIesErglu 61
Db      870 GCATTACACCTTAATCCCAAGACTTAATTGCAAGACATGGGTTAGATTCAACA 929
Qy      62 AAlIhIshAaAlaIySaBngIyAlaLeuProLySProlengIuLeuValaPaAlaIyS 81
Db      930 GCATTACATGATGCCAAGATGAGATTTCACCAACCTCTCGAGCTAGTGCAGT 989
Qy      82 GLyThLySTrPlIeValleuArgValaSPgluIlIaShnArgaPaValaIaLeuLeuLyS 101
Db      990 GGTGCCAAGTGAGTAGTGTGAGATGGAATCAAGCCTGATGATGACACTTTAAAC 1049
Qy      102 TyrValaBngIyThrCySgInThrThr 110
Db      1050 TACGTTGGTGGAGCTGTCAACACT 1076

RESULT 12
AAD42738
ID      AAD42738 standard; DNA; 1379 BP.
XX
AC      AAD42738;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Pokeweed PAP' DNA #1.
XX
KW      Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS      Phytolacca americana.
XX
PN      W0200233107-A2.
XX
PD      25-APR-2002.
XX
PF      15-OCT-2001; 2001MO-GB004593.
XX
PR      14-OCT-2000; 2000GB-00025217.
XX
PA      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI      Thomas CJR, Mcpherson MJ, Atkinson HD, Neelam A;
XX
DR      WPI; 2002-489891/52.
XX
PT      Inducing necrotic effect in specific cells of plant by transforming plant
XX      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      which acts in response to application of specific stimulus to plant.
XX
PS      Claim 5; Page 86; 87pp; English.
XX
CC      The invention relates to a method of inducing a necrotic effect in
CC      specific cells of a plant. The method involves transforming the plant
CC      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC      PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts
CC      in response to the application of a specific stimulus to the plant so as
CC      to facilitate expression of the pokeweed antiviral protein in specific
CC      cells of the plant. The method is useful for inducing a necrotic effect
CC      in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,41e-51 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5

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Best Local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AD42738 (1-1379)

QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 DB 750 GGAGTGAATGTCATTCATGAGAAACCGAAGCCGAATTCCTATTGTGTAGCCATCAAAATG 809
 QY 22 ValSerGluAlaAlaArgPheIleGluAsnGlnValIyThrAsnPheAsnArg 41
 DB 810 GTATCAGAGGCGCAGAAATTCAGATGATGAGATCGATGAAATCTAAATTTTAAACGA 869
 QY 42 AlaPheTyProAspProIyValIleAsnLeuGluIyTyTPGILySeriIleSerGlu 61
 DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 929
 QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
 DB 930 GCAATTCATGATGCGCAAGAAATGAGATTTTACCAAACTCTCGAGCTAGTGATGCCAGT 989
 QY 82 GlyThrIySTPILleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
 DB 990 GTGCCAAGTGAATGATGTTGAGAGTGAATCAAGCTGATGTAGCACTCTTAAC 1049
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 DB 1050 TACGTGTGGAGCTGTCAACAACT 1076

RESULT 13
 AD105787
 ID AD105787 standard; DNA; 1379 BP.
 AC AD105787;
 DT 15-APR-2004 (first entry)
 XX DNA encoding the wild-type pokeweed antiviral protein.
 XX
 KW ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
 KW cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
 KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
 KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
 KW de.
 KW
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag=a
 FT /product="wild-type pokeweed antiviral protein"
 XX
 PN W0200262952-A2.
 XX 15-AUG-2002.
 XX
 PD 01-FEB-2002; 2002WO-US002792.
 XX
 PR 02-FEB-2001; 2001US-0266396P.
 XX
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Turner NB, Hudak KA, Parikh B;
 XX WPI; 2003-156656/15.
 DR P-PSDB; AD105788.
 XX
 PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 PT or autoimmune disease.
 XX

PS Disclosure; SEQ ID NO 1; 51bp; English.

CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytoskeletal and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer, AIDS, viral infection or autoimmune
 CC diseases associated with proliferations of unwanted T-cells or B-cells.
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.

SEQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5,41e-51	Length:	1379
Score:	454.00	Matches:	90
Percent Similarity:	87.2%	Conservative:	5
Best Local Similarity:	82.6%	Mismatches:	14
Query Match:	79.8%	Indels:	0
DB:	10	Gaps:	0

US-09-978-274A-8 (1-110) x AD105787 (1-1379)

QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 DB 750 GGAGTGAATGTCATTCATGAGAAACCGAAGCCGAATTCCTATTGTGTAGCCATCAAAATG 809
 QY 22 ValSerGluAlaAlaArgPheIleGluAsnGlnValIyThrAsnPheAsnArg 41
 DB 810 GTATCAGAGGCGCAGAAATTCAGATGATGAGATCGATGAAATCTAAATTTTAAACGA 869
 QY 42 AlaPheTyProAspProIyValIleAsnLeuGluIyTyTPGILySeriIleSerGlu 61
 DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 929
 QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
 DB 930 GCAATTCATGATGCGCAAGAAATGAGATTTTACCAAACTCTCGAGCTAGTGATGCCAGT 989
 QY 82 GlyThrIySTPILleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
 DB 990 GTGCCAAGTGAATGATGTTGAGAGTGAATCAAGCTGATGTAGCACTCTTAAC 1049
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 DB 1050 TACGTGTGGAGCTGTCAACAACT 1076

RESULT 14
 ADG76061
 ID ADG76061 standard; DNA; 1378 BP.
 AC ADG76061;
 DT 11-MAR-2004 (first entry)
 XX
 DE American pokeweed antiviral protein (PAP) DNA Seqd 1.
 XX
 KW gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
 KW nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
 KW american pokeweed; retroviral.
 XX
 OS Phytolacca americana.
 XX
 PN W02003106479-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 17-JUN-2003; 2003WO-US019141.

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XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
XX replication, for inducing depurination of viral RNA, or for treating
XX viral infection in subject.
XX
XX Example 2; SEQ ID NO 1; 62pp; English.
XX
XX This invention relates to novel modified pokeweed antiviral proteins
XX (PAPs). Specifically, it refers to modifications relative to wild-type
XX PAP that confer increased activity towards viral RNA, particularly
XX retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
XX modified PAP also exhibits decreased activity towards ribosomal RNA
XX relative to wild-type PAP. The present invention describes a molecular
XX model of PAP-HIV RNA interactions that have been used for the rational
XX redesign of PAP mutants with potent anti-HIV activity, where
XX modifications have been introduced in regions other than the active site.
XX Accordingly, these mutants represent antiviral agents that can work as
XX nucleoside analogue inhibitors of reverse transcriptase, as well as viral
XX protease inhibitors that can be used for treating viral infections. As
XX such, they are useful for inhibiting viral replication and for
XX depurinating viral RNA. This polynucleotide sequence is the DNA encoding
XX the wild type american pokeweed antiviral protein (PAP) of the invention.
XX
XX Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.01e-50 Length: 1378
XX Score: 452.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.4% Indels: 0
XX DB: 12 Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x ADG76061 (1-1378)
XX
XX 2 G1yValAspSerPheProVallyrThGluAlaPhePheLeuValAla1leGlnMet 21
XX |||||
XX 749 GGAAGTGTATGTCATTCACCTGAGAAAACCGAACCCGAATTCCTATGTGTAGCCATACCAATG 808
XX
XX 22 ValSerGluAlaAlaArgPheLySTyrlleGluAsnGlnVallyrThrAsnPheAsnArg 41
XX |||||
XX 809 GTATCAGAGGCGACGACAGATTCAGATACATAGAGATCGGTGAAAACCTAATTTTAAACGA 868
XX
XX 42 AlaPheTyrrProAspProLySValIleAsnLeuGluGluLySTpGlyLyS1leSerGlu 61
XX |||||
XX 869 GCATTCACCCCTATATCCCAAGTAACTTATTCGAAGAGACATGGGGTAAACATTTCAACA 928
XX
XX 62 Alil1eHisAsnAlaLySAsnGlyAlaLeuProLySProLeuGlnLeuValAspAlaLyS 81
XX |||||
XX 929 GCATTCATATAGTCCAGCAAGATGAGTTTACCCAAACCTCTCGAGCTAGTGAAGCCAGT 988
XX
XX 82 GlyThrLySTp1leValIleuArgValAspGluIleAsnArgValAla1leuLeuLyS 101
XX |||||
XX 989 GGTGCCAAGTGAAGATGTGTGAGAGTGAATCAAGCTGATGTAGCACTCTTAAAC 1048
XX
XX 102 TyrValAsnGlyThrrCySglnThrThr 110
XX |||||
XX 1049 TACGTGTCTGGAGCTGTCAACAAC 1075
XX
XX RESULT 15
XX AAC87929
XX ID AAC87929 standard; DNA; 1379 BP.
XX
XX AAC87929;

```

```

XX 06-MAR-2001 (first entry)
XX
XX P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
XX PhytoIacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
XX biotherapeutic; fusion protein; immunocjugate; mutant; cytotoxic;
XX anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
XX
XX PhytoIacca americana.
XX
XX Key Location/qualifiers
XX CDS 225..1166
XX FT /*tag= a
XX FT /product= "pokeweed antiviral protein (PAP) "
XX
XX US6146628-A.
XX
XX 14-NOV-2000.
XX
XX 11-JUL-1995; 95US-00501253.
XX
XX 11-JUL-1995; 95US-00501253.
XX
XX (MINU ) UNIV MINNESOTA & RUTGERS.
XX (UTNE-) UNIV STATE NEW JERSEY.
XX
XX Uckun FM, Turner NE;
XX
XX WPI; 2001-040422/05.
XX P-PSDB; AAB36500.
XX
XX Immunocjugates useful for treating cancer and acquired immunodeficiency
XX syndrome, comprises mutant pokeweed anti-viral protein and a targeting
XX moiety that binds a cell surface receptor.
XX
XX Disclosure; Col 47-50; 32pp; English.
XX
XX The present invention describes a fusion protein or an immunocjugate
XX (1), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
XX acid substitution at residue 75, 97 or 176 of native PAP and a targeting
XX moiety that binds a cell surface receptor. (1) can have cytosolic and
XX anti-HIV activities, and is an inhibitor of cellular RNA or protein
XX synthesis. (1) is useful for treating AIDS and cancers including
XX leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
XX tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
XX colon cancer. Immunocjugates prepared using PAP mutants exhibit an
XX improved therapeutic index over immunocjugates containing either wild-
XX type PAP or variant PAP. The present sequence encodes the wild-type PAP,
XX which is given in the exemplification of the present invention
XX
XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.37e-50 Length: 1379
XX Score: 451.00 Matches: 89
XX Percent Similarity: 87.2% Conservative: 6
XX Best Local Similarity: 81.7% Mismatches: 14
XX Query Match: 79.3% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAC87929 (1-1379)
XX
XX 2 G1yValAspSerPheProVallyrThGluAlaPhePheLeuValAla1leGlnMet 21
XX |||||
XX 750 GGAAGTGTATGTCATTCACCTGAGAAAACCGAACCCGAATTCCTATGTGTAGCCATACCAATG 809
XX
XX 22 ValSerGluAlaAlaArgPheLySTyrlleGluAsnGlnVallyrThrAsnPheAsnArg 41
XX |||||
XX 810 GTATCAGAGGCGACGACAGATTCAGATACATAGAGATCGGTGAAAACCTAATTTTAAACGA 869
XX
XX 42 AlaPheTyrrProAspProLySValIleAsnLeuGluGluLySTpGlyLyS1leSerGlu 61

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Db      870 GCATTCAACCTTAATCCCAAGTACTTAATTGCAAGAGCATGGGTAAAGATTCAACA 929
Qy      62 AIAIEHISAANAAlaYsAangIyAlaleuProLysProLeuGluLeuValAspAlaLys 81
Db      930 GCAATTGATGATGCCAAGATGAGATTTTACCCAAACCTCTGAGCTAGTGATGCCAGT 989
Qy      82 GLyThrLySTPILeValLeuArgValAspGluIleAsnArgAspValAlaleuLeuLys 101
Db      990 GGTGCCAAGTGAATAGTGTGAGAGTGAATCAAGCTGATGTAGCACTTTAAAC 1049
Qy      102 TyrValAsnGlyThrCysGlnThr 110
Db      1050 TACGTTGGTGGAGCTGTCAAGCAACT 1076

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 1999.23 Seconds
(without alignments)
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Fgapop 6.0 , Fgapext 7.0
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gse81:*
10: gb_gse82:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	226	39.7	816	2	BR035038 MM02A01 M
C 2	226	39.7	993	2	BR035039 MM02A03 M
3	213.5	37.5	649	6	CA838757 CA838757 MCT020B02
4	213.5	37.5	649	6	CA839330 CA839330 MCT026C11
5	213.5	37.5	661	6	CA835532 CA835532 MCT038A11
6	213.5	37.5	671	6	CA839511 MCT028D04
7	213.5	37.5	689	6	CA833333 CA833333 MCS021A09

8	213.5	37.5	689	6	CA833383
9	200.5	35.2	639	6	CA835855
10	197	34.6	1033	2	BR035541
11	157	27.6	829	7	CN782289
12	151	26.5	405	8	T24255
13	140.5	24.7	1021	2	BR036639
14	130	22.8	1038	2	BR035546
15	121	21.3	267	1	AA856221
16	117.5	20.7	614	7	CN845658
17	115.5	20.3	837	1	AM053634
18	115	20.2	649	7	CN948289
19	112	19.7	1094	4	AY105813
20	111	19.5	639	2	BE037217
21	110	19.3	591	6	CA091595
22	108	19.0	642	9	CC751502
23	107	18.8	299	2	BF704840
24	107	18.8	513	2	BF585775
25	107	18.8	587	2	BF704654
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27	106	18.6	654	6	CA244111
28	104	18.3	420	6	CP227009
29	104	18.3	563	6	CA246414
30	104	18.3	646	6	CA187396
31	104	18.3	719	6	CA206790
32	104	18.3	742	6	CA084039
33	104	18.3	841	7	CO121195
34	103	18.1	616	6	CA077373
35	103	18.1	628	6	CA184471
36	103	18.1	649	6	CA083619
37	103	18.1	677	6	CA174183
38	103	18.1	698	6	CA221929
39	103	18.1	759	6	CA074628
40	102	17.9	653	6	CA260173
41	102	17.9	680	6	CA198271
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43	100	17.6	903	7	CO103587
44	98	17.2	654	6	CA173838
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ALIGNMENTS

RESULT 1
LOCUS BR035038/c 816 bp mRNA linear EST 07-JUN-2000
DEFINITION MM02A01 M Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION BR035038
VERSION BR035038.1 GI:8330047
KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Caryophyllales; Alceaceae; Mesembryanthemum.
1 (bases 1 to 816)

AUTHORS Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu

FEATURES
source Location/Qualifiers

1..816
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/cell_type="epidermal bladder cells"

SOURCE

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/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_id="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
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ORIGIN

Alignment Scores:

Pred. No.:	2.16e-18	Length:	649
Score:	213.50	Matches:	50
Percent Similarity:	60.6%	Conservative:	16
Best Local Similarity:	45.9%	Mismatches:	34
Query Match:	37.5%	Indels:	9
DB:	6	Gaps:	3

US-09-978-274a-8 (1-110) x CA8393757 (1-649)

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Qy 2 G1YValAspSerPheProValIyThrG1uAlaPhePheLeuValAlaIleGlnMet 21
Db 166 GGTAAAGACATGACAGTCAGAGAAATGAGGCCAAATTCCTTGCTGATGCCATACAGATG 225
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Db 226 GTTCTGAGAGCAGCAGGTTCAAGTATATGAGTAAAGTAAACCAATGGCGTTAGAT 285
Qy 40 AsnArgAlaPheTyrrProAspProLyValIleAsnLeuG1uIySTyrlIySTyrlIe 59
Db 286 TATGAATGCTTCTTACCAGCCGAAATGCTGCTTTGGAGACCAATTTGGGGAGATT 345
Qy 60 SerG1uAlaIleHisAsnAlaIyAsnG1yAlaLeuPro-----Lys 73
Db 346 TCGCAGAGATTCTATGAGAGTCT---GGGGCGAAACCTGCTGTGATGAATCTTACACT 402
Qy 74 ProLeuG1uLeuValAlaPalaIySG1yThrIySTyrlIeValIleuArgValAspGluIle 93
Db 403 CCGATTCCGTTAAAGAAACCAATGATGATCCATGACGCGTGAATAGTTGACACTATT 462
Qy 94 AsnArgAspValAlaLeuLeuIySTyTyr 102
Db 463 AGACCTGAATAATGGGATATCTCAAGTTTC 489
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RESULT 4
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11.5,
mRNA sequence.

ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astroceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada

MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.

FEATURES

SOURCE

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/organism="Mesembryanthemum crystallinum"
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/clone_id="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
```

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-18	Length:	649
Score:	213.50	Matches:	50
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Query Match:	37.5%	Indels:	9
DB:	6	Gaps:	3

US-09-978-274a-8 (1-110) x CA839330 (1-649)

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Qy 2 G1YValAspSerPheProValIyThrG1uAlaPhePheLeuValAlaIleGlnMet 21
Db 166 GGTAAAGACATGACAGTCAGAGAAATGAGGCCAAATTCCTTGCTGATGCCATACAGATG 225
Qy 22 ValSerG1uAlaAlaArgPheIySTyrlIeG1uAaG1nValIySThrAsnPh----- 39
Db 226 GTTCTGAGAGCAGCAGGTTCAAGTATATGAGTAAAGTAAACCAATGGCGTTAGAT 285
Qy 40 AsnArgAlaPheTyrrProAspProLyValIleAsnLeuG1uIySTyrlIySTyrlIe 59
Db 286 TATGAATGCTTCTTACCAGCCGAAATGCTGCTTTGGAGACCAATTTGGGGAGATT 345
Qy 60 SerG1uAlaIleHisAsnAlaIyAsnG1yAlaLeuPro-----Lys 73
Db 346 TCGCAGAGATTCTATGAGAGTCT---GGGGCGAAACCTGCTGTGATGAATCTTACACT 402
Qy 74 ProLeuG1uLeuValAlaPalaIySG1yThrIySTyrlIeValIleuArgValAspGluIle 93
Db 403 CCGATTCCGTTAAAGAAACCAATGATGATCCATGACGCGTGAATAGTTGACACTATT 462
Qy 94 AsnArgAspValAlaLeuLeuIySTyTyr 102
Db 463 AGACCTGAATAATGGGATATCTCAAGTTTC 489
```

RESULT 5
CA835532 661 bp mRNA linear EST 12-DEC-2002
LOCUS MCS038A11.160572 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS038A11.5, mRNA
sequence.

ACCESSION CA835532
VERSION CA835532.1 GI:26563297
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 661)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7 21mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
Location/Qualifiers

FEATURES
source

1..661
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS038A11"
/rbase_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM) "
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 2,22e-18 Length: 661
Score: 213.50 Matches: 50
Percent Similarity: 60.6% Conservative: 16
Best Local Similarity: 45.9% Mismatches: 34
Query Match: 37.5% Indels: 9
DB: Gaps: 3

US-09-978-274A-8 (1-110) x CA835532 (1-661)

QY 2 G|YValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 177 GGTAAACATCGACAGCTCAGAGAAATGAGCCAAATCTTGCTGATTCACATACAGATG 236
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPh----- 39
DB 237 GTTCTGAAGCAGCAGAGTTCAAGTATATTGAGGTAAAGTAAAGCAAAAGCGCTTAGAT 296
QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIle 59
DB 297 TATGAATGTTCTTAACCCGACCCGAAATGCTGCTTTGGAGACCAATTTGGGGGAAGATT 356
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro-----Lys 73
DB 357 TCGCGAGGAGATTCAAGAGAGTCT--GGGGGAAACCTGCTGTATGAATCTTTACACT 413
QY 74 ProLeuGluLeuValAlaAspAlaLysGlyThrLysTyrIleValLeuArgValAspGluIle 93
DB 414 CCGATTCGCTTAAAGAAACCAATGTGATCATCGAGAGGTGAATAGGTGACACTATT 473
QY 94 AsnArgAspValAlaLeuLeuLysTyr 102
DB 474 AGACCTGAATGGGATTACTCAAGTTTC 500

RESULT 6

CA839511
LOCUS
DEFINITION

CA839511 671 bp mRNA linear EST 12-DEC-2002
MCT028D04 172117 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA839511
CA839511.1 GI:26567276
EST.
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 671)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

1..671
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/rbase_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM) "
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.: 2,26e-18 Length: 671
Score: 213.50 Matches: 50
Percent Similarity: 60.6% Conservative: 16
Best Local Similarity: 45.9% Mismatches: 34
Query Match: 37.5% Indels: 9
DB: Gaps: 3

US-09-978-274A-8 (1-110) x CA839511 (1-671)

QY 2 G|YValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 166 GGTAAACATCGACAGCTCAGAGAAATGAGCCAAATCTTGCTGATTCACATACAGATG 225
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPh----- 39
DB 226 GTTCTGAAGCAGCAGAGTTCAAGTATATTGAGGTAAAGTAAAGCAAAAGCGCTTAGAT 285
QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIle 59
DB 286 TATGAATGTTCTTAACCCGACCCGAAATGCTGCTTTGGAGACCAATTTGGGGGAAGATT 345
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro-----Lys 73

Db 346 TCGCAGAGATTGATGAGTGCT---GGGGCGAAACCTGCTGTATGATCTTTACCT 402
 Qy 74 ProleugluLeuValaAspAlaIysGlyThrIysTrpIleValaIysArgValaAspGluIle 93
 Db 403 CGGATTCGCTTTAAAGAAACCAATGCTATCATGACGCGATGAAGGTGACACTATT 462
 Qy 94 AsnArgAspValaAlaLeuLeuIysTyr 102
 Db 463 AGACCTGAATGGGATGACTCAAGTTTC 489
 RESULT 7
 LOCUS CA833333 689 bp mRNA linear EST 12-DEC-2002
 DEFINITION MCS021A09.151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.
 ACCESSION CA833333
 VERSION CA833333.1 GI:26561098
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 689)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERs
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: A column: 09
 Seq primer: T3 20mer
 High quality sequence stop: 689.
 FEATURES
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 1. 689
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS021A09"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.34e-18 Length: 689
 Score: 213.50 Matches: 50
 Percent Similarity: 60.6% Conservative: 16
 Best Local Similarity: 45.9% Mismatches: 34
 Query Match: 37.5% Indels: 9
 Gaps: 3
 DB: 6
 US-09-978-274A-8 (1-110) x CA833333 (1-689)
 Qy 2 G|YValaIspSerPheProValaIysThrGluAlaPheLeuLeuValaAlaIleGlnMet 21
 Db 177 GGTAAAGACATGACAACTGACAGAAATGAGGCAAAATTCCTGCTGATTCGACATGATG 236

Qy 22 ValSerGluAlaAlaArgPheIysThrIleGluAsnGlnValaIysThrAspHe----- 39
 Db 237 GTTCTGAAGCAGCAGAGTTCAAGATATTTAGATAGGTAAGCAAAAGTGCCTTAGAT 296
 Qy 40 AsnArgAlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIle 59
 Db 297 TATGATGCTTCTTAACCGAACCGAAATGCTGCTTTGGAGACCAATGGCGGAAGATT 356
 Qy 60 SerGluAlaIleHisAsnAlaIysAsnGlyValaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTGATGAGTGCT---GGGGCGAAACCTGCTGTATGATCTTTACCT 413
 Qy 74 ProleugluLeuValaAspAlaIysGlyThrIysTrpIleValaIysArgValaAspGluIle 93
 Db 414 CGGATTCGCTTTAAAGAAACCAATGCTATCATGACGCGATGAAGGTGACACTATT 473
 Qy 94 AsnArgAspValaAlaLeuLeuIysTyr 102
 Db 474 AGACCTGAATGGGATGACTCAAGTTTC 500
 RESULT 8
 LOCUS CA833383
 DEFINITION MCS021F04.152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA sequence.
 ACCESSION CA833383
 VERSION CA833383.1 GI:26561148
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 689)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERs
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: F column: 04
 Seq primer: T3 20mer
 High quality sequence stop: 689.
 FEATURES
 source
 1. 689
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS021F04"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.34e-18 Length: 689

Score: 213.50 Matches: 50
 Percent Similarity: 60.6% Conservative: 16
 Best Local Similarity: 45.9% Mismatches: 34
 Query Match: 37.5% Indels: 9
 DB: 6 Gaps: 3

US-09-978-274A-8 (1-110) x CA835855 (1-689)

QY 2 G|VAlaAspSerPheProValIySthrGlUAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 177 GGTAAAGCATCGCACTCAGAAATGAGCCAAATCTTGCTGATGCTCATACAGATG 236
 QY 22 ValSerGlUAlaIaAaGpPheTyrlleGlUaSnGlnValIySthraPhe----- 39
 Db 237 GTTCTGAAGCAGCAAGTTCAGATATATGAGGTAAAGTGAACCAAGTGGCTTAGAT 296
 QY 40 AsnArgAlaPheTyrrProAspProIySValIleAsnLeuGlnGluIySTPglYlyle 59
 Db 297 TATGAATCGTTCTTACCAGCCGAAATGCTCTTTGGAGACCAATGGGGAGATT 356
 QY 60 SerGlUAlaIleHisAsnAlaIyAsnGlyAlaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTCTATGAGAGTCT---GGGGCGAAACCTGCTGTATGAACTTTCACT 413
 QY 74 ProLeuGlnLeuValaPheAlaIyeglyThrlYrTrpIleValLeuArgValaPgluile 93
 Db 414 CCGATTCGGTTAAAGAAACCAATGATGATCCATGACGGTGAATAGGTGACACTAT 473
 QY 94 AsnArgAspValAlaLeuLeuTyrr 102
 Db 474 AGACCTGAATGGGATATCTCAAGTTC 500

RESULT 9 639 bp mRNA linear EST 12-DEC-2002
 LOCUS CA835855
 DEFINITION MGS004G12.161218 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crasulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MGS004G12.5, mRNA sequence.

ACCESSION CA835855
 VERSION CA835855.1 GI:26563620
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 639)

AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL COMMENT Unpublished (1997)
 CONTACT: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 004 row: G column: 12
 Seq primer: T3 20mer
 High quality sequence strop: 639.

FEATURES
 SOURCE location/Qualifiers
 1..639

/organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MGS004G12"
 /issue_type="leaf"
 /dev_stage="five-week-old"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,28e-16 Length: 639
 Score: 200.50 Matches: 50
 Percent Similarity: 60.0% Conservative: 16
 Best Local Similarity: 45.5% Mismatches: 34
 Query Match: 35.2% Indels: 10
 DB: 6 Gaps: 3

US-09-978-274A-8 (1-110) x CA835855 (1-639)

QY 2 G|VAlaAspSerPheProValIySthrGlUAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 177 GGTAAAGCATCGCACTCAGAAATGAGCCAAATCTTGCTGATGCTCATACAGATG 236
 QY 22 ValSerGlUAlaIaAaGpPheTyrlleGlUaSnGlnValIySthraPhe----- 39
 Db 237 GTTCTGAAGCAGCAAGTTCAGATATATGAGGTAAAGTGAACCAAGTGGCTTAGAT 296
 QY 40 AsnArgAlaPheTyrrProAspProIySValIleAsnLeuGlnGluIySTPglYlyle 59
 Db 297 TATGAATCGTTCTTACCAGCCGAAATGCTCTTTGGAGACCAATGGGGAGATT 356
 QY 60 SerGlUAlaIleHisAsnAlaIyAsnGlyAlaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTCTATGAGAGTCT---GGGGCGAAACCTGCTGTATGAACTTTCACT 413
 QY 74 ProLeuGlnLeuValaPheAlaIyeglyThrlYrTrpIleValLeu-ArgValaPgluile 93
 Db 414 CCGATTCGGTTAAAGAAACCAATGATGATCCATGACGGTGAATAGGTGACACTAT 473
 QY 93 AsnArgAspValAlaLeuLeuTyrr 102
 Db 474 TAGACCTGAATGGGATATCTCAAGTTC 501

RESULT 10

BE036541 1033 bp mRNA linear EST 07-JUN-2000
 LOCUS MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION antiviral protein, mRNA sequence.

ACCESSION BE036541
 VERSION BE036541.1 GI:8331550
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 1033)
 AUTHORS Bohnert, H.J., Bohnert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C., Scarpa, G., Wheeler, M. and Zepeda, G.R.
 TITLE Functional Genomics of Plant Stress Tolerance
 JOURNAL COMMENT Unpublished (2000)

CONTACT: Michalowski, C.B.

University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697

Email: chm@u.arizona.edu
 An open reading frame exists.

FEATURES
 SOURCE location/Qualifiers
 1..1033

/organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"

/db_xref="taxon:3988"
/clone="pcr1345"
/note="Vector: lambdaZAPri; site_1: EcoRI, site_2: XhoI;
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPri according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN

Alignment Scores:

Pred. No.:	4,16e-10	Length:	405
Score:	151.00	Matches:	33
Percent Similarity:	61.6%	Conservative:	12
Best Local Similarity:	45.2%	Mismatches:	25
Query Match:	26.5%	Indels:	3
DB:	8	Gaps:	1

US-09-978-274A-8 (1-110) x T24255 (1-405)

Qy 8 VallyerPhrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArg 27
Db 77 ATTCAACCTGCTGCTCTTCTTATGCTTGCATCCAAATGATTTCAAGAGCGACAGGA 136
Qy 28 PheleTyTilleGluAenGlnVallyeThr-----AanPheAanArgAlaPheTyPro 45
Db 137 TTCAGATCACTTGAGGAGAAATCGCAGCATTTAGTCAACCGACATCTGCACCA 196
Qy 46 AspProLyValIleAenLeuGlnLyTyTyllyleSerGluAlaIleHis-As 65
Db 197 GATCTAGCGTAATTACACTTNAAGATAGTTGGGGAGACTTCCACTGCATTCAGGA 256
Qy 65 naAlaAanGlnValaleuProLyProLeuGlnLeu 77
Db 257 GTCTAACCAAGAGCCTTGTCTAGTCACATTCACCTG 293

RESULT 13
LOCUS BE036639 1021 bp mRNA linear EST 07-JUN-2000
DEFINITION MF03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:8331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzaceae; Mesembryanthemum.
1 (bases 1 to 1021)
REFERENCE Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
Ferreira,H., Kawasaki,S., McColough,A., Michalowski,C.B.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski,C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: chm@u.arizona.edu
AN OPEN READING FRAME EXISTS.
INSERT LENGTH: 1 Std Error: 0.00.
LOCATION/QUALIFIERS
1. 1021
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

FEATURES
source
1. 1021
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

/issue_type="apical meristem and leaf primordia"
/dev stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN

Alignment Scores:

Pred. No.:	3.87e-08	Length:	1021
Score:	140.50	Matches:	41
Percent Similarity:	61.9%	Conservative:	11
Best Local Similarity:	48.8%	Mismatches:	28
Query Match:	24.7%	Indels:	5
DB:	2	Gaps:	3

US-09-978-274A-8 (1-110) x BE036639 (1-1021)

Qy 11 GluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPheTyTyr 30
Db 665 GAGGCCAAATCTTGTGCTGATTTGCTATACAGATGTTTGGAGACGACGCTTTAAGTAT 724
Qy 31 IlleGluAenGln---VallyeThrAanPheAanArgAlaPheTyProAspProLyVal 49
Db 725 ATTGAAGTGGAGACCCAAAGTGTACATGCTCTTCAAAACCCGACCCGAAAGTG 784
Qy 50 IlleAenLeuGlnLyTyTyllyleSer---GluAlaIleHisAanAlaAen 68
Db 785 CTGAGTTTGGAGAGACAAATTTGGGAGATTTCCAGAAATTAAGACAGATCGCCGAA 844
Qy 69 GlnAlaLeuProLy-----ProLeuGlnLeuValaAenAlaAenGlnTyTyrTyr 86
Db 845 AACTGTTTTC-AAAATATTCACCGCGCATCTTCCAAATGCTGATGTTACATGGAAG 903
Qy 87 ValLeuArgVal 90
Db 904 GTGATTAAGGGTG 915

RESULT 14
LOCUS BE033546 1038 bp mRNA linear EST 07-JUN-2000
DEFINITION MF03A09 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein, mRNA sequence.
ACCESSION BE033546
VERSION BE033546.1 GI:8328555
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzaceae; Mesembryanthemum.
1 (bases 1 to 1038)
REFERENCE Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
Ferreira,H., Kawasaki,S., McColough,A., Michalowski,C.B.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski,C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: chm@u.arizona.edu
AN OPEN READING FRAME EXISTS.
LOCATION/QUALIFIERS
1. 1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

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1. 1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
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/issue_type="Root"
/dev stage="5-6 weeks old"
/clone_lib="MP"
/note="Vector: Bluescript SK+, site_1: EcoRI; site_2:
XhoI"

ORIGIN
1. 1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/issue_type="Root"
/dev stage="5-6 weeks old"
/clone_lib="MP"
/note="Vector: Bluescript SK+, site_1: EcoRI; site_2:
XhoI"

US-09-978-274A-8 (1-110) X BE033546 (1-1038)

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29 LYSIYCIIEGLUASHGInVal---LysThrAsnPhesAsnArgAlaphetyrProAspPro 47

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27 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

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AA856221

LOCUS	267 bp	mRNA	linear	EST 20-FEB-2001
DEFINITION	L30-24273 Ice plant Lambda Uni-Zap XR expression library, 30 hours			

NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2 similar to Ribosome inactivating protein precursor (antiviral protein), mRNA sequence.

VERSION AA856221.1 GI:2944523

SOURCE ORGANISM	Strain
Mesembryanthemum crystallinum (common iceplant)	1100
Mesembryanthemum crystallinum	1101

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Rosales

1 (bases 1 to 267)
caryophyllales; Alzooaceae; Mesembryanthemum

ADINOKS Cubanah, U.C.
TITLE An expressed sequence tag database for the common ice plant

JOURNAL
mesemioyancnemum crystallinum
unpublished (1997)

Department of Biochemistry
contact: cubin@uic.edu

UNIVERSITY OF NEVADA
MS200, Reno, NV 89557-0014, USA

Fax: 775-784-1650

PCR Primers

BACKWARD: T3

Seq primer: T3

FEATURES	Location/Qualifiers
Source	1 357

Source

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/organism="Mesembryanthemum crystallinum"
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/db_xref="taxon:3544"
/catalytic_His30-243"

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/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev stage="Six week old"

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/clone_11b="Ice plant Lambda Uni-Zap XR expression  
library. 30 hours NaCl treatment"
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/home="vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site 2: XhoI"
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US-09-978-274A-8 (1-110) x AA856221 (1-267)

2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21

DB 104 GGTAGACATCGACAACTCAGAGAATGAGGCCAAATCTTGCTGATTGCCATACAGATG 163

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[illegible]

CONFIDENTIAL

Search completed: April 9, 2006, 06:20:23

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 120.071 Seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPVKTAEAFLLVAIQ.....DEINRDVALLKYVNGTCQTT 110

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=numan40.cdi
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	454	79.8	1195	2	US-08-373-858-1
2	454	79.8	1195	2	US-08-342-786B-1
3	454	79.8	1195	2	US-08-500-611-1
4	454	79.8	1195	2	US-08-500-694-1
5	454	79.8	1195	3	US-07-865-169-1
6	454	79.8	1195	3	US-07-865-169-2
7	454	79.8	1195	3	US-09-005-273-1
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9	454	79.8	1195	6	PCT-US96-11546-1

10	451	79.3	1379	3	US-08-501-253A-1	Sequence 1, Appl1
11	399	70.1	918	2	US-08-138-636-1	Sequence 1, Appl1
12	399	70.1	918	2	US-08-319-622A-1	Sequence 1, Appl1
13	399	70.1	918	2	US-08-471-564-1	Sequence 1, Appl1
14	213.5	37.5	813	2	US-07-901-707-11	Sequence 11, Appl1
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16	213.5	37.5	813	2	US-07-988-430-11	Sequence 11, Appl1
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18	213.5	37.5	813	2	US-08-425-336-11	Sequence 11, Appl1
19	213.5	37.5	813	2	US-08-488-113B-11	Sequence 11, Appl1
20	213.5	37.5	813	2	US-08-477-464B-11	Sequence 11, Appl1
21	213.5	37.5	813	2	US-08-646-360-11	Sequence 11, Appl1
22	213.5	37.5	813	2	US-08-621-803-246	Sequence 246, App
23	213.5	37.5	813	3	US-08-839-765-11	Sequence 11, Appl1
24	213.5	37.5	813	3	US-09-136-389-11	Sequence 11, Appl1
25	213.5	37.5	813	3	US-09-217-352-246	Sequence 246, App
26	213.5	37.5	813	3	US-09-610-838-11	Sequence 11, Appl1
27	213.5	37.5	813	3	US-09-711-485-11	Sequence 11, Appl1
28	213.5	37.5	813	6	PCT-US92-09487-11	Sequence 11, Appl1
29	213.5	37.5	813	6	PCT-US92-09487-57	Sequence 57, Appl1
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33	212.5	37.3	1003	2	US-08-621-803-252	Sequence 252, App
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36	212.5	37.3	1072	2	US-09-217-352-250	Sequence 250, App
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38	196.5	34.5	1855	3	US-09-551-151A-35	Sequence 35, Appl1
39	192	33.7	1855	2	US-08-356-786-7	Sequence 7, Appl1
40	192	33.7	1140	2	US-08-218-303-15	Sequence 15, Appl1
41	192	33.7	1140	2	US-08-338-793D-60	Sequence 60, Appl1
42	192	33.7	1605	2	US-08-356-786-9	Sequence 9, Appl1
43	192	33.7	1698	2	US-09-785-921A-1	Sequence 1, Appl1
44	192	33.7	1731	3	US-09-785-921A-2	Sequence 2, Appl1
45	192	33.7	1731	3	US-09-785-921A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoacta
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Dady & Dady
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

Alignment Scores:
Pred. No.: 4,26e-52 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 2

US-09-978-274A-8 (1-110) x US-08-373-858-1 (1-1195)

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QY 82 G1YTHIRLYSTRP11LEVALLEUARGVALASPG1UL1LEASARGAPVALA1ALEULELYS 101
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QY 102 TYRVALASNG1YTHRCYSGINTHTHR 110
DB 858 TACGTGTGGAGACTGTGACAGCAACT 884

RESULT 2
US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234el Expression Vector for Phytolacca
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana L.
IMMEDIATE SOURCE:
CLONE: PAP
US-08-342-786B-1

Alignment Scores:
Pred. No.: 4,26e-52 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 2

US-09-978-274A-8 (1-110) x US-08-342-786B-1 (1-1195)

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US-08-500-611-1

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RESULT 4
US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
; GENERAL INFORMATION:
; APPLICANT: Turner, Milgum E.
; TITLE OF INVENTION: DnaB Encoding Pokeweed Antiviral Protein
; TITLE OR INVENTION: Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ierner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,694
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; TELEX: 139-125
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
; FEATURES:
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
US-08-500-694-1

Alignment Scores:
Pred. No.: 5.17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 2 Gaps: 0

US-09-978-2744-8 (1-110) x US-08-500-694-1 (1-1379)
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QY 42 ALAPHELYTPROABPPOLYSVALLAENLEUGLULYSTRGLYSTRILESERGLU 61
DB 870 GCATTCACCTTAATCCCAAGACTTAATTTGCAAGACACATGGGGTAAGATTCAACA 929
QY 62 ALAIIHIAASNAALAYASANGYALALEUPROLYSPROLEUGLUDEUVALAEPALAYS 81
DB 930 GCATTCACCTTAATCCCAAGACTTAATTTGCAAGACACATGGGGTAAGATTCAACA 929
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QY 102 TYRVALASNGLYTHRCYSGINTHTHR 110
DB 1050 TACGTTGGTGAGACTGTGACACACT 1076

RESULT 5
US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940

GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-865-169-1

Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.24 Conservative: 5
Best Local Similarity: 82.64 Mismatches: 14
Query Match: 79.84 Indels: 0
DB: 3 Gaps: 0

US-09-978-274a-8 (1-110) x US-07-865-169-1 (1-1379)
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DB 810 GTRTCAGAGCGAGCAGATTCAGATGACATGAGAACTAGTGAATCTAATTTTACAGA 869
QY 42 ALAPHELYTPROABPPOLYSVALLAENLEUGLULYSTRGLYSTRILESERGLU 61
DB 870 GCATTCACCTTAATCCCAAGACTTAATTTGCAAGACACATGGGGTAAGATTCAACA 929
QY 62 ALAIIHIAASNAALAYASANGYALALEUPROLYSPROLEUGLUDEUVALAEPALAYS 81
DB 930 GCATTCACCTTAATCCCAAGACTTAATTTGCAAGACACATGGGGTAAGATTCAACA 929
QY 82 GLYTHRYSTRIPLEVALLEUARGVALAEPGLULIENARGAPVALAALAEULEULYS 101
DB 990 GGTCGCAAGTGATGATGTTGAGATGATGAATCAAGCTGATGATGACACTCTTAAC 1049
QY 102 TYRVALASNGLYTHRCYSGINTHTHR 110
DB 1050 TACGTTGGTGAGACTGTGACACACT 1076

RESULT 6
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940

GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-865-169-2

Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.24 Conservative: 5
Best Local Similarity: 82.64 Mismatches: 14

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3
Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 3
US-09-978-274A-8 (1-110) x US-09-005-273-3 (1-1379)
QY 2 G1YValAspSerPheProValIyThrGluAlaPheHeuLeuValAlaIleGlnMet 21
DB 750 GGAGTGAATGTCATTCAGTGAAGAAACCGAACCGAATTCCTATTCGATGCAATCAATG 809
QY 22 ValSerGluAlaAlaArgPheIyTyrIleGluAsnGlnValIyThrAsnPheAsnArg 41
DB 810 GATCAAGGCGAGCAATTCATCACTAGAGATCAAGTGAAGAACTAATTTTACAGCA 869
QY 42 AlaPheTyrProAspProIyValIleAsnLeuGluGluIyTyrGlyIyVilSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGATGGGGTMAATTTCAACA 929
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
DB 930 GCAATTCATGATGCGCAAGATGAGATTACCAACCTTCGAGCTAGTGAATGCCAGT 989
QY 82 GlyThrIySTrPileValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
DB 990 GGTGCCAAGTGAATGATGTTTGAAGTGAATGAATCAAGCCTGATGTCATTTAAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGAGTGTCAACAAC 1076
RESULT 9
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Tamer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Litlenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1
Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 6
US-09-978-274A-8 (1-110) x PCT-US96-11546-1 (1-1379)
QY 2 G1YValAspSerPheProValIyThrGluAlaPheHeuLeuValAlaIleGlnMet 21
DB 750 GGAGTGAATGTCATTCAGTGAAGAAACCGAACCGAATTCCTATTCGATGCAATCAATG 809
QY 22 ValSerGluAlaAlaArgPheIyTyrIleGluAsnGlnValIyThrAsnPheAsnArg 41
DB 810 GATCAAGGCGAGCAATTCATCACTAGAGATCAAGTGAAGAACTAATTTTACAGCA 869
QY 42 AlaPheTyrProAspProIyValIleAsnLeuGluGluIyTyrGlyIyVilSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGATGGGGTMAATTTCAACA 929
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
DB 930 GCAATTCATGATGCGCAAGATGAGATTACCAACCTTCGAGCTAGTGAATGCCAGT 989
QY 82 GlyThrIySTrPileValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101

Db 990 GGTGCAAGTGAATAGTGTGAGAGTGAATCAAGCTGATGACCTTAAC 1049
 Qy 102 TyrValaenglyThrCysGlnThrThr 110
 Db 1050 TACGTTGTGGAGCTGTCAAGCAACT 1076

RESULT 10

US-08-501-253A-1
 Sequence 1, Application US/08501253A
 Patent No. 6146628

GENERAL INFORMATION:
 APPLICANT: Uekun, Patih
 APPLICANT: Tumer, Nilgun
 TITLE OF INVENTION: Biotherapeutic Agents Comprising
 NUMBER OF INVENTION: Recombinant PAP and PAP Mutants
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Merchant & Gould
 STREET: 90 South 7th Street, 3100 No. 6146628west Center
 CITY: Minneapolis
 STATE: MN
 COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/501,253A
 FILING DATE: 11-JUL-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Kettleberger, Denise M.
 REGISTRATION NUMBER: 33,924
 REFERENCE/DOCKET NUMBER: 600,323US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-9081
 TELEFAX: 612-332-5300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 225..1163

US-08-501-253A-1

Alignment Scores:

Pred. No.: 1.32e-51 Length: 1379
 Score: 451.00 Matches: 89
 Percent Similarity: 87.2% Conservative: 6
 Best Local Similarity: 81.7% Mismatches: 14
 Query Match: 79.3% Indels: 0
 DB: 3 Gaps: 0

US-09-978-274A-8 (1-110) x US-08-501-253A-1 (1-1379)

Qy 2 G1ValaSerPheProVallyeThrGlnAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 750 GAGGTATGTCATTCACCTGAGAAAACCAAGCCGAATTCCTATTGTGATGCCATTCAGATG 809
 Qy 22 ValSerGlnAlaAlaArgPheLeuValIleGlnAlaGlnVallyeThrAspPheAsnArg 41
 Db 810 GATACAGAGCAGCAAGATTCAGATACATAGAGATCAGGTAAGAACTAATTTTAAACA 869
 Qy 42 AlaPheThrProAspProlyeValIleAsnLeuGlnGlnlyeThrGlyIleSerGln 61
 Db 870 GCATTCACCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGTAAAGATTTCACA 929

Qy 62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProlyeProLeuGlnLeuValAlaPalaIlys 81
 Db 930 GCATTCATGATGATGAGATGAGATGATTTACCCAAACCTCTCAGCTAGTGGATGCCAGT 989
 Qy 82 G1ThrlyeTrpIleValIleuArgValaAspGlnIleAsnArgAspValAlaIleuLeuIys 101
 Db 990 GGTGCAAGTGAATAGTGTGAGAGTGAATCAAGCTGATGACCTTAAC 1049
 Qy 102 TyrValaenglyThrCysGlnThrThr 110
 Db 1050 TACGTTGTGGAGCTGTCAAGCAACT 1076

RESULT 11

US-08-138-636-1
 Sequence 1, Application US/08138636
 Patent No. 5348865

GENERAL INFORMATION:
 APPLICANT: Moon, Young-Ho
 APPLICANT: Jeon, Hong-Seoh
 APPLICANT: Choi, Kyu-Wan
 APPLICANT: Lee, Kwan-Ho
 APPLICANT: Kim, Man-Keun
 TITLE OF INVENTION: No. 5348865e1 Genome Coding PhytoIacca Antiviral
 NUMBER OF INVENTION: Protein and a Recombinant Expression Vector Therefor
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSER: DARBY & DARBY
 STREET: 805 THIRD AVE.
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,636
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, S. Peter
 REGISTRATION NUMBER: 25,351
 REFERENCE/DOCKET NUMBER: 0136/08818
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 527-7700
 TELEFAX: (212) 753-6237
 TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 918 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: PhytoIacca insularis
 IMMEDIATE SOURCE:
 CLONE: antiviral protein (PIP)

US-08-138-636-1

Alignment Scores:

Pred. No.: 9.13e-45 Length: 918
 Score: 399.00 Matches: 79
 Percent Similarity: 80.7% Conservative: 9
 Best Local Similarity: 72.5% Mismatches: 21
 Query Match: 70.1% Indels: 0
 DB: 2 Gaps: 0

US-09-978-274A-8 (1-110) x US-08-138-636-1 (1-918)

QY 2 GYVAlAspSerheProVallystrGluAlaPhepheuValAlaIleGlnmet 21
DB 517 GGAGTACGCTACTGAGAGAACGGAAGCTGAATCTCTACTGAGCATACCAATG 576

QY 22 ValSerGluAlaAlaArgPheLystrYrIleGluAsnGlnVallystrAenPheAsnArg 41
DB 577 GTATCAGAGCAGCAGATTCAGATCATAGAGATCAATGAAATATTTTAAACA 636

QY 42 AlaphetYrProAspProlyValIleAsnLeuGluGlystrGlylyIleSerGlu 61
DB 637 CCATTCACCCCTATCCCAAGTACTATATTCAGAGACATGGGGTAAAGATTCTTCA 696

QY 62 AlAlIleHisAsnAlaLyAsnGlyAlaLeuProlyAspProleuGluLeuValAspAlaLy 81
DB 697 GCAATTCATGCTCCAGAAATGAGGTTTACCATCTCTACAGCTAGTCATGCCAAT 756

QY 82 GYThrLystrIleValleuArgValAspGluIleAsnArgAspValAlaLeuLeuLy 101
DB 757 GGTCGAATTCGATAGTGTGAGAGTCGATGAATCAAGCTGATGTGTCACTTTAAC 816

QY 102 TyrValAsnGlyThrCysGlnThr 110
DB 817 TACGTATTGGAGCTGCCAGAGAACT 843

RESULT 12
US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/0A445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SRO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: PhytoIacca Insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Alignment Scores:
Pred. No.: 9.13e-45 Length: 918
Score: 399.00 Matches: 79
Percent Similarity: 80.7% Conservative: 21
Best Local Similarity: 72.5% Mismatches: 0
Query Match: 70.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-08-319-622A-1 (1-918)

QY 2 GYVAlAspSerheProVallystrGluAlaPhepheuValAlaIleGlnmet 21
DB 517 GGAGTACGCTACTGAGAGAACGGAAGCTGAATCTCTACTGAGCATACCAATG 576

QY 22 ValSerGluAlaAlaArgPheLystrYrIleGluAsnGlnVallystrAenPheAsnArg 41
DB 577 GTATCAGAGCAGCAGATTCAGATCATAGAGATCAATGAAATATTTTAAACA 636

QY 42 AlaphetYrProAspProlyValIleAsnLeuGluGlystrGlylyIleSerGlu 61
DB 637 CCATTCACCCCTATCCCAAGTACTATATTCAGAGACATGGGGTAAAGATTCTTCA 696

QY 62 AlAlIleHisAsnAlaLyAsnGlyAlaLeuProlyAspProleuGluLeuValAspAlaLy 81
DB 697 GCAATTCATGCTCCAGAAATGAGGTTTACCATCTCTACAGCTAGTCATGCCAAT 756

QY 82 GYThrLystrIleValleuArgValAspGluIleAsnArgAspValAlaLeuLeuLy 101
DB 757 GGTCGAATTCGATAGTGTGAGAGTCGATGAATCAAGCTGATGTGTCACTTTAAC 816

QY 102 TyrValAsnGlyThrCysGlnThr 110
DB 817 TACGTATTGGAGCTGCCAGAGAACT 843

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326e1 Genome Coding PhytoIacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636

FILED DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phycolacca inularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Alignment Scores:
Pred. No.: 9,136-45 Length: 918
Score: 399.00 Matches: 79
Percent Similarity: 80.7% Conservative: 9
Best Local Similarity: 72.5% Mismatches: 21
Query Match: 70.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-08-471-564-1 (1-918)

QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 517 GGAATGACGTATTCATCTGAGAGAACCGAAGCTGAATTCCTACGTGTGATCAATATG 576
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 577 GTATCAGAGCGACGAGATTCAAGTACATAGAGTCAAGAGAACTAATTTTAAACGA 636
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIleSerGlu 61
DB 637 CCATTCAACCTATCCCAAGTACTTATTTGACGAGACATGGCGTAAGATTCTTCA 696
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 697 GCAATTCATGTGTCGACGAGATGAGTTTACCAATCCTCTACAGCTAGTCATGCCAAT 756
QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 757 GGTCAAAATTTGATGATGTTTAAAGATGATGAATCAAGCTGAATGTCTCTTAAAC 816
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 817 TACGTATTGGAGAGCTGCCAGAACT 843

RESULT 14
US-07-901-707-11
Sequence 11, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-901-707-11

Alignment Scores:
Pred. No.: 1,386-19 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
Gaps: 1

US-09-978-274A-8 (1-110) x US-07-901-707-11 (1-813)

QY 3 ValAspSerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
DB 433 ATAGACAAATATTAACCAACGAGATAGTACTCTATTTGTTTATTCAATAGGTG 492
QY 23 SerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAla 42
DB 493 TCTGAAACAGCTCATTCACCTTATTTGAGAACCAATTAAGAAATTAATCTTCAACAGAGA 552
QY 43 PheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAla 62
DB 553 ATTGCGCCCGGATATATACATACGCTTGAGAAATTAAGGGTAAATCTCTTCCAG 612
QY 63 IleHis--AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 613 ATCCGACATCAGGTGCAATGGAATGTTTTCGAGGACAGTGAATGAAACGTGCAAT 672
QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 673 GGCMAAAATATCTATGTGACCGGATGATCAAGTAAACCAAAATAGACCTCTTAAG 732
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 733 TGTGTCATTAAGATCCTTAAGACG 759

RESULT 15
US-07-901-707-57
Sequence 57, Application US/07901707

```
/ Patent No. 5376546
/ GENERAL INFORMATION:
/ APPLICANT: Bernhard, Susan L.
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Steve P.
/ APPLICANT: Lane, Julie A.
/ TITLE OF INVENTION: Materials Comprising and Methods of
/ TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ STREET: Street
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/901,707
/ FILING DATE: 19920619
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5376546and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27129/30910
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-5750
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 813 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-07-901-707-57

Alignment Scores:
Pred. No.: 1.38e-19 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 2 Gaps: 1

US-09-978-274a-8 (1-110) x US-07-901-707-57 (1-813)

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Db 433 ATAGACAAATTATTAACCAACGAGTAGCTTCTATTGGTTGTTATTCAATGCTG 492
Qy 23 SerGIuAlaAlaArgPheIyTyrlEgluAnGIuValIyThrAsnPheAsnArgAla 42
Db 493 TCTGAAACAGCTCGATTCACTTATTGAGAACCAATTAATAAATTACTTTCACAGAGA 552
Qy 43 PheTyrrProAspProIyValIleAsnLeuGIuIyTyrgIlyleIleSerGIuAla 62
Db 553 ATTGCGCCGGGGAATATACATCAGCTTGAGATTAATGGGGTAAACTCTCGTTCAG 612
Qy 63 ILeHts---AsnAlaIyAsnGIyAlaLeuProIySProLeuGIuLeuValAspAlaIyS 81
Db 613 ATCCGACATCAAGGTGCAATGGAATGTTTTCGAGGCAATTGAAATGGAACGTGCAAT 672
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Qy 82 GlyThrIyTyrrPileValLeuArgValAspGIuIleAsnArgAspValAlaLeuLeuIyS 101
Db 673 GGCATAAAATACATATGTCACCGCATGTCATCAAGTAACCAAAATAGCATCTTGAAAG 732
Qy 102 TyrValAsnGIyThrcYsgIntHrThr 110
Db 733 TTCGTGATTAAGATCTCTAAACGAGC 759
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Search completed: April 8, 2006, 14:01:58
Job time : 123.071 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 393.829 Seconds
(without alignments)
2309.713 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569
Sequence: 1 MGVDSPFKTEAFPLVAIQ.....DEINRDVALLKYNGTCQT 110

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-O=/abs/ABSSMB.spool/US09978274/rnat.07042006.173040.28552/app.query.fasta.1
-DB=Published_Applications_NA_Main -QPM=faetap -SUFFI=p2n.rnpbm
-MIMATCH=0.1 -LOOPEL=0 -UNITS=bits -START=1 -END=-1
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MILEN=0 -MAXLEN=200000000 -HOST=abs03h
-USRR=US09978274 @CGN 1.1 2039 @rnat.07042006.173040.28552 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	569	100.0	333	US-09-978-274A-7 Sequence 7, Appl1
2	564	99.1	792	US-09-978-274A-3 Sequence 3, Appl1
3	564	99.1	945	US-09-978-274A-1 Sequence 1, Appl1
4	519	91.2	1092	US-09-978-274A-19 Sequence 19, Appl1
5	454	79.8	1366	US-09-978-274A-31 Sequence 31, Appl1
6	454	79.8	1376	US-10-467-009-1 Sequence 1, Appl1
7	454	79.8	1379	US-09-978-274A-30 Sequence 30, Appl1

8	454	79.8	1379	US-11-106-187-1 Sequence 1, Appl1
9	213.5	37.5	813	US-09-765-527-246 Sequence 246, App
10	213.5	37.5	813	US-10-127-860-11 Sequence 11, Appl1
11	213.5	37.5	1176	US-10-717-243-11 Sequence 11, Appl1
12	213.5	37.5	1176	US-10-074-596-2 Sequence 2, Appl1
13	213.5	37.5	2407	US-11-084-080-25 Sequence 25, App
14	212.5	37.3	955	US-09-765-527-258 Sequence 258, App
15	212.5	37.3	1003	US-09-765-527-252 Sequence 252, App
16	212.5	37.3	1072	US-09-765-527-250 Sequence 250, App
17	212.5	37.3	1500	US-10-964-195-12 Sequence 12, Appl1
18	212.5	37.3	1527	US-10-074-596-10 Sequence 10, Appl1
19	209.5	36.8	1542	US-10-926-711A-11 Sequence 11, Appl1
20	200	35.1	855	US-11-106-187-20 Sequence 20, Appl1
21	200	35.1	934	US-09-978-274A-32 Sequence 32, Appl1
22	200	35.1	934	US-11-106-187-3 Sequence 3, Appl1
23	200	35.1	1517	US-10-964-195-10 Sequence 10, Appl1
24	196.5	34.5	1855	US-10-394-511-35 Sequence 35, Appl1
25	192	33.7	1698	US-09-785-921A-1 Sequence 1, Appl1
26	192	33.7	1698	US-10-618-560-1 Sequence 1, Appl1
27	192	33.7	1731	US-09-785-921A-2 Sequence 2, Appl1
28	192	33.7	1731	US-09-785-921A-3 Sequence 3, Appl1
29	192	33.7	1731	US-10-618-560-2 Sequence 2, Appl1
30	192	33.7	1731	US-10-618-560-3 Sequence 3, Appl1
31	192	33.7	1805	US-09-785-921A-10 Sequence 10, Appl1
32	192	33.7	1805	US-10-618-560-10 Sequence 10, Appl1
33	192	33.7	1855	US-10-394-511-3 Sequence 3, Appl1
34	192	33.7	1855	US-10-394-511-5 Sequence 5, Appl1
35	192	33.7	1855	US-10-394-511-7 Sequence 7, Appl1
36	192	33.7	1855	US-10-394-511-9 Sequence 9, Appl1
37	192	33.7	1855	US-10-394-511-13 Sequence 13, Appl1
38	192	33.7	1855	US-10-394-511-15 Sequence 15, Appl1
39	192	33.7	1855	US-10-394-511-17 Sequence 17, Appl1
40	192	33.7	1855	US-10-394-511-19 Sequence 19, Appl1
41	192	33.7	1855	US-10-394-511-21 Sequence 21, Appl1
42	192	33.7	1855	US-10-394-511-23 Sequence 23, Appl1
43	192	33.7	1855	US-10-394-511-25 Sequence 25, Appl1
44	192	33.7	1855	US-10-394-511-27 Sequence 27, Appl1
45	192	33.7	1855	US-10-394-511-29 Sequence 29, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-7
Sequence 7, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Ackinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-7

Alignment Scores:

Pred. No.: 2.31e-73
Score: 569.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 333
Matches: 110
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-7 (1-333)

QY 1 MetGlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGln 20
DB 1 ATGGGGATTGATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTGGAGCCATCCAA 60

QY 21 MetValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsn 40
DB 61 ATGGTTTCAGAGGCGAGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATATTTAAAT 120

QY 41 ArgAlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIYVleSeriSer 60
DB 121 AGAGCATTCCTACCCCTGATCCCAAGTAATTAATTTGGAGGAGAGAGTGGGCAAAATCTCT 180

QY 61 GluAlaIleIleHisAsnAlaIleAsnGluValAlaLeuProIleYrPheGluLeuValAspAla 80
DB 181 GAGGCAATTCACATGCAAGAAATGGGGCTTTACCCCAACCACTGAGCTAGTGATGCC 240

QY 81 LysGlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
DB 241 AAAGGTRCCAGTGAGTGTCTTAAAGTGATGAATCAATCTGATGTGGCACTCTCTT 300

QY 101 LysYrValAsnGlyThrCysGlnThrThr 110
DB 301 AAGTACGTATATGGAACCTGTGACAGCAACT 330

RESULT 2
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Ackinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phycolacca americana
; US-09-978-274A-3

Alignment Scores:
Pred. No.: 4.47e-72 Length: 792
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-3 (1-792)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 463 GAGGTTATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTAGATCCCAATG 522

QY 22 ValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsnArg 41
DB 523 GTTTCAGAGGCGAGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATATTTAAATGA 582

QY 42 AlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIYVleSeriSerGlu 61
DB 583 GCATTCCTACCTGATCCCAAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAG 642

QY 62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleYrPheGluLeuValAspAlaIle 81
DB 62 ATATTTTCTGATTCCTCGTAAAAAAGAGGCTTTTCTTACGTAGATCCCAATG 680

DB 643 GCATTCACAAATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTAGTGCACAA 702

QY 82 GlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuYs 101
DB 703 GGTACCAAGGAGTGTCTTAAAGTGATGAATCAATCTGATGTGGCACTCTTAAG 762

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 763 TACGTTATATGGAACCTGTGACAGCAACT 789

RESULT 3
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Ackinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Phycolacca americana
; US-09-978-274A-1

Alignment Scores:
Pred. No.: 5.79e-72 Length: 945
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-1 (1-945)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 532 GAGGTTATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTAGATCCCAATG 591

QY 22 ValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsnArg 41
DB 592 GTTTCAGAGGCGAGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATATTTAAATGA 651

QY 42 AlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIYVleSeriSerGlu 61
DB 652 GCATTCCTACCTGATCCCAAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAG 711

QY 62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleYrPheGluLeuValAspAlaIle 81
DB 712 GCATTCACATGCGCAAGATGGGCTTTACCCAAACCACTTGAAGTGTAGTGCACAA 771

QY 82 GlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuYs 101
DB 772 GGTACCAAGGAGTGTCTTAAAGTGATGAATCAATCTGATGTGGCACTCTTAAG 831

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 832 TACGTTATATGGAACCTGTGACAGCAACT 858

RESULT 4
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher

```

; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:
Pred. No.: 2,866-65 Length: 1092
Score: 519.00 Matches: 101
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 91.2% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-19 (1-1092)

QY 2 GlyValAspSerPheProValIlyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 463 GGAAGTGGATTCATTCCTCGTAAACCTGAGGCTTTTCTACTGTCATCCAAATG 522

QY 22 ValSerGluAlaAlaArgPheIleTyrlleGluAsnGluValIlyThrAsnPhenArg 41
Db 523 GTTTCAGAGGCGAGCGCATTCAGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 582

QY 42 AlaPheTyrrProAspProIlyValIleAsnLeuGluGluIlyTyrrGlyIlyseGlu 61
Db 583 GCATTTACCTGATCCCAAGATTAATTAATTCGAGAGGAGGAGGAGGAGGAGGAGGAG 642

QY 62 AlaIleHisAsnAlaIlyAsnGlyAlaLeuProIlyPheLeuGluLeuValAspAlaIys 81
Db 643 GCAATTCACAAATGCGCAAGATGAGGCTTTACCAACCAATGAGCTAGTGAGTCCAAA 702

QY 82 GlyThrIlySTPrlleValleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
Db 703 GGTACCAAGTGTAGTCTTAGAGTGTAGTAATCAATCGTAGTGGCACTCCTTAAG 762

QY 102 Tyr 102
Db 763 TAC 765

RESULT 5
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
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; ORGANISM: Phytolacca americana
US-09-978-274A-31

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Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-31 (1-1368)

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Db 750 GGAAGTGGATTCATTCCTCGTAAACCTGAGGCTTTTCTACTGTCATCCAAATG 809

QY 22 ValSerGluAlaAlaArgPheIleTyrlleGluAsnGluValIlyThrAsnPhenArg 41
Db 810 GTATCAGAGCGAGCAAGATTCAGTACTAGAGATCAAGTGAAGCAATTAATTTTAACGA 869

QY 42 AlaPheTyrrProAspProIlyValIleAsnLeuGluGluIlyTyrrGlyIlyseGlu 61
Db 870 GCATTTACCTGATCCCAAGATTAATTAATTCGAGAGGAGATGGGTAAAGATTCAACA 929

QY 62 AlaIleHisAsnAlaIlyAsnGlyAlaLeuProIlyPheLeuGluLeuValAspAlaIys 81
Db 930 GCAATTCACAAATGCGCAAGATGAGGCTTTACCAACCTCGAGCTAGTGAGTGGCCAGT 989

QY 82 GlyThrIlySTPrlleValleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
Db 990 GGTCCAAAGTGTAGTCTTAGAGTGTAGTAATCAAGCTGATGTAGCACTTAAAC 1049

QY 102 TyrValAsnGlyThrCysGlnThr 110
Db 1050 TACGTGTGTGGAGCTGTCAAGCAACT 1076

RESULT 6
US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467,009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

Alignment Scores:
Pred. No.: 1,386-55 Length: 1376
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 8 Gaps: 0

US-09-978-274A-8 (1-110) x US-10-467-009-1 (1-1376)

QY 2 GlyValAspSerPheProValIlyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 747 GGAAGTGGATTCATTCCTCGTAAACCTGAGGCTTTTCTACTGTCATCCAAATG 806
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QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 807 GTATCAGAGGCGACCAAGATTCAAGTACATGAGAAATCAGGTGAAATCTAATTTTAAACAGA 866
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrPglLysIleSerGlu 61
DB 867 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAAGATTTCACA 926
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 927 GCATTCAATGATCCCAAGATGAGGTTTACCCAAACCTCTCGAGTAGTGATGCCAGT 986
QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 987 GGTGCCAAGTGATGTTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAC 1046
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1047 TACGTTGGTGGAGCTGTCAAGCAACT 1073

RESULT 7
US-09-978-274A-30
; Sequence 30, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:
Pred. No.: 1,39e-55 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-30 (1-1379)
QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GAGAGTATGTCATCTACTGAGAAACCGAAGCCGAATTCCTTGTGTAGCCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GTATCAGAGGCGACCAAGATTCAAGTACATGAGAAATCAGGTGAAATCTAATTTTAAACAGA 869
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrPglLysIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 930 GCATTCAATGATCCCAAGATGAGGTTTACCCAAACCTCTCGAGTAGTGATGCCAGT 989
QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GGTGCCAAGTGATGTTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAC 1049
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QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGCTGTCAAGCAACT 1076

RESULT 8
US-11-106-187-1
; Sequence 1, Application US/1106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUNER, NITGON E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Alignment Scores:
Pred. No.: 1,39e-55 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 10 Gaps: 0

US-09-978-274A-8 (1-110) x US-11-106-187-1 (1-1379)
QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GAGAGTATGTCATCTACTGAGAAACCGAAGCCGAATTCCTATGTGTAGCCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GTATCAGAGGCGACCAAGATTCAAGTACATGAGAAATCAGGTGAAATCTAATTTTAAACAGA 869
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrPglLysIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 930 GCATTCAATGATCCCAAGATGAGGTTTACCCAAACCTCTCGAGTAGTGATGCCAGT 989
QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GGTGCCAAGTGATGTTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGCTGTCAAGCAACT 1076

RESULT 9
US-09-765-527-246
; Sequence 246, Application US/09765527
; Patent No. US2002006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
```

TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "gelonin"
SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246
Alignment Scores:
Pred. No.: 1,24e-20 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 3 Gaps: 1
US-09-978-274A-8 (1-110) x US-09-765-527-246 (1-813)
QY 3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
Db 433 ATGACCAATTAATAACCAACGAGATAGCTTCTATTGGTTGTTATTCAATGCGTG 492
QY 23 SerGluAlaIaIaArgPheIysTyrIleGluAsnGlnValIysThrAsnPheAsnArgAla 42
Db 493 TCTGAAGCACTGCATTCACCTTATTGAGAACCAATTAAATAACTTTCAACAGAGA 552
QY 43 PheTyrProAspProIysValIleAsnLeuGlnIuIysTyrGlyIysIleSerGluAla 62
Db 553 ATTCGCCCGCGAATAATATACATCAGCTTGAGAAATTAATCGGCTAAACTCTGTTCCAG 612
QY 63 ILeHis---AsnAlaIysAsnGlyAlaLeuProIysPheLeuGlnLeuValAspAlaIys 81
Db 613 ATCCGACATCAGGTGCAATGGAATGTTTCGAGAGGCAAGTTGAATTGGAACGTGCAAT 672
QY 82 G1YThrIysTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
Db 673 GCGCAAAATAATACATATGTCACCGCAGTTGATCAAGTAATAAACCAATAATGCACTTTGAG 732
QY 102 TyrValAsnGlyThrCysGlnThrThr 110

Db 733 TTCCTCGATAAAGATCCCTAAACGAGC 759
RESULT 10
US-10-127-890-11
Sequence 11, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-127-890-11
Alignment Scores:
Pred. No.: 1,24e-20 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 6 Gaps: 1
US-09-978-274A-8 (1-110) x US-10-127-890-11 (1-813)
QY 3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
Db 433 ATGACCAATTAATAACCAACGAGATAGCTTCTATTGGTTGTTATTCAATGCGTG 492

Db 433 ATAGACATTAATAACCAACGAGATGCTAGTCTCTATTGTTGTTATTCAATGGTG 492
 Qy 23 SerGIuAlAlaIaArgPheIySTyrlIeGIuAenGIuValIySThrAenPheAenAArgAla 42
 Db 493 TCTGAAGCAGCTCGATTCACTTATATGAGAACCAATATGAATACCTTCAACGAGA 552
 Qy 43 PheTy-PrOAsPProLySValIleAenIeUGluIuIySTpGIySTySleSergIuAla 62
 Db 553 ATTCGCCCGCGGATTAATACATACAGCTTGAAGATTAATGGGGTAACTCTGTTCCAG 612
 Qy 63 ILeHs---AenAlaIySAenGIyAlaIeUProLySProLeUGluIeUValAAspAlaIyS 81
 Db 613 ATCCGACATCAGGTGGAATGGAATGTTTCGAGGCGAGCTTGAATTTGAACGCAAT 672
 Qy 82 GIyThrIySTpIleValIleAArgValAAspGIuIleAenAArgAspValAlaIeUleUyS 101
 Db 673 GGCAGAAAATACTATGTGTACCGGACGTGATCAAGTAAGTAACCAAAATAGACCTTGAAG 732
 Qy 102 TyrValAenGIyThrCySGInThr 110
 Db 733 TTGCTGATTAAGATCTCTAAACGAGC 759
 RESULT 11
 US-10-717-243-11
 ; Sequence 11, Application US/10717243
 ; Publication No. US2005054835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Caroli, Stephen F.
 ; Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; Proteins
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/717,243
 ; FILING DATE: 18-Nov-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-9155
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 813 base pairs

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 ; US-10-717-243-11
 Alignment Scores:
 Pred. No.: 1,248-20 Length: 813
 Score: 213.50 Matches: 47
 Percent Similarity: 61.5% Conservative: 20
 Best Local Similarity: 43.1% Mismatches: 41
 Query Match: 37.5% Indels: 1
 Gaps: 1
 DB: 9
 US-09-978-274A-8 (1-110) x US-10-717-243-11 (1-813)
 Qy 3 ValAspSerPheProValIySThrGIuAlaPhePheIeUleUValAlaIleGIuMetVal 22
 Db 433 ATAGACATTAATAACCAACGAGATGCTAGTCTCTATTGTTGTTATTCAATGGTG 492
 Qy 23 SerGIuAlAlaIaArgPheIySTyrlIeGIuAenGIuValIySThrAenPheAenAArgAla 42
 Db 493 TCTGAAGCAGCTCGATTCACTTATATGAGAACCAATATGAATACCTTCAACGAGA 552
 Qy 43 PheTy-PrOAsPProLySValIleAenIeUGluIuIySTpGIySTySleSergIuAla 62
 Db 553 ATTCGCCCGCGGATTAATACATACAGCTTGAAGATTAATGGGGTAACTCTGTTCCAG 612
 Qy 63 ILeHs---AenAlaIySAenGIyAlaIeUProLySProLeUGluIeUValAAspAlaIyS 81
 Db 613 ATCCGACATCAGGTGGAATGGAATGTTTCGAGGCGAGCTTGAATTTGAACGCAAT 672
 Qy 82 GIyThrIySTpIleValIleAArgValAAspGIuIleAenAArgAspValAlaIeUleUyS 101
 Db 673 GGCAGAAAATACTATGTGTACCGGACGTGATCAAGTAAGTAACCAAAATAGACCTTGAAG 732
 Qy 102 TyrValAenGIyThrCySGInThr 110
 Db 733 TTGCTGATTAAGATCTCTAAACGAGC 759
 RESULT 12
 US-10-074-596-2
 ; Sequence 2, Application US/10074596
 ; Publication No. US2003017633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENBLUM, MICHAEL G.
 ; APPLICANT: CHEUNG, LAWRENCE
 ; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
 ; TITLE OF INVENTION: MAKING THEROF
 ; FILE REFERENCE: CLFR-007US
 ; CURRENT APPLICATION NUMBER: US/10/074,596
 ; CURRENT FILING DATE: 2002-02-12
 ; PRIOR APPLICATION NUMBER: 60/268,402
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1176
 ; TYPE: DNA
 ; ORGANISM: Gelonium multiferum
 ; US-10-074-596-2
 Alignment Scores:
 Pred. No.: 2,138-20 Length: 1176
 Score: 213.50 Matches: 47
 Percent Similarity: 61.5% Conservative: 20
 Best Local Similarity: 43.1% Mismatches: 41
 Query Match: 37.5% Indels: 1
 Gaps: 1
 DB: 6
 US-09-978-274A-8 (1-110) x US-10-074-596-2 (1-1176)

QY 3 ValAspSerPheProValIlyThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
DB 594 ATAGACATTTAAACCAACGAGATAGTCTTATGTTGTTATTCATTAATGGTG 653
QY 23 SerGluAlaIleArgPheIlyThrIleGluGlnValIlyThrAsnPheAsnArgAla 42
DB 654 TCTGAAGACGCTCGATTCACCTTATTTAGAACCAAAATAGAAATACCTTTCACAGAGA 713
QY 43 PheTyrrProAspProIlyValIleAsnLeuGluGluIlySTPGLYIlyIleSerGluAla 62
DB 714 ATTCGCCCGGAGATTAATACATGACCTTGAGATTAATGGGTAACTCTCGTCCAG 773
QY 63 ILeHis--AsnAlaIlyAsnGlyAlaLeuProIlyProLeuGluLeuValAspAlaIly 81
DB 774 ATCCGACATCAGGTGCAATGATGTTTTCGAGGACGATTAATGGAACGTGCAAT 833
QY 82 GlyThrIlySTPILeValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIly 101
DB 834 GGCAGAAAATCTATGTCACCGCATGATCAAGTAAACCAAAATAGACACTTGAAG 893
QY 102 TyrrValAsnGlyThrCySGlnThrThr 110
DB 894 TTCGTGCATTAAGATCCTAAACGAGC 920

RESULT 13
US-11-084-080-25
Sequence 25, Application US/11084080
Publication No. US20050238642A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSCH, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25
LENGTH: 2407
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VB6-845-gelionin
US-11-084-080-25

Alignment Scores:
Pred. No.: 6,08e-20 Length: 2407
Score: 213.50 Matches: 46
Percent Similarity: 62.1% Conservatives: 18
Best Local Similarity: 44.7% Mismatches: 38
Query Match: 37.5% Indels: 1
DB: 10 Gaps: 1

US-09-978-274a-8 (1-110) x US-11-084-080-25 (1-2407)

QY 3 ValAspSerPheProValIlyThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
DB 1257 ATAGACATTTAAACCAACGAGATAGTCTTATGTTGTTATTCATTAATGGTG 1316
QY 23 SerGluAlaIleArgPheIlyThrIleGluGlnValIlyThrAsnPheAsnArgAla 42
DB 1317 TCTGAAGACGCTCGATTCACCTTATTTAGAACCAAAATAGAAATACCTTTCACAGAGA 1376

QY 43 PheTyrrProAspProIlyValIleAsnLeuGluGluIlySTPGLYIlyIleSerGluAla 62
DB 1377 ATCCGCCCGGAGATTAATACATGACCTTGAGATTAATGGGTAACTCTCGTCCAG 1436
QY 63 ILeHis--AsnAlaIlyAsnGlyAlaLeuProIlyProLeuGluLeuValAspAlaIly 81
DB 1437 ATCCGACATCAGGTGCAATGATGTTTTCGAGGACGATTAATGGAACGTGCAAT 1496
QY 82 GlyThrIlySTPILeValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIly 101
DB 1497 GGCAGAAAATCTATGTCACCGCATGATCAAGTAAACCAAAATAGACACTTGAAG 1556
QY 102 TyrrValAsn 104
DB 1557 TTCGTGCAT 1565

RESULT 14
US-09-978-258
Sequence 258, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 66..944
NAME/KEY: misc_feature
LOCATION: residues 1-65
OTHER INFORMATION: /label= BcORI
/note="residues 1-65 comprise EcorI site to beginning of pel B."
NAME/KEY: misc_feature
LOCATION: AA 1-32
OTHER INFORMATION: /label= pel B
/note="pel B is the leader sequence from the pectate lyase

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; gene of Erwinia carotovora."
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 23-273
; OTHER INFORMATION: /label= "gelonin"
; /note="gelonin (see U.S. Patent No. 5,416,202)."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 274-275
; OTHER INFORMATION: /label= BagI
; /note="BagI cloning site."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 276-279
; OTHER INFORMATION: /label= cleavage linker
; /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
; site."
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 280-293
; OTHER INFORMATION: /label= peptide sequence
; /note="BPI-derived peptide."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 945-954
; OTHER INFORMATION: /label= XhoI
; /note="residues 945-955 comprise stop codon and XhoI site."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 258
;
; US-09-765-527-258
;
; Alignment Scores:
; Pred. No.: 2.2e-20 Length: 955
; Score: 212.50 Matches: 46
; Percent Similarity: 62.1% Conservatives: 18
; Best Local Similarity: 44.7% Mismatches: 38
; Query Match: 37.3% Indels: 1
; Gaps: 1
;
; US-09-978-274A-8 (1-110) x US-09-765-527-258 (1-955)
;
; QY 3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
; : : : : :
; Db 564 ATAGACATTAATAACCAAGGAGATAGCTTCTCTATTGTTGTTATTCAATGGTG 623
;
; QY 23 SerGluAlaAlaArgPheLysTyrIleGluGlnGlnValLysThrAsnPheAsnArgAla 42
; : : : : :
; Db 624 TCTGAACAGCTGATTCACCTTATTGAGAACCAAAATTGAATACTTTCACACAGGA 683
;
; QY 43 PheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGluAla 62
; : : : : :
; Db 684 ATTCGCCCGCGCAATTAATACATCACTTGAGAAATATGGGTAAACTCTGTTCCAG 743
;
; QY 63 IleHis--AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
; : : : : :
; Db 744 ATCCGACATCAGGTGCAATGGAATGTTTCGAGGCACTGATTGGAACGTGCAAT 803
;
; QY 82 GlyThrLysTyrIleValLeuArgValAspGluIleAsnArgPheValAlaLeuLeuLys 101
; : : : : :
; Db 804 GGCAGAAAAATCACTATGTCACCGCAGTGTGATCAAGTAAACCAAAATGCACTTTGAG 863
;
; QY 102 TyrValAsn 104
; : : : : :
; Db 864 TTCGTTCAT 872
;
; RESULT 15
; US-09-765-527-252
; Sequence 252: Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..992
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label= EcoRI
; /note="residues 1-65 comprise EcoRI site to beginning of pel
; B."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 1-22
; OTHER INFORMATION: /label= pel B
; /note="pel B is the leader sequence from the pectate lyase
; gene of Erwinia carotovora."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 23-273
; OTHER INFORMATION: /label= "gelonin"
; /note="gelonin (see U.S. Patent No. 5,416,202)."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 274-275
; OTHER INFORMATION: /label= BagI
; /note="BagI cloning site."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 276-279
; OTHER INFORMATION: /label= cleavage linker
; /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
; site."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 280-309
; OTHER INFORMATION: /label= peptide sequence
; /note="BPI-derived peptide."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 993-1011
; OTHER INFORMATION: /label= XhoI
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/note="residues 993-1003 comprise stop codon and XhoI site."
SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-765-527-252

Alignment Scores:

Pred. No.:	2,366-20	Length:	1003
Score:	212.50	Matches:	46
Percent Similarity:	62.1%	Conservative:	18
Best Local Similarity:	44.7%	Mismatches:	38
Query Match:	37.3%	Indels:	1
DB:	3	Gaps:	1

US-09-978-274a-8 (1-110) x US-09-765-527-252 (1-1003)

```
QY      3 ValaspSerPheProValIysThrGIuAlaPhePheLeuValAlaIleGIuMetVal 22
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      564 ATAGCAATTATTAACCAACGAGATAGCTAGTCTCTATTGGTTGTTATTCAAATGCTG 623
QY      23 SerGIuAlaAlaArgPheIysTyrIleGIuEngIuValIysThrAsnPhesnArgAla 42
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      624 TCTGAGCAGCTCGATTCTCCTTATGTGAGAACCAATTAGAAATTAACCTTCAACAGAGA 683
QY      43 PheTyrProaspProIysValIleasnEngIuGIuIysTyrGIuIysIleSerGIuAla 62
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      684 ATTGCCCCGGCGAAATPAATACATCAGCCTTGAGATAATAGGGTAAACTCTCGTTCAG 743
QY      63 IleHis--AsnAlaIysAsnGIuAlaLeuProIysProLeuGIuLeuValAspAlaIys 81
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      744 ATCCGACATCAGGTGCAATGCAATGTTTCGAGGCACTTGAAATGGAACGTGCATAT 803
QY      82 GLyThrIysTyrPileValLeuArgValAspGIuIleAsnArgaspValAlaIleuLeuIys 101
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      804 GGCATAAAATACTATGTCACCGCAGTTGATCAAGTAAACCAAAATATGCACTTGAAAG 863
QY      102 TyrValasn 104
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      864 TTCGTGCAAT 872
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Search completed: April 9, 2006, 03:12:39
Job time : 396.829 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 288.537 Seconds
(without alignments)
1525.144 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569
Sequence: 1 MGVDSPVYKTRAPFLVAIQ.....DEINRDVALLKYNGTCQT 110

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=Published Applications NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=numa40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abes03p
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA_New:*
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5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	79.8	1360	14	US-11-010-795-19
2	200	35.1	934	14	US-11-010-795-21

3	196.5	34.5	1855	8	US-10-893-584-35	Sequence 35, App1
4	195.5	34.4	1813	8	US-10-893-584-245	Sequence 245, App
5	194	34.1	1810	8	US-10-893-584-168	Sequence 168, App
6	193.5	34.0	1807	8	US-10-893-584-196	Sequence 196, App
7	192	33.7	807	14	US-11-010-795-23	Sequence 23, App1
8	192	33.7	1623	8	US-10-893-584-273	Sequence 273, App
9	192	33.7	1819	8	US-10-893-584-238	Sequence 238, App
10	192	33.7	1822	8	US-10-893-584-175	Sequence 175, App
11	192	33.7	1822	8	US-10-893-584-182	Sequence 182, App
12	192	33.7	1825	8	US-10-893-584-231	Sequence 231, App
13	192	33.7	1828	8	US-10-893-584-210	Sequence 210, App
14	192	33.7	1831	8	US-10-893-584-161	Sequence 161, App
15	192	33.7	1834	8	US-10-893-584-203	Sequence 203, App
16	192	33.7	1837	8	US-10-893-584-154	Sequence 154, App
17	192	33.7	1837	8	US-10-893-584-266	Sequence 266, App
18	192	33.7	1843	8	US-10-893-584-259	Sequence 259, App
19	192	33.7	1849	8	US-10-893-584-252	Sequence 252, App
20	192	33.7	1855	8	US-10-893-584-3	Sequence 3, App1
21	192	33.7	1855	8	US-10-893-584-5	Sequence 5, App1
22	192	33.7	1855	8	US-10-893-584-7	Sequence 7, App1
23	192	33.7	1855	8	US-10-893-584-9	Sequence 9, App1
24	192	33.7	1855	8	US-10-893-584-13	Sequence 13, App1
25	192	33.7	1855	8	US-10-893-584-15	Sequence 15, App1
26	192	33.7	1855	8	US-10-893-584-17	Sequence 17, App1
27	192	33.7	1855	8	US-10-893-584-19	Sequence 19, App1
28	192	33.7	1855	8	US-10-893-584-21	Sequence 21, App1
29	192	33.7	1855	8	US-10-893-584-23	Sequence 23, App1
30	192	33.7	1855	8	US-10-893-584-25	Sequence 25, App1
31	192	33.7	1855	8	US-10-893-584-27	Sequence 27, App1
32	192	33.7	1855	8	US-10-893-584-29	Sequence 29, App1
33	192	33.7	1855	8	US-10-893-584-31	Sequence 31, App1
34	192	33.7	1855	8	US-10-893-584-33	Sequence 33, App1
35	192	33.7	1855	8	US-10-893-584-37	Sequence 37, App1
36	192	33.7	1855	8	US-10-893-584-39	Sequence 39, App1
37	192	33.7	1855	8	US-10-893-584-48	Sequence 48, App1
38	192	33.7	1855	8	US-10-893-584-50	Sequence 50, App1
39	192	33.7	1855	8	US-10-893-584-52	Sequence 52, App1
40	192	33.7	1855	8	US-10-893-584-54	Sequence 54, App1
41	192	33.7	1855	8	US-10-893-584-74	Sequence 74, App1
42	192	33.7	1855	8	US-10-893-584-77	Sequence 77, App1
43	192	33.7	1855	8	US-10-893-584-80	Sequence 80, App1
44	192	33.7	1855	8	US-10-893-584-83	Sequence 83, App1
45	192	33.7	1855	8	US-10-893-584-86	Sequence 86, App1

ALIGNMENTS

RESULT 1
US-11-010-795-19
: Sequence 19, Application US/11010795
: Publication No. US20060005271A1
: GENERAL INFORMATION:
: APPLICANT: TUMER, NILGUN E.
: APPLICANT: DI, RONG
: TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
: TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
: FILE REFERENCE: OCTRS 3.0-065
: CURRENT APPLICATION NUMBER: US/11/010,795
: PRIOR APPLICATION NUMBER: 2004-12-13
: PRIOR FILING DATE: 2003-12-12
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 19
: LENGTH: 1360
: TYPE: DNA
: ORGANISM: Phytolacca americana
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (207)..(1145)
: US-11-010-795-19
Alignment Scores:

Pred. No.: 1,58e-52 Length: 1360
 Score: 454.00 Matches: 90
 Percent Similarity: 87.2% Conservative: 5
 Best Local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 DB: 14 Gaps: 0

US-09-978-274A-8 (1-110) x US-11-010-795-19 (1-1360)

QY 2 GlyValAspSerPheProValLyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 Db 732 GGAGTATGTCATCTCACTGAGAAACCGAAGCCCAATTCCTATTGTAGCCATCAATG 791
 QY 22 ValSerGluAlaAlaArgPheLyThrIleGluAsnGlnValLyThrAsnPheAsnArg 41
 Db 792 GTATCAGGCGACGACGATTCATCACTAGAGATGAGTACGCTGAAATTTTAAACA 851
 QY 42 AlaPheTyrProAspProLyValIleAsnLeuGluGlyTyrGlyLySerGlu 61
 Db 852 GCATTCAACCTATCCCAAGTACTTAATTGCAAGACATGGGGTAAGATTCAACA 911
 QY 62 AlaIleHisAsnAlaLyAsnGlyValAlaLeuProLySerProLeuGluLeuValAspAlaLys 81
 Db 912 GCAATTCATGATGCCAAGATGAGTTTACCCAAACCTCTCGAGTATGAGATGCCAGT 971
 QY 82 GlyThrLyThrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
 Db 972 GGAGCCAGGAGTATGCTTGAAGTGAATCAAGCTGATATGACACTTTAAAC 1031
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 Db 1032 TACGTGTGGAGAGCTCTCAGACAACT 1058

RESULT 2

US-11-010-795-21
 ; Sequence 21, Application US/11010795
 ; Publication No. US2006005271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TUMER, NITGUN E.
 ; APPLICANT: DI, RONG
 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
 ; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
 ; FILE REFERENCE: OCIRS 3.0-085
 ; CURRENT APPLICATION NUMBER: US/11/010,795
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: 60/529,348
 ; PRIOR FILING DATE: 2003-12-12
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 21
 ; LENGTH: 934
 ; TYPE: DNA
 ; ORGANISM: Phytolacca americana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(930)
 US-11-010-795-21

Alignment Scores:

Pred. No.: 1.94e-17 Length: 934
 Score: 200.00 Matches: 47
 Percent Similarity: 62.0% Conservative: 20
 Best Local Similarity: 43.5% Mismatches: 29
 Query Match: 35.1% Indels: 12
 DB: 14 Gaps: 5

US-09-978-274A-8 (1-110) x US-11-010-795-21 (1-934)

QY 9 LyThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 28
 Db 544 AAAAATAGAGCTGAATTTCTTCTTATGACCTTCAATAGGTACTGAGGCAATCAAGGTTT 603
 QY 29 LyThrIleGluAsnGlnValLyThrAsnPheAsnArgAla-----PheTyrProAsp 46

Db 604 AAATATCTGAGAAACAGGAAAGCTAAATTTGATGATGCCAATGGGTATCAGCCAGAT 663
 QY 47 ProLyValIleAsnLeuGluGlyTyrGlyLyIleSerGluAlaIleHisAsnAla 66
 Db 664 CTTAAAGCTATTTCCTTACGAGAAATTTGGACAGTGTTCATAGGCTATT-----GCA 717
 QY 67 LyAsnGly-----AlaLeuProLySerProLeuGluLeuValAspAlaLys 81
 Db 718 AAAGTTGGACACCTCCGGTATATGATCTTACTTATCTGAGACCTTAAAGATGAGAAT 777
 QY 82 GlyThrLyThrIleValLeuArgValAspGluIleAsnArgAspVal--AlaLeuLeu 100
 Db 778 AATTAACCTTGACTACGCGCACCATGAAAGCACTTAAGACGATTAAGCACTTATGACCTCTTA 837
 QY 101 LyThrValAsnGlyThrCysGln 108
 Db 838 ACCCAGCTT-----ACTTGCAG 855

RESULT 3

US-10-893-584-35
 ; Sequence 35, Application US/10893584
 ; Publication No. US20050272048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borgford, Thor
 ; APPLICANT: Braun, Curtis
 ; APPLICANT: Purac, Admit
 ; APPLICANT: Stoll, Dominik
 ; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
 ; TITLE OF INVENTION: Viral or Parasitic Infections
 ; FILE REFERENCE: 10447-025
 ; CURRENT APPLICATION NUMBER: US/10/893,584
 ; CURRENT FILING DATE: 2004-07-19
 ; PRIOR APPLICATION NUMBER: US 09/551,151
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: US 09/403,752
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 10/089,058
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 274
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 1855
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PAP-246 insert
 US-10-893-584-35

Alignment Scores:

Pred. No.: 1.43e-16 Length: 1855
 Score: 196.50 Matches: 44
 Percent Similarity: 53.3% Conservative: 21
 Best Local Similarity: 36.1% Mismatches: 40
 Query Match: 34.5% Indels: 17
 DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-35 (1-1855)

QY 2 GlyValAspSerPheProValLyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 Db 580 GGAGGACTGAGCTTCCAACTCTGCTGCTCTCTT-----ATTAATTCATCCAAATG 633
 QY 22 ValSerGluAlaAlaArgPheLyThrIleGluAsnGlnValLyThr-----AsnPhe 39
 Db 634 ATTTCAAGACGACGAAATTCATATATTGAGGAGAAATGCGCACGAGAAATTAGGTAC 693
 QY 40 AsnArgAlaPheTyrProAspProLyValIleAsnLeuGluGlyTyrGlyLyLysIle 59
 Db 694 AACCGAGATCTGCACCAATCTTACGTTAATTAACATTGAGATATATTGGGAGAGCTT 753
 QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyValAlaLeuProLySerProLeuGluLeuValAsp 79

```

Db      75 TCCAGCTCAATTCAGAGTCTAAACAAGAGCCTTTGCTAGTCCAAATTCAGCTCAAGA 81
Qy      80 AAlayegjlyThrystrpIleValleuArjValAspIuileasnArjAspValAlaleu 99
Db      814 CGTAATGGTTCGCAAAATTCAGTGTGTACAGATGATATTAATCCCTATCATAGCTCTC 873
Qy      100 LeuIystr-----ValaenGlyThr 106
Db      874 AAGGTATATAGATGGCGACCTCCACCATGCTACAGTTTCTGGGGGTGTAAATGATCG 933
Qy      107 CygGln 108
Db      934 TGTAGA 939

RESULT 4
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtie
; APPLICANT: Purac, Admit
; TITLE OF INVENTION: Stoll, Dominik
; TITLE OF INVENTION: Richn-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.: 1,91e-16 Length: 1813
Score: 195.50 Matches: 44
Percent Similarity: 54.8% Conservative: 19
Best Local Similarity: 38.3% Mismatches: 41
Query Match: 34.4% Indels: 11
DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-245 (1-1813)
Qy      2 GlyValAspSerPheProValIystrGluAlaPhePheLeuValAlaIleGlnMet 21
Db      580 GGTGGCATCTCAAGCTTCACACTGTGGCTGCTCTT-----ATAATTGCATCCAAAG 633
Qy      22 ValSerGluAlaAlaArjPheIystrIleGluAsnGlnValIystr-----AsnPhe 39
Db      634 ATTTCAGAGCAGACGAATTCGAATTAATTTAGCGGAGAAATCGCCAGCAATTAGGTAC 693
Qy      40 AsnArjAlaPheIystrProAspProIyValIleAsnLeuGluGluIystrGlyIystrIle 59
Db      694 AACCGAGATCTGCACCGATCTCTAGCGGTAAATTACCTTGAAATATGTTGGGGGAGACTT 753
Qy      60 SerGluAlaIleHleAsnAlaIyAsnGlnIyAlaLeuProIyProLeuGluLeuValAsp 79
Db      754 TCCAGCTCAATTCAGAGCTCTAACCAAGAGCCTTTGCTAGTCCAAATTCAGCTGCMAAG 813
Qy      80 AAlayegjlyThrystrpIleValleuArjValAspGluileasnArjAspValAlaleu 99
Db      814 CGTAATGGTTCGCAAAATTCAGTGTGTACAGATGATATTAATCCCTATCATAGCTCTC 873
Qy      100 LeuIystr-----ValaenGlyThrCys 107

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Db      874  ATGGTGTATGATGCGGACCGACGAGCAGTAGTGGCGGGGCGCTGT  918
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RESULT 5
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OR INVENTION: Richin-like Toxin Variants for Treatment of Cancer,
; TITLE OR INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 1810
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-168

Alignment Scores:
Pred. No.: 3,08e-16 Length: 1810
Score: 194.00 Matches: 43
Percent Similarity: 55.3% Conservative: 20
Best Local Similarity: 37.7% Mismatches: 41
Query Match: 34.1% Indels: 10
DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-168 (1-1810)
QY      2  GLYVALASPSEPHETHRVALLYSHTRGUALAPHEPHELEUENVALAALLIGINMET  21
Db      580  GGGGGACACTCAGCTTCACACTCTGGCTGCTTCCTT-----ATGAATTGCACCAATG  633
QY      22  VALSEGLUALALALARGPHELYSTYRIILEGLUNSGINVALYSTH-----ASPHE  39
Db      634  ATTTCGAAAGCAGCAGNATTCCAATATATTAGGAGAAATGCCACAGAGAAATTAGGTAC  693
QY      40  ASNARGALAPHERY-PROASPETHRVALLIENLENGUINGULYSTPGLYSTYLE  59
Db      694  AACCGAGAGCTGCACCGATCTAGCTGATTTACATTGAGAAATAGTTGGGGAGACTT  753
QY      60  SEGLUALAILLEHISANALALYBANGLYALALEUPOLYSPROLEUGLULEVALASP  79
Db      754  TCACATGCACATTCAGAAGAGCTAACCCAGAGACCTTCTGACCAATTCACTGAAAGA  813
QY      80  ALALYGLYTHRYSTRIPILEVALLEUARGVALASGILULEASNARGPVALAALALEU  99
Db      814  CGTAATGCTTCCAATTCAGTGTGTAGCATGTGATTAATTAATCCCTATCATAGCTCT  873
QY      100  LEULYSTY-----VALASNGLYTHRYYS  107
Db      874  ATGGTGTATGATGCTCTCCGCAAGAGAAATTGACGGGAGCGTGT  915

RESULT 6
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir

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APPLICANT: Stoll, Dominik
FEATURE:
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
LENGTH: 1807
TYPE: DNA
ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:
Pred. No.: 3.61e-16 Length: 1807
Score: 193.50 Matches: 44
Percent Similarity: 55.8% Conservative: 19
Best Local Similarity: 38.9% Mismatches: 41
Query Match: 34.0% Indels: 9
DB: Gaps: 3

US-09-978-274a-8 (1-110) x US-10-893-584-196 (1-1807)
QY 2 GlyValAspSerPheProValIyThrGluAlaPheHeuLeuValAlaIleGlnMet 21
Db 580 GGTGGCACTCAGCTTCCAACTCTGCTGCTCTT-----ATTAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheIyTyrlIeGluAsnGlnValIyThr-----AsnPhe 39
Db 634 ATTTCAGAGACGACAAATTCATATATATGAGGAGAAATGCCACAGAAATTAAGGTAC 693
QY 40 AsnArgAlaPheTyrrProAspProIySValIleAsnLeuGluIyIySTPGLyLeIle 59
Db 694 AACCGAGATCTGCACGACGATCTAGCGTATTAACATTGAGAAATTAAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaIyAsnGlnValAlaLeuProIySProIeGluLeuValAsp 79
Db 754 TCCACTCGCAATTCAGAGCTTAACCAAGAGCCCTTGTCTAGTCCAAATTCACCTGCAAGA 813
QY 80 AlaIySgIyThrlYsTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeu 99
Db 814 CGTAATGTTCCAAATTCAGTGTGACATGTGATATTAATCCCATATCATAGCTCTC 873
QY 100 LeuIySTYr-----ValAsnGlyThrCys 107
Db 874 ATGGGTATAGATGCCGACGACGAGTAGTCGGCGGGTGT 912

RESULT 7
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NIGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
```

```
ORGANISM: Ricinus communis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(804)
US-11-010-795-23

Alignment Scores:
Pred. No.: 2.08e-16 Length: 807
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274a-8 (1-110) x US-11-010-795-23 (1-807)
QY 2 GlyValAspSerPheProValIyThrGluAlaPheHeuLeuValAlaIleGlnMet 21
Db 472 GGTGGCACTCAGCTTCCAACTCTGCTGCTCTT-----ATTAATTGCATCCAAATG 525
QY 22 ValSerGluAlaAlaArgPheIyTyrlIeGluAsnGlnValIyThr-----AsnPhe 39
Db 526 ATTTCAGAGACGACAAATTCATATATATGAGGAGAAATGCCACAGAAATTAAGGTAC 585
QY 40 AsnArgAlaPheTyrrProAspProIySValIleAsnLeuGluIyIySTPGLyLeIle 59
Db 586 AACCGAGATCTGCACGACGATCTAGCGTATTAACATTGAGAAATTAAGTTGGGGAGACTT 645
QY 60 SerGluAlaIleHisAsnAlaIyAsnGlnValAlaLeuProIySProIeGluLeuValAsp 79
Db 646 TCCACTCGCAATTCAGAGCTTAACCAAGAGCCCTTGTCTAGTCCAAATTCACCTGCAAGA 705
QY 80 AlaIySgIyThrlYsTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeu 99
Db 706 CGTAATGTTCCAAATTCAGTGTGACATGTGATATTAATCCCATATCATAGCTCTC 765
QY 100 LeuIySTYr 102
Db 766 ATGGGTAT 774

RESULT 8
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admlr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Alignment Scores:
Pred. No.: 5.08e-16 Length: 1623
Score: 192.00 Matches: 41
```


Percent Similarity: 58.3%
Best Local Similarity: 39.8%
Query Match: 33.7%
Gaps: 2

Conservative: 19
Matches: 39
Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-273 (1-1623)

QY 2 G1YValaAspSerPheProVallyThrglualAphPheLeuValAlaIleGlnMet 21
DB 469 GGTGGCACTCAAGCTTCCAACTGCTGCTCTT-----ATAATTGATCCAAATG 522
QY 22 ValSerGlualAlaArgPheLySTyTllegluAengluVallyThr-----AsnPhe 39
DB 523 ATTTCAGAGACGACCAAGATTCCTAGATATATGAGGAGAAATGCGACGCAAGATTAAGTAC 582
QY 40 AsnArgAlaPheTyRProAspProLySValIleAsnLeuGluGluLySTyTllySile 59
DB 583 AACCGAGATCTGCACCAAGATCTTACGTAATTAACATTAAGTATGAGGAGACTT 642
QY 60 SerGlualAlaIleHisAsnAlaLySaengluValaleuProLySProLeuGluLeuValaAsp 79
DB 643 TCCACTGCAATTCAGAGCTTCAACCAAGAGCTTGTCTAGTCAATTCACACTGCAGAGA 702
QY 80 AlAlayeglyThrLySTyTlPleValleuArgValaAspGluIleAsnArgAspValAlaLeu 99
DB 703 CGTATGCTTCCAAATTCAGTGTAGTACGATGATATTAATCCATATCAATGCTCTC 762
QY 100 LeuLySTyR 102
DB 763 ATGGTGAT 771

RESULT 9

US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braum, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-238

Alignment Scores:
Pred. No.: 5.88e-16 Length: 1819
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-238 (1-1819)

QY 2 G1YValaAspSerPheProVallyThrglualAphPheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAAGCTTCCAACTGCTGCTCTT-----ATAATTGATCCAAATG 633

QY 22 ValSerGlualAlaArgPheLySTyTllegluAengluVallyThr-----AsnPhe 39
DB 634 ATTTCAGAGACGACCAAGATTCCTAGATATATGAGGAGAAATGCGACGCAAGATTAAGTAC 693

QY 40 AsnArgAlaPheTyRProAspProLySValIleAsnLeuGluGluLySTyTllySile 59
DB 694 AACCGAGATCTGCACCAAGATCTTACGTAATTAACATTAAGTATGAGGAGACTT 753

QY 60 SerGlualAlaIleHisAsnAlaLySaengluValaleuProLySProLeuGluLeuValaAsp 79
DB 754 TCCACTGCAATTCAGAGCTTCAACCAAGAGCTTGTCTAGTCAATTCACACTGCAGAGA 813

QY 80 AlAlayeglyThrLySTyTlPleValleuArgValaAspGluIleAsnArgAspValAlaLeu 99
DB 814 CGTATGCTTCCAAATTCAGTGTAGTACGATGATATTAATCCATATCAATGCTCTC 873

QY 100 LeuLySTyR 102
DB 874 ATGGTGAT 882

RESULT 10

US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braum, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175

Alignment Scores:
Pred. No.: 5.89e-16 Length: 1822
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-175 (1-1822)

QY 2 G1YValaAspSerPheProVallyThrglualAphPheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAAGCTTCCAACTGCTGCTCTT-----ATAATTGATCCAAATG 633
QY 22 ValSerGlualAlaArgPheLySTyTllegluAengluVallyThr-----AsnPhe 39
DB 634 ATTTCAGAGACGACCAAGATTCCTAGATATATGAGGAGAAATGCGACGCAAGATTAAGTAC 693
QY 40 AsnArgAlaPheTyRProAspProLySValIleAsnLeuGluGluLySTyTllySile 59
DB 694 AACCGAGATCTGCACCAAGATCTTACGTAATTAACATTAAGTATGAGGAGACTT 753
QY 60 SerGlualAlaIleHisAsnAlaLySaengluValaleuProLySProLeuGluLeuValaAsp 79
DB 754 TCCACTGCAATTCAGAGCTTCAACCAAGAGCTTGTCTAGTCAATTCACACTGCAGAGA 813

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QY 80 AlAlaYsGlyThrIySTrPileValLeuAArgValAspGluIleAsnAArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACAGATGATATATATATCCCTATCATAGCTCTC 873
QY 100 LeuIySTyr 102
DB 874 ATGGTGTAT 882

RESULT 11
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-182

Alignment Scores:
Pred. No.: 5.99e-16 Length: 1822
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-182 (1-1822)
QY 2 G1VAlAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAGCTTCCAACCTCGGCTCGTCTTT-----ATAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheIySTyrIleGluAsnGlnValIySThr-----AsnPhe 39
DB 634 ATTTCAAGACAGCAAGATTCATATATTTGAGGAGAAATGCCAGAGAAATTAGGTAC 693
QY 40 AsnArgAlaPheIySTyrProAspProIyValIleAsnLeuGluIySTyrGlyIyValIle 59
DB 694 AACCGAGATCTGCACCAAGATCTTAGCGTAATTACATTGAGAAATAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProlLeuGluLeuValAsp 79
DB 754 TCCACTGCATTCAGAGCTTAACCAAGAGAGCTTTGCTAGTCCAAATTCAGCAAGA 813
QY 80 AlAlaYsGlyThrIySTrPileValLeuAArgValAspGluIleAsnAArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACAGATGATATATATATCCCTATCATAGCTCTC 873
QY 100 LeuIySTyr 102
DB 874 ATGGTGTAT 882

RESULT 12
US-10-893-584-231
```

```
; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231

Alignment Scores:
Pred. No.: 5.9e-16 Length: 1825
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-231 (1-1825)
QY 2 G1VAlAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAGCTTCCAACCTCGGCTCGTCTTT-----ATAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheIySTyrIleGluAsnGlnValIySThr-----AsnPhe 39
DB 634 ATTTCAAGACAGCAAGATTCATATATTTGAGGAGAAATGCCAGAGAAATTAGGTAC 693
QY 40 AsnArgAlaPheIySTyrProAspProIyValIleAsnLeuGluIySTyrGlyIyValIle 59
DB 694 AACCGAGATCTGCACCAAGATCTTAGCGTAATTACATTGAGAAATAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProlLeuGluLeuValAsp 79
DB 754 TCCACTGCATTCAGAGCTTAACCAAGAGAGCTTTGCTAGTCCAAATTCAGCAAGA 813
QY 80 AlAlaYsGlyThrIySTrPileValLeuAArgValAspGluIleAsnAArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACAGATGATATATATATCCCTATCATAGCTCTC 873
QY 100 LeuIySTyr 102
DB 874 ATGGTGTAT 882

RESULT 13
US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
```

;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent Ver. 2.0
;; SEQ ID NO 210
;; LENGTH: 1828
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-210

Alignment Scores:
Pred. No.: 5,91e-16 Length: 1828
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-210 (1-1828)

QY 2 GlyValAspSerPheProValIleThrGluAlaPheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTGACCTTCCAACTCTGCTGCTCTT-----ATAATTGCAATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLeuTyrIleGluAsnGlnValIleThr-----AsnDhe 39
DB 634 ATTTCAAGAGCAGCAGATTCCTCAATATTTAGGAGGAGAAATGCCGACGAGAAATTAGTAC 693
QY 40 AsnArgAlaPheTyrProAspProIleValIleAsnLeuGluGluTyrGlyLysIle 59
DB 694 AACCGAGATCTGCACCAAGATCTTACGTAATTAACACTTGAGAAATGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProIleProLeuGluLeuValAsp 79
DB 754 TCACCTGCAATTCAGAGCTTACCAAGAGCCTTGTACTGCAATTCGAACTGCAAGA 813
QY 80 AlaIleGlyThrIleTyrPileValIleuArgValAspGluIleAsnArgAspValAlaLeu 99
DB 814 CGTATGTTCCAAATTCAGTGTACGATGTGATATTAATCCATCATAGCTCTC 873
QY 100 LeuLysTyr 102
DB 874 ATGGTGAT 882

RESULT 14
US-10-893-584-161
;; Sequence 161, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Rich-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent Ver. 2.0
;; SEQ ID NO 161
;; LENGTH: 1831

;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-161

Alignment Scores:
Pred. No.: 5,93e-16 Length: 1831
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-161 (1-1831)

QY 2 GlyValAspSerPheProValIleThrGluAlaPheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTGACCTTCCAACTCTGCTGCTCTT-----ATAATTGCAATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLeuTyrIleGluAsnGlnValIleThr-----AsnDhe 39
DB 634 ATTTCAAGAGCAGCAGATTCCTCAATATTTAGGAGGAGAAATGCCGACGAGAAATTAGTAC 693
QY 40 AsnArgAlaPheTyrProAspProIleValIleAsnLeuGluGluTyrGlyLysIle 59
DB 694 AACCGAGATCTGCACCAAGATCTTACGTAATTAACACTTGAGAAATGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProIleProLeuGluLeuValAsp 79
DB 754 TCACCTGCAATTCAGAGCTTACCAAGAGCCTTGTACTGCAATTCGAACTGCAAGA 813
QY 80 AlaIleGlyThrIleTyrPileValIleuArgValAspGluIleAsnArgAspValAlaLeu 99
DB 814 CGTATGTTCCAAATTCAGTGTACGATGTGATATTAATCCATCATAGCTCTC 873
QY 100 LeuLysTyr 102
DB 874 ATGGTGAT 882

RESULT 15
US-10-893-584-203
;; Sequence 203, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Rich-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent Ver. 2.0
;; SEQ ID NO 203
;; LENGTH: 1831
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-203

Alignment Scores:
Pred. No.: 5,93e-16 Length: 1831
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 915.096 Seconds
(without alignments)
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Title: US-09-978-274A-3

Perfect score: 792
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	766	96.7	1092	3	US-09-978-274A-19
4	532.6	67.2	1379	3	US-09-978-274A-30
5	532.6	67.2	1379	10	US-11-106-187-1
6	529.4	66.8	1368	3	US-09-978-274A-31
7	518.2	65.4	1376	8	US-10-467-009-1
8	462	58.3	465	3	US-09-978-274A-5
9	328.4	41.5	333	3	US-09-978-274A-7
10	101	12.8	855	10	US-11-106-187-3
11	101	12.8	934	3	US-09-978-274A-32
12	101	12.8	934	10	US-11-106-187-3
13	86.4	10.9	765	6	US-09-792-793A-66
14	86.4	10.9	765	6	US-10-375-209A-66
15	86.4	10.9	984	3	US-09-792-793A-60
16	86.4	10.9	984	6	US-10-375-209A-60
17	86.4	10.9	993	3	US-09-792-793A-63
18	86.4	10.9	993	6	US-10-375-209A-63
19	86.4	10.9	999	3	US-09-792-793A-54
20	86.4	10.9	999	3	US-09-792-793A-57
21	86.4	10.9	999	6	US-10-375-209A-57
22	86.4	10.9	999	6	US-10-375-209A-57
23	84.2	10.6	935	9	US-10-919-750-4

24	83.8	10.6	2404	10	US-11-084-080-15	Sequence 15, Appl
25	83.8	10.6	2404	10	US-11-084-080-19	Sequence 19, Appl
26	83.8	10.6	2404	10	US-11-084-080-21	Sequence 21, Appl
27	83.8	10.6	2404	10	US-11-084-080-23	Sequence 23, Appl
28	83.8	10.6	2431	3	US-11-084-080-27	Sequence 27, Appl
29	82	10.4	1233	10	US-09-861-257-24	Sequence 24, Appl
30	82	10.4	1233	6	US-10-189-360-80	Sequence 80, Appl
31	81	10.2	804	3	US-09-861-257-37	Sequence 37, Appl
32	81	10.2	804	3	US-09-861-257-38	Sequence 38, Appl
33	81	10.2	804	6	US-10-189-360-22	Sequence 22, Appl
34	81	10.2	804	6	US-10-189-360-23	Sequence 23, Appl
35	75	9.5	1230	6	US-10-189-360-53	Sequence 53, Appl
36	75	9.5	1251	3	US-09-861-257-77	Sequence 77, Appl
37	75	9.5	1251	6	US-10-189-360-74	Sequence 74, Appl
38	75	9.5	1260	3	US-09-861-257-75	Sequence 75, Appl
39	75	9.5	1260	6	US-10-189-360-72	Sequence 72, Appl
40	75	9.5	1266	3	US-09-861-257-78	Sequence 78, Appl
41	75	9.5	1266	6	US-10-189-360-75	Sequence 75, Appl
42	75	9.5	1269	3	US-09-861-257-81	Sequence 81, Appl
43	75	9.5	1269	6	US-10-189-360-78	Sequence 78, Appl
44	75	9.5	1275	3	US-09-861-257-76	Sequence 76, Appl
45	75	9.5	1275	6	US-10-189-360-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1									
US-09-978-274A-3									
Sequence 3, Application US/09978274A									
Patent No. US20020116737A1									
GENERAL INFORMATION:									
APPLICANT: Thomas, Christopher									
APPLICANT: McPherson, Michael									
APPLICANT: Atkinson, Howard									
APPLICANT: Neelam, Anil									
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM									
FILE REFERENCE: 9341-028									
CURRENT APPLICATION NUMBER: US/09/978,274A									
CURRENT FILING DATE: 2001-10-15									
PRIOR APPLICATION NUMBER: 0025225.4									
PRIOR FILING DATE: 2000-10-14									
NUMBER OF SEQ ID NOS: 32									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 3									
LENGTH: 792									
TYPE: DNA									
ORGANISM: Phytolacca americana									
US-09-978-274A-3									
Query Match									
Best Local Similarity 100.0%; Score 792; DB 3; Length 792;									
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ATGATAAATACGATCACTTGGATGCGGAATGCCACATTAACAAATATGCACTT	60						
DB	1	ATGATAAATACGATCACTTGGATGCGGAATGCCACATTAACAAATATGCACTT	60						
QY	61	ATGGAATCTTCTGTAATCAAGGAAAGATCCAAAATTAATGCTATGCAATCAATG	120						
DB	61	ATGGAATCTTCTGTAATCAAGGAAAGATCCAAAATTAATGCTATGCAATCAATG	120						
QY	121	CTACCTGATCTAATTCGACCCCTTAAGTATTATGTTAAGCTCCAAAGTGCACCTTA	180						
DB	121	CTACCTGATCTAATTCGACCCCTTAAGTATTATGTTAAGCTCCAAAGTGCACCTTA	180						
QY	181	AAAACATTAACATTAAGTGCAGCAAAATTAATGCTATGCAATCAATG	240						
DB	181	AAAACATTAACATTAAGTGCAGCAAAATTAATGCTATGCAATCAATG	240						
QY	241	TTCAATGCAATTAAGTGTCTTACATATATTAATGATATTAACAAGCAGGACACT	300						
DB	241	TTCAATGCAATTAAGTGTCTTACATATATTAATGATATTAACAAGCAGGACACT	300						

QY 301 GATGTGAGAAATCTTTTGTCTCAAGTTCTAGTTCGTGTGTGCATGTCATTACTAC 360
DB 301 GATGTGAGAAATCTTTTGTCTCAAGTTCTAGTTCGTGTGTGCATGTCATTACTAC 360
QY 361 AATAGCTTAATTCGAGCAATGAGAAAGAGAGAAATGTAATCAAGATCCAA 420
DB 361 AATAGCTTAATTCGAGCAATGAGAAAGAGAGAAATGTAATCAAGATCCAA 420
QY 421 TTGGGAATTCGAATCTCAGCAATGATGAAATAATCTGTGAGTTGATTCATTCCT 480
DB 421 TTGGGAATTCGAATCTCAGCAATGATGAAATAATCTGTGAGTTGATTCATTCCT 480
QY 481 GTAAAACTGAGGCTTTTCTTCTAGTCCATCCAAATGTTTCAGAGGCGCGCA 540
DB 481 GTAAAACTGAGGCTTTTCTTCTAGTCCATCCAAATGTTTCAGAGGCGCGCA 540
QY 541 TTCAAGATCAATGAGAAAGCAAGTCAATTAATTTAATAGATCTTCAATCCATCC 600
DB 541 TTCAAGATCAATGAGAAAGCAAGTCAATTAATTTAATAGATCTTCAATCCATCC 600
QY 601 AATGTAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGCAAG 660
DB 601 AATGTAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGCAAG 660
QY 661 AATGGGCTTTACCCAAACCACTTGAGCTAGTGAGTCCAAAGGTACCAAGTGATGTT 720
DB 661 AATGGGCTTTACCCAAACCACTTGAGCTAGTGAGTCCAAAGGTACCAAGTGATGTT 720
QY 721 CTTAGAGTGAATGAATCAATCGTAGTGAGTCCCTTAAGTAACTTAATGAACTGT 780
DB 721 CTTAGAGTGAATGAATCAATCGTAGTGAGTCCCTTAAGTAACTTAATGAACTGT 780
QY 781 CAGACAACCTTA 792
DB 781 CAGACAACCTTA 792

RESULT 2

US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-1

Query Match 99.3%; Score 786.4; DB 3; Length 945;
Best Local Similarity 99.9%; Pred. No. 9.1e-219;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 AATAATACGATCACTTTGATGCTGAGAAATGCAACATTAACAAATATGCACTTTATG 63
DB 73 AATAATACGATCACTTTGATGCTGAGAAATGCAACATTAACAAATATGCACTTTATG 132
QY 64 GAATCTCTTCTGTAATCAAGGAAAGATCCAAATTAATATGCTATGCAATCAATGCTA 123
DB 133 GAATCTCTTCTGTAATCAAGGAAAGATCCAAATTAATATGCTATGCAATCAATGCTA 192

QY 124 CCGATTAATTAATGACCCCTTAAGTAACTTAATGTTAAGTCCAGGTGCAAACTTA 183
DB 193 CCGATTAATTAATGACCCCTTAAGTAACTTAATGTTAAGTCCAGGTGCAAACTTA 252
QY 184 ACCATTAACCTAATGCTGAGAGCAATTAATTAATGATGAGGCTAATTTGATCCCTTC 243
DB 253 ACCATTAACCTAATGCTGAGAGCAATTAATTAATGATGAGGCTAATTTGATCCCTTC 312
QY 244 AATGCAATTAAGTGTGTTACCATTAATTAATTAATTAATTAATTAATTAATTAATTA 303
DB 313 AATGCAATTAAGTGTGTTACCATTAATTAATTAATTAATTAATTAATTAATTAATTA 372
QY 304 GTGAGAAATCTCTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTAATCAAT 363
DB 373 GTGAGAAATCTCTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTAATCAAT 432
QY 364 AGCTTAATTCGACCAATGAGAAAGAGAGAAAGTAACTCAAGAAATCAAGTCAATG 423
DB 433 AGCTTAATTCGACCAATGAGAAAGAGAGAAAGTAACTCAAGAAATCAAGTCAATG 492
QY 424 GGAATTCAAATTAATCTCAGCAATGATCAATGAGAAATCTGAGAGTTGATTCATCCCTGTA 483
DB 493 GGAATTCAAATTAATCTCAGCAATGATCAATGAGAAATCTGAGAGTTGATTCATCCCTGTA 552
QY 484 AAAAATGAGGCTTTTCTTCTAGTGTAGCCATCAATGATGTTCAAGAGCGCGCATTC 543
DB 553 AAAAATGAGGCTTTTCTTCTAGTGTAGCCATCAATGATGTTCAAGAGCGCGCATTC 612
QY 544 AATGATTAATGAGAAAGCAATGCAAGTAAATTTAATAGAGCAATTCATCCCTGTA 603
DB 613 AATGATTAATGAGAAAGCAATGCAAGTAAATTTAATAGAGCAATTCATCCCTGTA 672
QY 604 GTAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGCAAGAT 653
DB 673 GTAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGCAAGAT 732
QY 724 AGAGTGAATGAATCAATGATGATGAGCACTCCCTTAATAGTAAATGAACTGTGAG 783
DB 793 AGAGTGAATGAATCAATGATGATGAGCACTCCCTTAATAGTAAATGAACTGTGAG 852
QY 784 ACAACTTA 791
DB 853 ACAACTTA 860

RESULT 3

US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cybetatin fusion
US-09-978-274A-19

Query Match 96.7%; Score 766; DB 3; Length 1092;
Best Local Similarity 100.0%; Pred. No. 9e-213;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGATAATATCATGATCCTTTGATGCTGAAATGCCACATTAACTAAATATGCCACTTT 60
Db 1 ATGATAATATCATGATCCTTTGATGCTGAAATGCCACATTAACTAAATATGCCACTTT 60
Qy 61 ATGAAATCTCTGTAATCAAGCGAAGATGCCAAAATCTAAATATGTAATGCCATCATG 120
Db 61 ATGAAATCTCTGTAATCAAGCGAAGATGCCAAAATCTAAATATGTAATGCCATCATG 120
Qy 121 CTACCTGATCTAATTCGACCCCTTAAGTCTTAATGTTAAGCTCCAAAGTGAACCTTA 180
Db 121 CTACCTGATCTAATTCGACCCCTTAAGTCTTAATGTTAAGCTCCAAAGTGAACCTTA 180
Qy 181 AAAACATTACATATGCTGAGACGAAATTAATTATGATGAGGCTATTCGATCC 240
Db 181 AAAACATTACATATGCTGAGACGAAATTAATTATGATGAGGCTATTCGATCC 240
Qy 241 TTCAATGSCAATAGTGTGCTTACATATTTAATGATATTAACAAGCCGAAGCCT 300
Db 241 TTCAATGSCAATAGTGTGCTTACATATTTAATGATATTAACAAGCCGAAGCCT 300
Qy 301 GATGTGAGAAATCTCTTGTCTCAAGTCTAGTCTGTTGCTGCAATGCTTAACCTAC 360
Db 301 GATGTGAGAAATCTCTTGTCTCAAGTCTAGTCTGTTGCTGCAATGCTTAACCTAC 360
Qy 361 AATAGCTTATATCCGACCAATGAAAGCAAGATTAATCTCAAGAAATCAAGTCCA 420
Db 361 AATAGCTTATATCCGACCAATGAAAGCAAGATTAATCTCAAGAAATCAAGTCCA 420
Qy 421 TTGGGAATTCGAATATCTGAGAGTGAATTTGGAATATCTGAGATGATTCATTCCT 480
Db 421 TTGGGAATTCGAATATCTGAGAGTGAATTTGGAATATCTGAGATGATTCATTCCT 480
Qy 481 GTAAATATGAGGCTTTTCTCTGAGTACCAATCCAAATGTTTTCAGAGGACGCGA 540
Db 481 GTAAATATGAGGCTTTTCTCTGAGTACCAATCCAAATGTTTTCAGAGGACGCGA 540
Qy 541 TTCAAGTACATAGAAACCAAGTCAAGCTAATTTAATAGAGCATTCCTGATCCC 600
Db 541 TTCAAGTACATAGAAACCAAGTCAAGCTAATTTAATAGAGCATTCCTGATCCC 600
Qy 601 AAAATATTAATCTTGGAGAGAAATGAGGCGAAATCTCTGAGCAATTCATATGCCAG 660
Db 601 AAAATATTAATCTTGGAGAGAAATGAGGCGAAATCTCTGAGCAATTCATATGCCAG 660
Qy 661 AATGGGCTTTTACCCAAACCACTGAGCTAGTGAATGCCAAAGTCAAGTGAATGTT 720
Db 661 AATGGGCTTTTACCCAAACCACTGAGCTAGTGAATGCCAAAGTCAAGTGAATGTT 720
Qy 721 CTAGAGTGAATGAATCAATCTGATGCTGACCTCTTAAGTACG 766
Db 721 CTAGAGTGAATGAATCAATCTGATGCTGACCTCTTAAGTACG 766
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RESULT 4
US-09-978-274A-30
; Sequence 30, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-30

Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 1.7e-144;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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Qy 5 TAAATAGATCACTTGTGATGCTGAAATGCCACATTAACTAAATATGCCACTTTATG 64
Db 292 TGAATACATATCTTACATATGTTGAAGTACACCAATTAGCAATATAGCCACTTTCTGA 351
Qy 65 AATCTCTTGTATCAAGCGAAGATGCCAAAATCTAAATATGTAATGCCATTCATGCTAC 124
Db 352 ATGATCTTGTATCAAGCGAAGATGCCAAAATCTAAATATGTAATGCCATTCATGCTAC 411
Qy 125 CTGATCTAATTCGACCCCTTAAGTCTTAATGTTAAGCTCCAAAGTGAACCTTAATA 184
Db 412 CCAATACAAATATCAAAATCCAAAGTATGTTGTTGAGCTCCAAAGTTCAAATTAATA 471
Qy 185 CCATTACATATGCTGAGACGAAATTAATTATGATGAGGCTATTCGATCCCTTCA 244
Db 472 CCATACATATGCTGAGACGAAATTAATTATGATGAGGCTATTCGATCCCTTCA 531
Qy 245 ATGGCAATTAAGTGTGTTACATATTAATTAATGATTAACAAGCCGAAGCCTGATG 304
Db 532 AAACCAATTAATGCTGTTACCAATCTTAATGATATCTGAGTACGAAAGCCGAAGT 591
Qy 305 TGAAGAAATCTCTTGTCTCAAGTCTGATGCTGCTGTTGCAATGCTTAATCAATA 364
Db 592 TAGAGCTACTCTTGTCCAAATGCCAATCTGCTGTTGTAATAAATCAATACTTTGATA 651
Qy 365 GCTTAATTCGACCAATGAAAGCAAGTCAAGTCAAGAAATCAAGTCAATGTTG 424
Db 652 GTGATATTCGAATCTGACATGATTAATGAAAGATTTCTGAGTGAATCTCAATCTGAGA 711
Qy 425 GAATTCAAATCTGACGATGACATTTGAAATATCTCTGAGTGAATTCCTCTGTAA 484
Db 712 GAATTCAAATCTGACATGATTAATGAAAGATTTCTGAGTGAATCTCAATCTGAGA 771
Qy 485 AAACTGAGGCTTTTCTCTGAGTACCAATCCAAATGTTTTCAGAGGACGCGATTC 544
Db 772 AAACCGAAGCCGAATCTTATGTTGATGCAATGATGATGATGATGATGATGATGAT 831
Qy 545 AGTACATAGAGAACCAAGTCAAGCTAATTTAATAGAGCATTCATCCGATCCCAAG 604
Db 832 AGTACATAGAGAACCAAGTCAAGCTAATTTAATAGAGCATTCATCCGATCCCAAG 891
Qy 605 TAAATTAATGAGAGAAATGAGGCGAAATCTCTGAGCAATTCATATGCCAAGATG 664
Db 892 TACTTAATTTGCAAGAGACATGAGGTAAGTTTCAACAGCAATTCATGATGCCAAGATG 951
Qy 665 GGGCTTATCCCAAAACCACTGAGTGAATGCCAAAGTCAAGTGAATGATTTCTTA 724
Db 952 GAGTTTATCCCAAAACCTCTGAGTGAATGCCAAAGTGAATGATGATGATGATGATGAT 1011
Qy 725 GAGTGAATGAATCAATCTGATGCTGACCTCTTAAGTGAATGAATGAACCTGTGAGA 784
Db 1012 GAGTGAATGAATCAATCTGATGCTGACCTCTTAAGTGAATGAATGAATGAATGAAT 1071
Qy 785 CAACTTA 791
Db 1072 CAACTTA 1078
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RESULT 5
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1

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/ GENERAL INFORMATION:
/ APPLICANT: TUMER, NILGUN E.
/ APPLICANT: WANG, PINGER
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106,187
/ PRIOR FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721,047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 1
/ LENGTH: 1379
/ TYPE: DNA
/ ORGANISM: PhytoIacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (225)..(1163)
US-11-106-187-1
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Query Match      67.2%; Score 532.6; DB 10; Length 1379;
Best Local Similarity 79.8%; Pred. No. 1.7e-144;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
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QY 5 TAAATACGATCACCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACTTATG 64
DB 292 TGAATCAATCACTCAATCAATGTTGGAAGTACCAACATTAACAAATATGCCACTTATG 351
QY 65 AATCTCTGATCAAGCAAGAAAGATCAAAATCTAATGCAATCAATGCTAC 124
DB 352 ATGATCTTCTGATGAGCAAGCAAGATCAAGTTAAATCTATGCAATCAATGCTAC 411
QY 125 CTGATCTAATTTGACCCCTAAGTACTTATGTTAGTCAAGGTCAAAGCTCAAACTTAA 184
DB 412 CCAATCAATATCAAAATCCAAAGTACGTTGTTAGTCCAAAGTTCAAAATTA 471
QY 185 CCATTACCTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAATATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 531
QY 245 ATGCAATTAAGTCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 304
DB 532 AAACCAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 591
QY 305 TGAAGATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 364
DB 592 TAGAGCTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 651
QY 365 GCTTATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 424
DB 652 GTCGATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 711
QY 425 GAATTAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 484
DB 712 GAATTAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 771
QY 485 AAACGAGCTTTTCTAATGCTGATCAATCAATGATTAATCAAGCAAGCAAGCTGAT 544
DB 772 AAACGAGCTTTTCTAATGCTGATCAATCAATGATTAATCAAGCAAGCAAGCTGAT 831
QY 545 AGTACATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 604
DB 832 AGTACATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 891
QY 605 TAAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 664
DB 892 TAAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 951
QY 665 GAGCTTTTACCAAACTCTGAGCTAGTGAATGCCAGCTGATGATGATGATGATGAT 724
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DB 952 GAGCTTTTACCAAACTCTGAGCTAGTGAATGCCAGCTGATGATGATGATGATGAT 1011
QY 725 GAGTGAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCTGAT 784
DB 1012 GAGTGAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCTGAT 1071
QY 785 CAACCTTA 791
DB 1072 CAACCTTA 1078
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RESULT 6
US-09-978-274A-31
/ Sequence 31, Application US/09978274A
/ Patent No. US20020116737A1
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Christopher
/ APPLICANT: McPherson, Michael
/ APPLICANT: Atkinson, Howard
/ APPLICANT: Neelam, Anil
/ TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
/ FILE REFERENCE: 9341-028
/ CURRENT APPLICATION NUMBER: US/09/978,274A
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 0025225.4
/ PRIOR FILING DATE: 2000-10-14
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 1368
/ TYPE: DNA
/ ORGANISM: PhytoIacca americana
US-09-978-274A-31
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Query Match      66.8%; Score 529.4; DB 3; Length 1368;
Best Local Similarity 79.5%; Pred. No. 1.4e-143;
Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
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QY 5 TAAATACGATCACCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACTTATG 64
DB 292 TGAATCAATCACTCAATCAATGTTGGAAGTACCAACATTAACAAATATGCCACTTATG 351
QY 65 AATCTCTGATCAAGCAAGAAAGATCAAAATCTAATGCAATCAATGCTAC 124
DB 352 ATGATCTTCTGATGAGCAAGCAAGATCAAGTTAAATCTATGCAATCAATGCTAC 411
QY 125 CTGATCTAATTTGACCCCTAAGTACTTATGTTAGTCAAGGTCAAAGCTCAAACTTAA 184
DB 412 CCAATCAATATCAAAATCCAAAGTACGTTGTTAGTCCAAAGTTCAAAATTA 471
QY 185 CCATTACCTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAATATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 531
QY 245 ATGCAATTAAGTCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 304
DB 532 AAACCAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 591
QY 305 TGAAGATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 364
DB 592 TAGAGCTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 651
QY 365 GCTTATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 424
DB 652 GTCGATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 711
QY 425 GAATTAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 484
DB 712 GAATTAATTAATGCTGCTTACCATATATTAATGATTAATCAAGCAAGCAAGCTGAT 771
QY 485 AAACGAGCTTTTCTAATGCTGATCAATCAATGATTAATCAAGCAAGCAAGCTGAT 544
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Db 772 AACCGAAGCCGAATTCTATTGTAGCCATACAAATGTATCAGAGGACGAAAGATTC 831
Qy 545 AGTACATGAGAACCAAGTCAAGCTATTTTAAATAGCAATTCTACCTTGATCCCAAG 604
Db 832 AGTACATGAGAAATCAGGTGAAATATTTTAAACAGCAATTCACCTTAATCCCAAG 891
Qy 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCAAGATG 664
Db 892 TACTTAATTTGCAAGAGACATGGGTAAAGTTTCAACGCAATTCATGATGCCAAGATG 951
Qy 665 GGGCTTAAACCAACCACTTGAGTGTAGTCCAAAGGTAACCAAGTGAATGTTCTTA 724
Db 952 GAGTTTAAACCAACCTCTCCAGCTAGTGAATGCCAGTGGCCAAAGTGAATGTTGA 1011
Qy 725 GAGTGAATGAATCAATGTGATGTGCACTCTTAATAGTTAAATGGAACCTGTGCA 784
Db 1012 GAGTGAATGAATCAAGCTGATGTGATGCACTTAAACTAGTGTGGAGCTGTGCA 1071
Qy 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 7
US-10-467-009-1

; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467,009
; CURRENT FILING DATE: 2003-08-01
; PRIORITY APPLICATION NUMBER: 60/266,396
; PRIORITY FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: *Physiolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

Query Match 65.4%; Score 518.2; DB 8; Length 1376;
Best Local Similarity 79.5%; Pred. No. 2.7e-140;
Matches 626; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

Qy 5 TAAATAGATCACTTGTGATGCTGAAATGCCACATTTAACAAATATGCGACCTTTATG 64
Db 292 TGAATACATCATCTACAAATGTGAAAGTACACACATTAGCAAAATAGCCACTTTTGA 351
Qy 65 AATCTCTTGTGATCAAGCAAGATCCAAATCTAAATGTCTATGCAATCAATGCTAC 124
Db 352 ATGATCTTGTGATGAGAGCAAGATCCAAATTTAAATGTCTATGCAATCAATGCTAC 411
Qy 125 CTGATCTAATTTGACCCCTTAAGTATTGTGTTAAGCTCAAGGTGCAAACTTAA 184
Db 412 CCAATACAAATACAAATCCAAAGTATGTTGTGAGCTCAAGGTTCAAATTA 471
Qy 185 CCATTAACATTAATGCTGAGAGCAATTAATTAACGTGATGGGCTATTTCTGATCCCTTCA 244
Db 472 CCATCAACATTAATGCTGAGAGCAATTAATTAATGATGGGCTATTTCTGATCCCTTGA 531
Qy 245 ATGCAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 304
Db 532 AAACCAATTAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 591
Qy 305 TGAAGATTAATCTTTGCTCAAGTTCTGATTTCTGTTGCAATGTCATTAATCAATTA 364
Db 592 TAGAGACTACTCTTTGGCCA---GCCAATCTCGTGTAGTAAACATTAATCTTGATA 648

Qy 365 GCTTAATTCGACCATGGAAGAAAGAAAGCAAGTAACTCAAGAAATCAATCCAAATG 424
Db 649 GTGATATTCCAACATTTGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 708
Qy 425 GAATTCAAATCTCAGCAGTGCATTTGAAAAATCTCTGAGTGAATTCATTTCCCTGTA 484
Db 709 GAATTCAAATCTCAGCAGTGAATTTGAAAAATTTCTGAGTGAATTCATTTCACTAGA 768
Qy 485 AAATGAGGCTTTTCTACTGTGTACCATCCAAATGTTTCAAGGACGCGGATTC 544
Db 769 AAACCGAAGCCGAATTCCTATTGTGTACCATCAAAATGTATCAGAGGCAAGATTC 828
Qy 545 AGTACATGAGAACCAAGTCAAGCTAATTTTAAATAGCAATTCATCCGATCCCAAG 604
Db 829 AGTACATGAGAAATCAGGTGAAATCTAATTTTAAACAGCAATTCACCTTAATCCCAAG 888
Qy 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGATG 664
Db 889 TACTTAATTTGCAAGAGACATGGGTAAAGTTTCAACAGCAATTCATGATGCCAAGATG 948
Qy 665 GGGCTTAAACCAACCACTTGAGTGTGATGCAAGTCCAAAGTCAAGTGAATGTTCTTA 724
Db 949 GAGTTTAAACCAACCTCTCCAGCTAGTGAATGCCAGTGGGCCAAGTGAATGTTGA 1008
Qy 725 GAGTGAATGAATCAATGTGATGTGCACTCTTAATAGTGTAAATGAAGAACCTGTGCA 784
Db 1009 GAGTGAATGAATCAAGCTGATGTGACACTTAACTAGTGTGGAGCTGTGCA 1068
Qy 785 CAACCTTA 791
Db 1069 CAACCTTA 1075

RESULT 8
US-09-978-274A-5

; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIORITY APPLICATION NUMBER: 0025225.4
; PRIORITY FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: *Physiolacca americana*
US-09-978-274A-5

Query Match 58.3%; Score 462; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATTCGATCACTTTGATGCTGAAATGCCACCTTAACAAATATGCAACTTT 60
Db 1 ATGATTAATTCGATCACTTTGATGCTGAAATGCCACCTTAACAAATATGCAACTTT 60
Qy 61 ATGGAATCTCTGATATCAAGCAAGATCCAAATCTAATAATGCTATGCAATGCAATG 120
Db 61 ATGGAATCTCTGATATCAAGCAAGATCCAAATCTAATAATGCTATGCAATGCAATG 120
Qy 121 CTACTGATATCAATTTGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCACAACTTA 180
Db 121 CTACTGATATCAATTTGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCACAACTTA 180

QY 181 AAAACCTTACCTAATGCTGAGACGAATTAATCTGATGGCTATTCGATCCC 240
DB 181 AAAACCTTACCTAATGCTGAGACGAATTAATCTGATGGCTATTCGATCCC 240
QY 241 TTGAATGCAATAGTGTCTGATCAATATTTAATGATATTAACCAACGCACT 300
DB 241 TTGAATGCAATAGTGTCTGATCAATATTTAATGATATTAACCAACGCACT 300
QY 301 GATGTGAGAAATCTTTTGTCTCAAGTCTGATCTGCTGTGTGCAATGCTCAATAC 360
DB 301 GATGTGAGAAATCTTTTGTCTCAAGTCTGATCTGCTGTGTGCAATGCTCAATAC 360
QY 361 AATGCTTATATCCGACCAATGAAAAGAAAGCAAGATTAATCAAGATCAAGTCCAA 420
DB 361 AATGCTTATATCCGACCAATGAAAAGAAAGCAAGATTAATCAAGATCAAGTCCAA 420
QY 421 TTGGGAATTCGAATCTCAGAGTGAATGGAATTAATCTCT 462
DB 421 TTGGGAATTCGAATCTCAGAGTGAATGGAATTAATCTCT 462

RESULT 9
US-09-978-274A-7
Sequence 7, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-7

Query Match 41.5%; Score 328.4; DB 3; Length 333;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 463 GGAATGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGATGCAATCAATG 522
DB 4 GGAATGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGATGCAATCAATG 522
QY 523 GTTTCAGAGGACGCGGATTCAGATGATAGAGCAACCAATCAATATTTAATAGA 562
DB 64 GTTTCAGAGGACGCGGATTCAGATGATAGAGCAACCAATCAATATTTAATAGA 562
QY 583 GCAATTCACCTGATCCCAAGTAATTAATCTGAGAGAGAGTGGGCAAAATCTCGAG 642
DB 124 GCAATTCACCTGATCCCAAGTAATTAATCTGAGAGAGAGTGGGCAAAATCTCGAG 642
QY 643 GCAATTCACCAATGCGCAAGATGCGGCTTACCCAAACCACTTGAAGTGAATGCCAA 702
DB 184 GCAATTCACCAATGCGCAAGATGCGGCTTACCCAAACCACTTGAAGTGAATGCCAA 702
QY 703 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCGATCTTAAG 762
DB 244 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCGATCTTAAG 762
QY 763 TACGTTAATGAACTGTGACAGCAACTTAA 792
DB 304 TACGTTAATGAACTGTGACAGCAACTTAA 792

RESULT 10
US-11-106-187-20
Sequence 20, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TURNER, NILDUN E.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 20
LENGTH: 855
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (855)
US-11-106-187-20

Query Match 12.8%; Score 101; DB 10; Length 855;
Best Local Similarity 53.3%; Pred. No. 1.8e-18;
Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

QY 19 TTTGATGCTGGAATGCAACCAATTAATCAATATGCAACCTTATGATCTCTGTAAT 78
DB 10 TTTGATGCTGGAATGCAACCAATTAATCAATATGCAACCTTATGATCTCTGTAAT 78
QY 79 CAAGCAAGATGCAATCAATCAATATGATGCAATGCAATGCAATGCAATGCAATGCA 138
DB 70 GCTGTGAAGAGCAAGAAATGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 129
QY 139 ACCCTTAATGATCTTATGCTTAAAGTTCGAAGTGAACCTTAAACCAATTAATG 198
DB 130 CAAGCAAGATGCAATGCTTAAAGTTCGAAGTGAACCTTAAACCAATTAATG 186
QY 199 CTGAGAGAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 258
DB 187 ATGAGAGAGAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 243
QY 259 CGTTACCAATTAATTAATGATTAATCAAGCAACGCAATGATGATGATGATGATGAT 318
DB 244 CGTTACCAATTAATTAATGATTAATCAAGCAACGCAATGATGATGATGATGATGAT 291
QY 319 TGTCTCAAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378
DB 292 TGTCTCAAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
QY 379 ATGAG 438
DB 352 ATGAG 411
QY 439 AGCAGTGAATGGAATTAATCTCTGAGATGATCA-----TTCCCTGTAA 486
DB 412 AGCAGTGAATGGAATTAATCTCTGAGATGATCA-----TTCCCTGTAA 471
QY 487 ACTGAGGCTTTTCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
DB 472 AATGAGGCTGAATTTCTTCTTATGATGATGATGATGATGATGATGATGATGATGAT 531
QY 547 TACATGAG 600
DB 532 TACATGAG 591
QY 601 AATGATTAATTAATGAG 655

Db 592 AAAGCTATTTCCCTAGAGAAAATTGGGACAGTGTCTTAAGTCATTGCAAAAG 646

RESULT 11

US-09-978-274A-32
Sequence 32, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelman, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 934
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-32

Query Match 12.8%; Score 101; DB 3; Length 934;
Best Local Similarity 53.3%; Pred. No. 1.9e-18;

Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

QY 19 TTTGATGCTGGAATATGCGACCATTAACAATAATGCAACCTTATGATCTCTGGTAAT 78
DB 85 TTTGACCTTGAGATGCGACACCGAATCTCTTAATTTTCTGACTAGTTTGGAGAA 144
QY 79 CAAGCGAAGATCCAAATCTAAATGCTATGCAATCAATGCTACTGATTAATTCG 138
DB 145 GCTGTGAAAGCAAGAAATTCATGCAATGATGTAATGGCCACAACTCATCGAA 204
QY 139 ACCCTTAAGTACTTATGCTTAAGCTCCAGAGTCAAACTTAACCTTAATG 198
DB 205 CAACCGAAGTATGTTGGTGAACCTCAATTCGATCTGCAATTC--ACATTTGCA 261
QY 199 CTGAGAGCAATATCTTATAGTATGAGGCTATCTGATCCCTCAATGGCAATAGT 258
DB 262 ATCAGAGGGGAACTTAATTTGGAGGCTATTTGACATTTTCAATGG--AAATGT 318
QY 259 CGTTACCATATATTAATGATTAATTAACAAGCACCGAAGCACTGATGAGATATCTT 318
DB 319 CGTTATCGATCTTCAAGATTCAGATTC--GATGCCAAGAGACGGTT 366
QY 319 TGTCTAAGTCTAGTCTCGTGTTCGATGCTCAATTCATTAAGTATTCGACC 378
DB 367 TGCCCCGGGGCAAAAGCAAGCCCTGGCACTCAGAAATATATCCCTATGAAAAGATTAC 426
QY 379 ATGAAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGGGAATTTCAATATCTC 438
DB 427 AAAGGATGGAATCAAAAGGTGGGGCTTAAGCTTAATTTAGGTTAAGAAAGATTAACCTC 486
QY 439 AGCAGTGAATGGAATAATCTCTGAGTTGATTCA-----TTCCCTGTAAAA 486
DB 487 AAGAGTGAATGGGTAAATCTACGGCAAGATCAAGATCAAGAGATTAACAAAA 546
QY 487 ACTGAGGCTTTTCTTACTGCTAGCAATCAATGTTTCAAGGCAAGGCAATTAAG 546
DB 547 AATGAGGCTAATTTCTTCTTAATAGCGTTCAATGTTTCTAGGCAATCAAGGTTCAAA 606
QY 547 TACATAGAGAACCAAGTCAAGATTAATTTTAAAT-----AGAGATTTCAACCGTATCCC 600
DB 607 TACATTGAGAACCAAGGAGGCTTAATTTGATGATGCCAATGGGTATCAGCCGATCTCT 666
QY 601 AAAGTAAATTAACTTGAAGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCGAATG 655

Db 667 AAAGCTATTTCCCTAGAGAAAATTGGGACAGTGTCTTAAGTCATTGCAAAAG 721

RESULT 12

US-11-106-187-3
Sequence 3, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NIGDUN E.
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 934
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(75)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (76)..(930)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
US-11-106-187-3

Query Match 12.8%; Score 101; DB 10; Length 934;
Best Local Similarity 53.3%; Pred. No. 1.9e-18;

Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

QY 19 TTTGATGCTGGAATATGCGACCATTAACAATAATGCAACCTTATGATCTCTGGTAAT 78
DB 85 TTTGACCTTGAGATGCGACACCGAATCTCTTAATTTTCTGACTAGTTTGGAGAA 144
QY 79 CAAGCGAAGATCCAAATCTAAATGCTATGCAATCAATGCTACTGATTAATTCG 138
DB 145 GCTGTGAAAGCAAGAAATTCATGCAATGATGTAATGGCCACAACTCATCGAA 204
QY 139 ACCCTTAAGTACTTATGCTTAAGCTCCAGAGTCAAACTTAACCTTAATG 198
DB 205 CAACCGAAGTATGTTGGTGAACCTCAATTCGATCTGCAATTC--ACATTTGCA 261
QY 199 CTGAGAGCAATATCTTATAGTATGAGGCTATTTGATCCCTCAATGGCAATAGT 258
DB 262 ATCAGAGGGGAACTTAATTTGGAGGCTATTTGACATTTTCAATGG--AAATGT 318
QY 259 CGTTACCATATATTAATGATTAATTAACAAGCACCGAAGCACTGATGAGATATCTT 318
DB 319 CGTTATCGATCTTCAAGATTCAGATTC--GATGCCAAGAGACGGTT 366
QY 319 TGTCTAAGTCTAGTCTCGTGTTCGATGCTCAATTCATTAAGTATTCGACC 378
DB 367 TGCCCCGGGGCAAAAGCAAGCCCTGGCACTCAGAAATATATCCCTATGAAAAGATTAC 426
QY 379 ATGAAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGGGAATTTCAATATCTC 438
DB 427 AAAGGATGGAATCAAAAGGTGGGGCTTAAGCTTAATTTAGGTTAAGAAAGATTAACCTC 486
QY 439 AGCAGTGAATGGAATAATCTCTGAGTTGATTCA-----TTCCCTGTAAAA 486
DB 487 AAGAGTGAATGGGTAAATCTACGGCAAGATCAAGATCAAGAGATTAACAAAA 546

Db 361 TACCAATGTCATCGAAGAACGCCAGATCAACCCAGGCGATCAATCCCGAAGAACTG 420
Qy 418 CAATTGGGAATTCAATATCTGACGATGACATTTGGAAAATCTCTGAGTTGATTCATTC 477
Db 421 GGTCTGGGTATTTATCTGCTGACGACGAGCATGGAAGCGTCAACAA--AAAGCTCGC 477
Qy 478 CTTGTAAAACTGAGGCTTTTCTTCTAGTACCATCAATAGTTTCAGAGGACG 537
Db 478 GTGTTAAAGACGAAGCCCGCTTCTGCTGATTCGCAATGATGACGCGAAGCCGCC 537
Qy 538 CGATTCAAGTACATAGAGAACCAAGTCAAGCTAATTTTAAATGAGCATTTACCTGAT 597
Db 538 CGTTCCGCTACATTCAGAACCTGCTCATCAAACTTCCGAAACAAGTTCAATTCGAG 597
Qy 598 CCCAAGTAAATTAATCTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACATGCC 657
Db 598 AATTAAGTCATTCAGTTGAGGTTAATTTGAAAAAATTTCCACCGCATTTATGTGAC 657
Qy 658 AAGAAATGGGCTTTACCCAA 677
Db 658 GCGAAGAACGTTTTCAA 677

RESULT 15
US-09-792-793A-60
; Sequence 60, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogging, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-792-793A-60

Query Match 10.9%; Score 86.4; DB 3; Length 984;
Best Local Similarity 47.5%; Pred. No. 3.5e-14;
Matches 323; Conservative 0; Mismatches 351; Indels 6; Gaps 2;

Qy 1 ATGATAAATACGATCACCTTGTATGCTGAAATGCCACCATTAACAATATGCCACCTT 60
Db 220 ATGATTAATAGTATTAATCTGACCTGTGATCGAACCGCGCAATATAGAGCTTC 279
Qy 61 ATGGAATCTTCTGATTAACGAGAAAGATTCAAAATCTAAATGCTATGACATACATG 120
Db 280 GTGATTAAGATTCGTAACAAGTAAGATCCGAATCTGAATACGGGTGACTGATATT 339
Qy 121 CTACCTGATTAATGACCCCTAAGTACTTATTTAGTTAAGTCAAGGTGCAAACTTA 180
Db 340 GCGGTATCGGTCCGCGAAGAAAGAAAGTTCTCGGCAATTAATTTCAAGTCCCGT 399
Qy 181 AAAACATTAACATAATGCTGAGACGAATTAATTAATGATGAGGCTATTTGATCCC 240
Db 400 GGCATGTTTCTCTGGGCTGAAAGCGCATTAACCTGATGTTGCTATCTGGCATG 459
Qy 241 TTCAATGGCAATAAGTGGT---TACCATATATTAATGATATTAACAAGACCGAAGC 297
Db 460 GATTAATGAAACGTAACCGGCTACTTCTTGACGAGATTACGAGCGCGAATTC 519

Qy 298 ACTGATGAGAAATACTCTTTTGCTCAAGTTTATGTTCTGCTGTTGCAATGTCATTAAAC 357
Db 520 ACTGCTCTGTTCCCGAGGCGACCATGCAAAACCAAAAGCATGGAATATACGGAAT 579
Qy 358 TACAATAGCTTATATCCGACCATGGAAGAAAGACAGAAATTAATCTCAAGAAATCAAGTC 417
Db 580 TACCAATGTCATTCGAGAAAGACGCGACATCAACCCAGGCGATCAATCCCGAAGAACTG 639
Qy 418 CAATTGGGAATTCAAATATCTCAGACATGACATTTGGAATAAATCTCTGAGATTTGATTCATTC 477
Db 640 GGTCTGGGTATTTATCTGCTGACGACGAGATGGAACGGTCAACAA--AAAGCTCGC 696
Qy 478 CTTGTAAAACTGAGGCTTTTCTTCTAGTACCATCAAAATGTTTCAGAGGACG 537
Db 697 GTGTTAAAGACGAAGCCCGCTTCTGCTGATGCAATTTGATGACGAGAACGCCGCC 756
Qy 538 CGATTCAAGTACATAGAGAACCAAGTCAAGCTAATTTTAAATGAGCATTTACCTGAT 597
Db 757 CGTTCCGCTACATTCAGAACCTGCTCATCAAACTTCCGAAACAAGTTCAATTCGAG 816
Qy 598 CCCAAGTAAATTAATCTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACATGCC 657
Db 817 AATTAAGTCATTCAGTTGAGGTTAATTTGAAAAAATTTCCACCGCATTTATGTGAC 876
Qy 658 AAGAAATGGGCTTTACCCAA 677
Db 877 GCGAAGAACGTTTTCAA 677

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OM nucleic - nucleic search, using sw model

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Title: US-09-978-274A-3

Perfect score: 792
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Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Published Applications NA_New:*
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532.6	67.2	1360	US-11-010-795-19	Sequence 19, Appl
2	101	12.8	934	US-11-010-795-21	Sequence 21, Appl
3	63	8.0	1623	US-10-893-584-273	Sequence 273, Appl
4	61.4	7.8	807	US-11-010-795-23	Sequence 23, Appl
5	61.4	7.8	1807	US-10-893-584-196	Sequence 196, Appl
6	61.4	7.8	1810	US-10-893-584-168	Sequence 168, Appl
7	61.4	7.8	1813	US-10-893-584-245	Sequence 245, Appl
8	61.4	7.8	1819	US-10-893-584-238	Sequence 238, Appl
9	61.4	7.8	1822	US-10-893-584-175	Sequence 175, Appl
10	61.4	7.8	1822	US-10-893-584-182	Sequence 182, Appl
11	61.4	7.8	1825	US-10-893-584-231	Sequence 231, Appl
12	61.4	7.8	1828	US-10-893-584-210	Sequence 210, Appl
13	61.4	7.8	1831	US-10-893-584-161	Sequence 161, Appl
14	61.4	7.8	1831	US-10-893-584-203	Sequence 203, Appl
15	61.4	7.8	1834	US-10-893-584-154	Sequence 154, Appl
16	61.4	7.8	1837	US-10-893-584-266	Sequence 266, Appl
17	61.4	7.8	1843	US-10-893-584-259	Sequence 259, Appl
18	61.4	7.8	1849	US-10-893-584-252	Sequence 252, Appl

19	61.4	7.8	1855	US-10-893-584-3	Sequence 3, Appl
20	61.4	7.8	1855	US-10-893-584-5	Sequence 5, Appl
21	61.4	7.8	1855	US-10-893-584-7	Sequence 7, Appl
22	61.4	7.8	1855	US-10-893-584-9	Sequence 9, Appl
23	61.4	7.8	1855	US-10-893-584-13	Sequence 13, Appl
24	61.4	7.8	1855	US-10-893-584-15	Sequence 15, Appl
25	61.4	7.8	1855	US-10-893-584-17	Sequence 17, Appl
26	61.4	7.8	1855	US-10-893-584-19	Sequence 19, Appl
27	61.4	7.8	1855	US-10-893-584-21	Sequence 21, Appl
28	61.4	7.8	1855	US-10-893-584-23	Sequence 23, Appl
29	61.4	7.8	1855	US-10-893-584-25	Sequence 25, Appl
30	61.4	7.8	1855	US-10-893-584-27	Sequence 27, Appl
31	61.4	7.8	1855	US-10-893-584-29	Sequence 29, Appl
32	61.4	7.8	1855	US-10-893-584-31	Sequence 31, Appl
33	61.4	7.8	1855	US-10-893-584-33	Sequence 33, Appl
34	61.4	7.8	1855	US-10-893-584-35	Sequence 35, Appl
35	61.4	7.8	1855	US-10-893-584-37	Sequence 37, Appl
36	61.4	7.8	1855	US-10-893-584-39	Sequence 39, Appl
37	61.4	7.8	1855	US-10-893-584-48	Sequence 48, Appl
38	61.4	7.8	1855	US-10-893-584-50	Sequence 50, Appl
39	61.4	7.8	1855	US-10-893-584-52	Sequence 52, Appl
40	61.4	7.8	1855	US-10-893-584-54	Sequence 54, Appl
41	61.4	7.8	1855	US-10-893-584-74	Sequence 74, Appl
42	61.4	7.8	1855	US-10-893-584-77	Sequence 77, Appl
43	61.4	7.8	1855	US-10-893-584-80	Sequence 80, Appl
44	61.4	7.8	1855	US-10-893-584-83	Sequence 83, Appl
45	61.4	7.8	1855	US-10-893-584-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NIIIGUN E.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
FILE REFERENCE: OCIRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,348
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 1360
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: CDS
LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 67.2%; Score 532.6; DB 14; Length 1360;
Best Local Similarity 79.8%; Pred. No. 4.5e-129;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY	5	TAATATGATCAGCTTGTAGCTGGAAATGCCACATTAACAATATGCCACCTTATNG	64
DB	274	TGAATACATCATTTATCAATGTGGAGTACCAATTAACAATATGACCACTTTTGA	333
QY	65	AATCTCTGTAATCAAGCAAGATCAAAACTTAATGCTATGCAATCAATGCTAC	124
DB	334	ATGATCTTGTGAATGAGGAGGAGATCAAGTTTAAATGCTATGCAATGCTGC	393
QY	125	CTGATTAATTAATGACCCCTTAAGTCTTATGTTAAGTCCAGTGCAACTTAAAA	184
DB	394	CCAATCAATTAATCAAAATCAAGTACGTGTGGTGAAGTCCAAAGTTCAATTAATA	453

```
Qy 185 CCATTACACTAATGCTGAGACGAATACTATACGTATGGGCTATTCTGATCCCTTCA 244
    |||||
Db 454 CCATCACACTAATGCTGAGACGAATCAATTTGATGATGGGTTATTCGATCCCTTTG 513
Qy 245 ATGGCAATAGTGTCTTACCATATATTTAATGATATTAACAAGCAGAAACGACTGATG 304
    |||||
Db 514 AAACCAATTAATGTCGTACCATATCTTTAATGATATCTCAGGTACGAAACGCGCAATG 573
Qy 305 TGGAGATACTCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTATACATTA 364
    |||||
Db 574 TTAGACTACTCTTTGCCCAATGCCAATTCCTCGTGTAGTAAACATTAATCTTGATA 633
Qy 365 GCTTATATCCGACATGAAAGAAAGACAGATTAATCTCAAGAAATCAAATCCAAATGG 424
    |||||
Db 634 GTGATATCCCAATGGAATCAAAAGCGGAGTAAATCAAGAAATCAAGATCCAACTGG 693
Qy 425 GAATTCATAATCTCAGAGTGAATTTGAAAAATCTCTGAGATGTTCAATTCCTCTTAA 484
    |||||
Db 694 GAATTCATAATCTCAGAGTGAATTTGAAAAATTTCTGAGATGTTCAATTCCTGAGA 753
Qy 485 AAACGAGGCTTTTCTACTGTGAGCCATCCAAATGTTTCAAGGACGCGATTTCA 544
    |||||
Db 754 AAACGAGGCGAATTCCTATTGTGATCCATACAAATGTTATCAGAGGACGAAATTTCA 813
Qy 545 AGTACATAGAAACCAAGTCAAGCTAATTTTAATAGACATTCATCTGATCCCAAG 604
    |||||
Db 814 AGTACATAGAAATCAGGTGAAATCTAATTTTAAACAGACATTCACCTTAATCCCAAG 873
Qy 605 TAATTAATCTGGAGAAATGGGGCAAAATCTCTGAGCAATTCACAAATGCCAAGATG 664
    |||||
Db 874 TACTTAATTTGCAAGACATGGGGTAAGATTTCAACAGCAATTCAGATGCCAAGATG 933
Qy 665 GGGCTTTAACCAACCACTGAGTATGATGATGCCAAAGGTACCAAGTGAATGTTCTTA 724
    |||||
Db 934 GAATTTTAAACCAACCTCTGAGCTATGATGATGCCAGTGTGCCAAGTGAATGTTGA 993
Qy 725 GAGTGATGAATCAATCGTATGTGGCACTCTTAAAGTACGTTAATGAAACCTGTGAGA 784
    |||||
Db 994 GAGTGATGAATCAAGCTGATGTAGCACTTTAACTAGTTGGTGGAGCTGTGAGA 1053
Qy 785 CAACCTTA 791
    |||||
Db 1054 CAACCTTA 1060
    |||||
```

RESULT 2

```
US-11-010-795-21
/ Sequence 21, Application US/11010795
/ Publication No. US2006005271A1
/ GENERAL INFORMATION:
/ APPLICANT: TUMER, NITGUN E.
/ APPLICANT: DI, RONG
/ TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
/ TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
/ FILE REFERENCE: OCINS 3.0-085
/ CURRENT APPLICATION NUMBER: US/11/010.795
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 60/529,348
/ PRIOR FILING DATE: 2003-12-12
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 21
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(930)
US-11-010-795-21
```

Query Match 12.8%; Score 101; DB 14; Length 934;
Best Local Similarity 53.3%; Pred. No. 2.8e-16;
Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

```
Qy 19 TTTGATGCTGGAATGCGACCATTAACAATATGCCACTTATGGAATCTTTCGTAAT 78
    |||||
Db 85 TTTGATGCTGGAATGCGACCATTAACAATATGCTTATTTTGTGACTAGTTTGGCAGAA 144
Qy 79 CAAGCAAGATGCAAAACTAAATGCTATGCGATCAATGCTACCTGATTAATTTG 138
    |||||
Db 145 GCTGTATGAGACAAAGAAATTTGATCATGTCATGAAATGATATGCGCAACACCTCACTGAA 204
Qy 139 ACCCTTAAGTACTTATTTGTTAAGTCCCAAGTGCACCACTTAACCAATTAACATG 198
    |||||
Db 205 CAACCAAGATGCTGTGTTGACCTCAATTCGATCTGGAACATTC--ACATTAAGCA 261
Qy 199 CTGAGACGAATATCTTAATACGTATGAGGCTATTCGATCCCTTCAATGCAATTAAGT 258
    |||||
Db 262 ATGAGAAAGGGAACCTTATTTTGGAGGCTATTCGACATTTACATG--AAATATG 318
Qy 259 GCTTACATTAATTTAATGATTAATTAAGACCAAGCAAGCACTGATGTGAAATCTTT 318
    |||||
Db 319 CGTTATCGATCTTCAAGATTCAGAAATCC-----GATGCCCAAGACCGTT 366
Qy 319 TGCTCAAGTCTAGTCTCGTGTGCAATGTCATTAATCAATAGCTTAATATCCGACC 378
    |||||
Db 367 TGCCCCGGGACAAAGCAAGCCTGGCACTCAGAAATTAATATCCCTAATGAAAGAGTTAC 426
Qy 379 ATGAAAAAGAAAGCAGAAATGTAATCTCAAGAAATCAAGTCCAAATGGAAATTCATATCTC 438
    |||||
Db 427 AAAGGATGGAATCAAAAGGATGGGGCTAGAACCTTAATTTAGGTTAGGAAGATTAACATC 486
Qy 439 AGCAGTGAATTTGAAAAATCTCTGAGTTGATTC-----TTCCCTGTAAAA 486
    |||||
Db 487 AAGAGTCGAATGGGTAAAACTACGCAAGATGCAACGATCAGAAAGATTAACAAAA 546
Qy 487 ACTGAGGCTTTTCTTACTGTGATGCCATCAATGTTTCAAGGACAGCGCATTCAG 546
    |||||
Db 547 AATGAGGCTGAATTTTCTTATAGCGCTTCAATGTTACTGAGGCAATCAAGTTCAAA 606
Qy 547 TACATGAGAACCAAGTCAAGCTAATTTTAAT-----AGACATTCACCTGATCC 600
    |||||
Db 607 TACATGAGAACCAAGTCAAGCTAATTTTAATTTGATGATGCCAATGGTATCAGCAATCT 666
Qy 601 AAGTAATTAATCTTGAGAGAGAAATGGGCAAAATCTCTGAGCAATTCACATG 655
    |||||
Db 667 AAGCTAATTTCCCTAGAGAAAAATTTGGACAAGTGTTCCTAAGTCAATTCACAAAG 721
    |||||
```

RESULT 3

```
US-10-893-584-273
/ Sequence 273, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Adamir
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ PRIOR FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 273
/ LENGTH: 1623
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
```


OTHER INFORMATION: Ricin-like toxin (YSL10054)
US-10-893-584-273

Query Match 8.0%; Score 63; DB 8; Length 1623;
Best Local Similarity 54.0%; Pred. No. 3e-06;
Matches 154; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 545
DB 486 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 545
QY 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
DB 546 AATATTTAGAGGAGAAATGCGCAGAGATTAGTACACCGAGATCTGCACCGAGATCC 605
QY 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGCAATTCACATGCCAA 659
DB 606 TAGGTAATTAACACTTGAGAAATAGTGGGGGAGACTTTCACCTGCAATTCAGAGCTTAA 665
QY 660 GAATGGGCTTTTACCACCAACCACTGAGTATGATGATGATGATGATGATGATGATGAT 719
DB 666 CCAAGAGGCTTTTGTACTATCCATTCACATGCAAGAGATGATGATGATGATGATGATGAT 725
QY 720 TCTTAGAGTGATGAATCAATCGTATGATGATGATGATGATGATGATGATGATGATGAT 764
DB 726 GTACAGATGTAGTATTAATCCATCATGATGATGATGATGATGATGATGATGATGATGAT 770

RESULT 4

US-11-010-795-23
Sequence 23, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILDUN B.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OF INVENTION: RESISTANT TO TRICHOHEMBE FUNGAL TOXINS
FILE REFERENCE: OCIRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,348
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 23
LENGTH: 807
TYPE: DNA
ORGANISM: Ricinus communis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(804)
US-11-010-795-23

Query Match 7.8%; Score 61.4; DB 14; Length 807;
Best Local Similarity 53.7%; Pred. No. 6e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 545
DB 489 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 548
QY 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
DB 549 AATATTTAGAGGAGAAATGCGCAGAGATTAGTACACCGAGATCTGCACCGAGATCC 608
QY 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGCAATTCACATGCCAA 659
DB 609 TAGGTAATTAACACTTGAGAAATAGTGGGGGAGACTTTCACCTGCAATTCAGAGCTTAA 668
QY 660 GAATGGGCTTTTACCACCAACCACTGAGTATGATGATGATGATGATGATGATGATGATGAT 719
DB 669 CCAAGAGGCTTTTGTACTATCCATTCACATGCAAGAGATGATGATGATGATGATGATGAT 728

QY 720 TCTTAGAGTGATGAATCAATCGTATGATGATGATGATGATGATGATGATGATGATGAT 764
DB 729 GTACAGATGTAGTATTAATCCATCATGATGATGATGATGATGATGATGATGATGATGAT 773

RESULT 5

US-10-893-584-196
Sequence 196, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
LENGTH: 1807
TYPE: DNA
ORGANISM: B. coli
US-10-893-584-196

Query Match 7.8%; Score 61.4; DB 8; Length 1807;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 545
DB 597 AACTGAGGCTTTTCTTCTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCA 656
QY 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
DB 657 AATATTTAGAGGAGAAATGCGCAGAGATTAGTACACCGAGATCTGCACCGAGATCC 716
QY 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGCAATTCACATGCCAA 659
DB 717 TAGGTAATTAACACTTGAGAAATAGTGGGGGAGACTTTCACCTGCAATTCAGAGCTTAA 776
QY 660 GAATGGGCTTTTACCACCAACCACTGAGTATGATGATGATGATGATGATGATGATGATGAT 719
DB 777 CCAAGAGGCTTTTGTACTATCCATTCACATGCAAGAGATGATGATGATGATGATGATGAT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGATGATGATGATGATGATGATGATGATGATGAT 764
DB 837 GTACAGATGTAGTATTAATCCATCATGATGATGATGATGATGATGATGATGATGATGAT 881

RESULT 6

US-10-893-584-168
Sequence 168, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151


```
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175
```

Query Match 7.8%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;

Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

```
QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGCGCGCATTCAA 545
DB 597 AACTGCGCTGCTTCTTCTTAAATTTGATCCAAATGATTTTCAGAGGAGCAATTC 656
QY 546 GTACATGAGAACCAAGTCAAGTAAATTTT-----AATGAGCATTTCACTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGCAATTAAGTATGATCAACCGAGATCTGCACCAATCC 716
QY 600 CAAATGATTAATTAATGAGGAGAAATGCGCAAAATCTGAGCAATTCACATGCCAA 659
DB 717 TAGGTAAATTAACCTTGAAATGAGTGGGAGACTTTCACCTGCAATTCAGAGTCTAA 776
QY 660 GAATGAGGCTTTTACCAACCACTTGAAGTATGAGTCCAAAGGTACCAAGTGAATAGT 719
DB 777 CCAAGGAGCTTTGCTGATGCTCAATTCACACTGCAAGAGTAAATGCTTCAATTCAGGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGATGCGCACTCTCTTAAGTA 764
DB 837 GTACGATGTGATTAATTAATCCCTATCATAGTCTCATGCTGTA 881
```

RESULT 10

```
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 182
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-182
```

Query Match 7.8%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;

Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

```
QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGCGCGCATTCAA 545
DB 597 AACTGCGCTGCTTCTTCTTAAATTTGATCCAAATGATTTTCAGAGGAGCAATTC 656
QY 546 GTACATGAGAACCAAGTCAAGTAAATTTT-----AATGAGCATTTCACTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGCAATTAAGTATGATCAACCGAGATCTGCACCAATCC 716
QY 600 CAAATGATTAATTAATGAGGAGAAATGCGCAAAATCTGAGCAATTCACATGCCAA 659
DB 717 TAGGTAAATTAACCTTGAAATGAGTGGGAGACTTTCACCTGCAATTCAGAGTCTAA 776
QY 660 GAATGAGGCTTTTACCAACCACTTGAAGTATGAGTCCAAAGGTACCAAGTGAATAGT 719
DB 777 CCAAGGAGCTTTGCTGATGCTCAATTCACACTGCAAGAGTAAATGCTTCAATTCAGGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGATGCGCACTCTCTTAAGTA 764
DB 837 GTACGATGTGATTAATTAATCCCTATCATAGTCTCATGCTGTA 881
```

RESULT 11

```
US-10-893-584-231
; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231
```

Query Match 7.8%; Score 61.4; DB 8; Length 1825;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;

Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

```
QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGCGCGCATTCAA 545
DB 597 AACTGCGCTGCTTCTTCTTAAATTTGATCCAAATGATTTTCAGAGGAGCAATTC 656
QY 546 GTACATGAGAACCAAGTCAAGTAAATTTT-----AATGAGCATTTCACTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGCAATTAAGTATGATCAACCGAGATCTGCACCAATCC 716
QY 600 CAAATGATTAATTAATGAGGAGAAATGCGCAAAATCTGAGCAATTCACATGCCAA 659
```

Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGGAGACTTTCCACTGCAATTCAAGAGCTTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAGGATCAAGTGGATAGT 719
Db 777 CCAGAGGAGCCTTTGCTAGTGTCAATTCACATCGCAAGACGTAAGCTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCATGCTGATGTCGACCTCTTAAGTA 764
Db 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 12

US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:

; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: E. coli

US-10-893-584-210

Query Match 7.8%; Score 61.4; DB 8; Length 1828;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTTCTACTGTAGCCATCCAAATGTTTCAGAGGACGGCATTCAA 545
Db 597 AACTCGGCTCGTCTCTTATTAATTCATCCAAATGATTCAGAGGACGACGATTCGA 656
Qy 546 GTTCATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCATTTCACTTGATCC 599
Db 657 ATATATTGAGGAGAAATGCGACGAAATTAAGTACACCGAGANTCTGACACCAATGCC 716
Qy 600 CAAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAAATGCCAA 659
Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGGAGACTTTCCACTGCAATTCAGAGCTTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAGGATCAAGTGGATAGT 719
Db 777 CCAGAGGAGCCTTTGCTAGTGTCAATTCACATCGCAAGACGTAAGCTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCATGCTGATGTCGACCTCTTAAGTA 764
Db 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 13

US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:

; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik

; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli

Query Match 7.8%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTTCTACTGTAGCCATCCAAATGTTTCAGAGGACGGCATTCGA 545
Db 597 AACTCGGCTCGTCTCTTATTAATTCATCCAAATGATTCAGAGGACGACGATTCGA 656
Qy 546 GTTCATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCATTTCACTTGATCC 599
Db 657 ATATATTGAGGAGAAATGCGACGAAATTAAGTACACCGAGANTCTGACACCAATGCC 716
Qy 600 CAAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAAATGCCAA 659
Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGGAGACTTTCCACTGCAATTCAGAGCTTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAGGATCAAGTGGATAGT 719
Db 777 CCAGAGGAGCCTTTGCTAGTGTCAATTCACATCGCAAGACGTAAGCTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCATGCTGATGTCGACCTCTTAAGTA 764
Db 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 14

US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:

; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli

US-10-893-584-203

Query Match 7.8%; Score 61.4; DB 8; Length 1831;

Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTGAAGGCGAGCGCATTTCA 545
DB 597 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTGAAGGCGAGCGCATTTCA 545
QY 546 GTACATAGAGAACCAAGTCAAGTCAATTTT-----AATAGAGCATTTCAACCTGATCC 599
DB 657 ATATATTAGAGGAGAAATGCGCAGCAATTTAGTACACCGAGATCTGCAACGATCC 716
QY 600 CAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAA 659
DB 717 TAGGTATTAATACCTGAGAAATGTTGGGGGAGACTTCCACTGCAATTCAGAGTCTTA 776
QY 660 GAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGTACCAAGTGAATGT 719
DB 777 CCAGAGACCTTGTGTAGTCCAAATTCACATGCAAGAGTATGTTCCAAATTCAGTGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGTGGCACTCTTAAGTA 764
DB 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTA 881

RESULT 15

US-10-893-584-154
; Sequence 154; Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 1834
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-154

Query Match 7.8%; Score 61.4; DB 8; Length 1834;

Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTGAAGGCGAGCGCATTTCA 545
DB 597 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTGAAGGCGAGCGCATTTCA 545
QY 546 GTACATAGAGAACCAAGTCAAGTCAATTTT-----AATAGAGCATTTCAACCTGATCC 599
DB 657 ATATATTAGAGGAGAAATGCGCAGCAATTTAGTACACCGAGATCTGCAACGATCC 716
QY 600 CAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAA 659
DB 717 TAGGTATTAATACCTGAGAAATGTTGGGGGAGACTTCCACTGCAATTCAGAGTCTTA 776
QY 660 GAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGTACCAAGTGAATGT 719
DB 777 CCAGAGACCTTGTGTAGTCCAAATTCACATGCAAGAGTATGTTCCAAATTCAGTGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGTGGCACTCTTAAGTA 764

DB 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTA 881

Search completed: April 9, 2006, 04:47:50
Job time : 691.524 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 1124.2 Seconds
(without alignments)
2309.713 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 1617
Sequence: 1 MKVMVVVVTLMIAIAAP.....VIISTYYNYSNIGDPEGF 314

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=published Applications_NA_Main -OPMT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPLC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=biosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext
-HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03h
-USER=US09978274 @CGN_1_1.2039 @runat_07042006_173040_28552 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main.*

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1617	100.0	945	3	US-09-978-274A-1
2	1352	83.6	792	3	US-09-978-274A-3
3	1307	80.8	1092	3	US-09-978-274A-19
4	1235.5	76.4	1379	3	US-09-978-274A-30
5	1235.5	76.4	1379	10	US-11-106-187-1
6	1227.5	75.9	1368	3	US-09-978-274A-31
7	1224	75.7	1376	8	US-10-467-009-1

8	788	48.7	465	3	US-09-978-274A-5	Sequence 5, Appl1
9	564	34.9	333	3	US-09-978-274A-7	Sequence 7, Appl1
10	511	31.6	934	3	US-09-978-274A-32	Sequence 32, Appl1
11	511	31.6	934	10	US-11-106-187-3	Sequence 3, Appl1
12	480.5	29.7	855	10	US-11-106-187-20	Sequence 20, Appl1
13	378.5	22.4	935	9	US-10-919-750-4	Sequence 38, Appl1
14	361.5	22.4	804	3	US-09-861-257-38	Sequence 23, Appl1
15	361.5	22.1	804	6	US-10-189-360-23	Sequence 35, Appl1
16	357.5	22.1	804	3	US-09-861-257-35	Sequence 20, Appl1
17	357.5	22.1	804	6	US-10-189-360-20	Sequence 37, Appl1
18	356.5	22.0	804	3	US-09-861-257-37	Sequence 30, Appl1
19	356.5	22.0	804	6	US-10-189-360-22	Sequence 22, Appl1
20	355.5	22.0	804	3	US-09-861-257-22	Sequence 22, Appl1
21	355.5	22.0	804	3	US-09-861-257-36	Sequence 36, Appl1
22	355.5	22.0	804	6	US-10-189-360-19	Sequence 19, Appl1
23	355.5	22.0	804	6	US-10-189-360-21	Sequence 21, Appl1
24	348	21.5	999	3	US-09-792-793A-54	Sequence 54, Appl1
25	348	21.5	999	6	US-10-375-209A-54	Sequence 54, Appl1
26	345.5	21.4	993	3	US-09-792-793A-63	Sequence 63, Appl1
27	345.5	21.4	993	6	US-10-375-209A-63	Sequence 63, Appl1
28	344	21.3	765	3	US-09-792-793A-66	Sequence 66, Appl1
29	344	21.3	765	6	US-10-375-209A-66	Sequence 66, Appl1
30	344	21.3	984	3	US-09-792-793A-60	Sequence 60, Appl1
31	344	21.3	984	6	US-10-375-209A-60	Sequence 60, Appl1
32	344	21.3	999	3	US-09-792-793A-57	Sequence 57, Appl1
33	344	21.3	999	6	US-10-375-209A-57	Sequence 57, Appl1
34	339	21.0	1260	3	US-09-861-257-75	Sequence 75, Appl1
35	339	21.0	1260	6	US-10-189-360-72	Sequence 72, Appl1
36	337	20.8	1269	3	US-09-861-257-81	Sequence 81, Appl1
37	337	20.8	1269	6	US-10-189-360-78	Sequence 78, Appl1
38	337	20.8	1299	3	US-09-861-257-80	Sequence 80, Appl1
39	337	20.8	1299	6	US-10-189-360-77	Sequence 77, Appl1
40	335	20.7	765	3	US-09-861-257-23	Sequence 23, Appl1
41	335	20.7	765	6	US-10-189-360-79	Sequence 79, Appl1
42	335	20.7	1230	6	US-10-189-360-53	Sequence 53, Appl1
43	335	20.7	1233	3	US-09-861-257-24	Sequence 24, Appl1
44	335	20.7	1233	6	US-10-189-360-80	Sequence 80, Appl1
45	335	20.7	1251	3	US-09-861-257-77	Sequence 77, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US2002016737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-1

Alignment Scores:
Pred. No.: 6.75e-189
Score: 1617.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 945
Matches: 314
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-2 (1-314) x US-09-978-274A-1 (1-945)

QY 1 MetLysValMetLeuValValValThrLeuIleAlaIlePheLeuIleAlaIleProThr 20
DB 1 ATGAAAGTATGCTTGTAGTGTGAGCCTTAATGCGGGCTCATTTGCTGCACCACT 60

QY 21 SerThrCysAlaIleLeuThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
DB 61 TCACATGTCGCCATAATACGATCACCTTGATGCGAAATGCCACATTACCAATAT 120

QY 41 AlaThrPheMetGlySerLeuArgAsnGlnAlaLysAspProLysPheLysCysTy 60
DB 121 GCCACCTTATGAAATCTCTCGTAATCAGCGAAAGATCCAAACCTCAAAATCTATGGC 180

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGln 80
DB 181 ATACCAATGCTACTGATCTAATTCGACCCCTTAAGTACTTATGGTTAAGCTCCAAAGT 240

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLysTyValMetGlyTy 100
DB 241 GCMAACCTAAACCAATTACACTAATGCTGAGACGAATATTAATTATACGTGAGGCTAT 300

QY 101 SerAspProPheAsnGlnLysLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
DB 301 TCTGATCCCTCAATGCGCAATAGTGTCTTACCAATATTAATATATTAACACACACC 360

QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 361 GAACGACATGATGTGAGAAATCTCTTGTCTCAAGTTCTAAGTTCTGTGTGCAATGTCC 420

QY 141 IleAsnTyAsnSerLysTyProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
DB 421 ATTAATACAAATGACTTATATCCGACCATGAAAGAAAGCAAGATTAATCAAAATAT 480

QY 161 GlnValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 481 CAAGTCCAAATGGAAATTCMAAATACACGAGATGCAATGGAAATATCTGTGAGTTGAT 540

QY 181 SerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
DB 541 TCATTCCTGTAAATCTGAGGCTTTTCTTCTGATGTCGATCCAAATGCTTCCAGG 600

QY 201 AlaAlaArgPheLysTyIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
DB 601 GCAGCCGCAATTCAGATACATAGAGAACCAAGTCAAGCTAATTTATAGACATTCAC 660

QY 221 ProAspProLysValIleAsnLeuGluGluLysTyIleGlyLysIleSerGluAlaIleHis 240
DB 661 CCTGATCCCAAAAGTAAATTAATTTGGAGAGAAAGTGGGGCAAAATCTCTGAGCAATTCAC 720

QY 241 AsnAlaLysAsnGlyValLeuProLysPheLeuGluLeuValAspAlaLysGlyThrLys 260
DB 721 AATGCCAAAGATGGGCTTTACCCCAACCACTTGAGCTAGTGCACCAAGGTACCAAG 780

QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLysTyValAsn 280
DB 781 TGGATAGTCTTGAAGTGAATCAATCGATGTGGCACTCCTTAAGTACGTTAAT 840

QY 281 GlyThrCysGlnThrThrTyrgIlnAsnAlaMetPheSerGlnValIleIleSerThrTy 300
DB 841 GGAACCTGTGACCAACTTACCAAAATGCGATGTTCTTCMAAGTTTAAATTTCTACTTAT 900

QY 301 TyrAsnTyMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
DB 901 TATTAATTATATGTCTAATCTTGATCTAATTTGAAGGATTC 942

APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 3
LENGTH: 792
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-3

Alignment Scores:
Pred. No.: 2,85e-156 Length: 792
Score: 1352.00 Matches: 262
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 83.6% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-2 (1-314) x US-09-978-274A-3 (1-792)

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DB 4 ATTAATACATCACTTATATGCTGAATATGCACCATTAACCAATATGCCACCTTATG 63

QY 45 GluSerLeuArgAsnGlnAlaLysAspProLysLysCysTyrgLysIleProMetLeu 64
DB 64 GAATCTCTCGTAATCAACGAAAGATCCAAATCTAAATGCTATAGGCATACCAATGCTA 123

QY 65 ProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 84
DB 124 CCGATTAATTAATTCGACCCCTTAAGTCTTATGTTAAGTCTCAAGTGCACCAAGTCAAA 183

QY 85 ThrIleThrLeuMetLeuArgArgAsnLeuTyValMetGlyTySerAspProPhe 104
DB 184 ACATTAATCACTAATGCTGAGCAAGAAATACCTTATAGTATGGGCTATTCGATCCCTTC 243

QY 105 AsnGlyAsnLysCysArgTyHisIlePheAsnAspIleThrSerThrGluArgThrAsp 124
DB 244 AATGGCAATAGATGTGTTACCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 303

QY 125 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyArg 144
DB 304 GTGGAAATATACCTTTGCTCAAGTTCTAATGTTCTGTGTGCAATGTCCATTAATCAAT 363

QY 145 SerLeuTyProThrMetGluLysLysValGluValAsnSerArgAsnGlnValGlnLeu 164
DB 364 AGCTTAATATCCAGCATGAGAAAGAAAGCAAGATTAATCAAGAAATCAAGTCCAAATG 423

QY 165 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 184
DB 424 GGAATTCAAATACCTGACGATGACATGTGAAATAATCTCGAGTTGATTCATTCCTGTGA 483

QY 185 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 204
DB 484 AAACCTGAGGCTTTTCTTACTGTGAGCAATCCAAATGTTTCAGAGGACAGGCGCATTC 543

QY 205 LysTyrgIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyProAspProLys 224
DB 544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGCAATTCATCCCTGATCCCAAA 603

QY 225 ValIleAsnLeuGluGluLysTyrgLysIleSerGluAlaIleHisAsnAlaLysAsn 244
DB 604 GATATTAATCTGAGAGAAAGTGGGCAAAATCTCGAGGCAATTCACATGCCAAGAT 663

QY 245 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrgIleValLeu 264
DB 664 GGGGCTTACCCCAACCACTTAGCTAGTGAATGCCAAAGATGATCCAAAGTGAATGTTCTT 723

Db 459 TCAAAATMAAAACCACTACACCTAATGCTAGAGCAAAACATTTGTATGATGCGTTAT 518
QY SerAspProPheAnGlyAenLysCyAArgTyrHisIlePheAnApIleThrSerThr 120
Db 519 TCTGATCCCTTTGAAACCAATTAATGCTGTTACATATCTTTATGATGATCGGTACT 578
QY 121 GluArgThrAspValGluAnthrLeuCySerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATCTCGTGTAGTAAAAAC 638
QY 141 IleAnThrAsnSerLeuTyrProThrMetGluLysValAlaGluValaAnSerArgAsn 160
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QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerSerSerSerSerGlyValAlaAsp 180
Db 699 CAGGTCCAACTGGGAATTCAAATCTGACAGCAATTAATTTGGAAAGATTTCTGAGTGATG 758
QY 181 SerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCATCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATTAACAAATGCTATCAGAG 818
QY 201 AlaAlaArgPheLeuTyrIleGlnGluAnGlnValIleThrAsnPheAnArgAlaPheTyr 220
Db 819 GCAGCAAGATTCAGATACATAGAGAAATCAGGTGAAAATTAATTTTAAACAGACATTCAC 878
QY 221 ProAspProLysValIleAnThrLeuGlnGluLysTyrGlyIleSerGluAlaIleHis 240
Db 879 CCAATCCCAATCTTAATTTTTCAGAGACATGGGGTAAAGATTTTTCACAGCAATTCAT 938
QY 241 AsnAlaLysAnGlyAlaLeuProLysProLeuGlnLeuValAlaAspAlaLysGlyThrLys 260
Db 939 GATGCCAAGATTCAGATTTTAAACCAAACTCTGAGCTAGTGATGCCAGTGGGCCAAG 998
QY 261 TrpIleValLeuArgValAlaAspGluIleAnThrAspValAlaLeuLeuLysTyrValAsn 280
Db 999 TGGATAGTGTGAGAGTGAATCAACCTGAGTGAAGTCTTAATCTGAGTGGT 1058
QY 281 GlyThrCysGlnThrThrTyr--GlnAnAlaMetPheSerGlnIleIleSerThr 299
Db 1059 GCGAGCTGCAGCAACTTAACCAAAATGCCATGTTTCTCACTTAATATGCTACT 1118
QY 300 TyrTyrAsnTyrMetSerAnLeuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATTATAATACATGGTAACTTGGTGAATCTATTGAAGATTC 1163

RESULT 5
US-11-106-187-1
/ Sequence 1, Application US/11106187
/ Publication No. US20050183162A1
/ GENERAL INFORMATION:
/ APPLICANT: TURNER, NITGUN E.
/ APPLICANT: WANG, PINGR
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106,187
/ PRIOR FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721,047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 1
/ LENGTH: 1379
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (225)..(1163)

US-11-106-187-1
Alignment Scores:
Pred. No.: 1,799-141 Length: 1,379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 10 Gaps: 2

US-09-978-274a-2 (1-314) x US-11-106-187-1 (1-1379)
QY 1 MetLysValMetLeuValValValAlaThrLeuIleAlaThrPheLeuIleAlaAlaProThr 20
Db 225 ATGAGATTCATGCTGCTGTTGATGACATATCAATA-----TGGCTCATTTCTGACCAACT 278
QY 21 SerThrCysAlaIleAnThrIleThrPheAnPheAlaGlyAnAlaThrIleAnLysTyr 40
Db 279 TCAACTGGGCTGTGATACATCAATCAATGTTGGAAGTACCACTTACCAATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAnGlnAlaLysAspProLysCysTyrGly 60
Db 339 GCCACTTTCTGATATGATCTTCTGATGAGCAAGATCCAGTTTAATGCTATGGA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGly 80
Db 399 ATACCAATGCTGCGCAATCAATAATCAATCAATCAATGATGATGATGATGATGATGATGAT 458
QY 81 AlaAnThrLeuThrIleThrLeuMetLeuArgArgAsnAnThrTyrValMetGlyTyr 100
Db 459 TCAAAATMAAAACCACTACACCTAATGCTAGAGCAAAACATTTGTATGATGCGTTAT 518
QY 101 SerAspProPheAnGlyAenLysCyAArgTyrHisIlePheAnApIleThrSerThr 120
Db 519 TCTGATCCCTTTGAAACCAATTAATGCTGTTACATATCTTTATGATGATCGGTACT 578
QY 121 GluArgThrAspValGluAnthrLeuCySerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATCTCGTGTAGTAAAAAC 638
QY 141 IleAnThrAsnSerLeuTyrProThrMetGluLysValAlaGluValaAnSerArgAsn 160
Db 639 ATAACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerSerSerSerSerGlyValAlaAsp 180
Db 699 CAGGTCCAACTGGGAATTCAAATCTGACAGCAATTAATTTGGAAAGATTTCTGAGTGATG 758
QY 181 SerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCATCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATTAACAAATGCTATCAGAG 818
QY 201 AlaAlaArgPheLeuTyrIleGlnGluAnGlnValIleThrAsnPheAnArgAlaPheTyr 220
Db 819 GCAGCAAGATTCAGATACATAGAGAAATCAGGTGAAAATTAATTTTAAACAGACATTCAC 878
QY 221 ProAspProLysValIleAnThrLeuGlnGluLysTyrGlyIleSerGluAlaIleHis 240
Db 879 CCAATCCCAATCTTAATTTTTCAGAGACATGGGGTAAAGATTTTTCACAGCAATTCAT 938
QY 241 AsnAlaLysAnGlyAlaLeuProLysProLeuGlnLeuValAlaAspAlaLysGlyThrLys 260
Db 939 GATGCCAAGATTCAGATTTTAAACCAAACTCTGAGCTAGTGATGCCAGTGGGCCAAG 998
QY 261 TrpIleValLeuArgValAlaAspGluIleAnThrAspValAlaLeuLeuLysTyrValAsn 280
Db 999 TGGATAGTGTGAGAGTGAATCAACCTGAGTGAAGTCTTAATCTGAGTGGT 1058
QY 281 GlyThrCysGlnThrThrTyr--GlnAnAlaMetPheSerGlnIleIleSerThr 299
Db 1059 GCGAGCTGCAGCAACTTAACCAAAATGCCATGTTTCTCACTTAATATGCTACT 1118
QY 300 TyrTyrAsnTyrMetSerAnLeuGlyAspLeuPheGluGlyPhe 314

Db 1119 TATTATATATACATGTTAATCTTGATCTAATTTGAAAGATTC 1163

RESULT 6

US-09-978-274A-31

Sequence 31, Application US/09978274A

Patent No. US2002011673A1

GENERAL INFORMATION:

APPLICANT: Thomas, Christopher

APPLICANT: McPherson, Michael

APPLICANT: Atkinson, Howard

APPLICANT: Neelam, Anil

TITLE OF INVENTION: PLANT CELL DEATH SYSTEM

FILE REFERENCE: 9341-028

CURRENT APPLICATION NUMBER: US/09/978, 274A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 0025225.4

PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 31

LENGTH: 1368

TYPE: DNA

ORGANISM: *Phytolacca americana*

US-09-978-274A-31

Alignment Scores:

Pred. No.:	1.72e-140	Length:	1368
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-09-978-274A-31 (1-1368)

QY 1 MetLyValMetLeuValValValThreulelealrpleuilealaProthr 20

Db 225 ATGAAGCATGCTGTGGTGACAAATCAATA-----TGGCTCATCTTGCACT 278

QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40

Db 279 TCAACTGGGCTGGATGATCAATCATCATGTTGAAGTACCACTAGCAATAC 338

QY 41 AlaThrPheMetGlnSerLeuArgAsnGlnAlaIleAspProLysLeuLysCysTyGly 60

Db 339 GCCACTTTTGGAAATGATCTTGGTAATGAAGCGAAAGATCCAACTTTAAATGCTATGA 398

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyIleuValLysLeuGlnGly 80

Db 399 ATACCAATGCTGCCCATATCAATCAATCAATCAATCGTTGGTTGAGCTCCAAAGT 458

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100

Db 459 TCAAAATTAATAAACATCACTATGCTGAGAGAAACATTTGTATGTGATGGTAT 518

QY 101 SerAspProPheAsnGlnLysLeuLysCysArgTyHisIlePheAsnAspIleThrSerThr 120

Db 519 TCTGATCCCTTTGAAACCAATTAATGTCTTACCATATCTTATGATATCTCAGTACT 578

QY 121 GlnArgThrAspValGlnAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140

Db 579 GAAGCCCAAGATGATGAGACTACTCTTGCCCAATCCAAATTCGTGTATGAAANAAC 638

QY 141 IleAsnTyAsnSerLeuTyProThrMetGlnLysLysAlaGlnValAsnSerArgAsn 160

Db 639 ATAACTTTGATAGTGCATATCAACATGTGAATCAAAAGCGGAGTAATCAAGAGT 698

QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180

Db 699 CAGGTCCAACTGGGAATTCAAATACTGACAGATTAATTTGAAAGATTTCTGGAGTGATG 758

QY 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGln 200

Db 759 TCATTCATGAGAAACCAAGCCGATTCCTATGGTACCATACAAATGATACAG 818

QY 201 AlaAlaArgPheLysTyIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220

Db 819 GCAGCAAGATTCAGATCAATGAGAAATCAGGTGAAATTAATTTAACAAGCATTCAC 878

QY 221 ProAspProLysValIleAsnLeuGlnLysTyThrGlyLysIleSerGlnAlaIleHis 240

Db 879 CCAATCCCAAGATTCATTAATTTGCAAGAACATGGGGTAAGATTCAACAGCAATTCAT 938

QY 241 AsnAlaLysAsnGlnValAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260

Db 939 GATGCCAAGATGAGATTTTACCCAACCTCTGAGCTAGTATGCAATGATGCCAG 998

QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLysTyValAsn 280

Db 999 TGGATGTGTGTGAGAGGTGAATCAACCTGATGTACACTTAAACTACGTTGGT 1058

QY 281 GlyThrCysGlnThrThrTyThr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299

Db 1059 GGAGCTGTCAAGCACTTAATTAACCAAAATGCCATGTTCTCAACTTAATGATGCTACT 1118

QY 300 TyrTyAsnTyIleMetSerLeuLysAspLeuPheGlnGlyPhe 314

Db 1119 TATTATATATACATGTTAATCTTGATCTAATTTGAAAGATTC 1163

RESULT 7

US-10-467-009-1

Sequence 1, Application US/10467009

Publication No. US20040241673A1

GENERAL INFORMATION:

APPLICANT: RUTGERS, THE STATE UNIVERSITY

TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS

FILE REFERENCE: OCIRS 3.4-076

CURRENT APPLICATION NUMBER: US/10/467, 009

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: 60/266,396

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1376

TYPE: DNA

ORGANISM: *Phytolacca americana*

FEATURE:

NAME/KEY: CDS

LOCATION: (225) ..(1160)

US-10-467-009-1

Alignment Scores:

Pred. No.:	4.7e-140	Length:	1376
Score:	1224.00	Matches:	239
Percent Similarity:	86.0%	Conservative:	32
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	75.7%	Indels:	4
DB:	8	Gaps:	3

US-09-978-274A-2 (1-314) x US-10-467-009-1 (1-1376)

QY 1 MetLyValMetLeuValValValThreulelealrpleuilealaProthr 20

Db 225 ATGAAGCATGCTGTGGTGACAAATCAATA-----TGGCTCATCTTGCACT 278

QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40

Db 279 TCAACTGGGCTGTGATCAATCATCATGTTGAAGTACCACTTAGCAATAC 338

QY 41 AlaThrPheMetGlnSerLeuArgAsnGlnAlaIleAspProLysLeuLysCysTyGly 60

Db 339 GCCACTTTTCTGAATGATCTTGTATGAAGCGAAAGATCCAAAGTTTAAATGCTATGGA 398

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyIleuValLysLeuGlnGly 80

US-09-978-274A-2 (1-314) x US-09-978-274A-7 (1-333)

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QY 178 G|VAlAspSerPheProValIleThGluAlaPhePheLeuValAlaIleG|Met 197
Db 4 GGAATTGATTCATTCCTCGTAAAGAGAGGCTTTTTCATCGTAGCCATCAAAATG 63
QY 198 ValSerGluAlaAlaArgPheLeuValIleGluAlaValIleThAsnPheAsnArg 217
Db 64 GTTTCAGAGGAGGCGCATTCAGTACATAGAGAACCAAGTCAGACATTAATTTATAGA 123
QY 218 AlA|PheTyrProAspProLysValIleAsnLeuGluGlySTPGLYV|SerGlu 237
Db 124 GCATTTCACCTGATCCCAAGTATATATTGAGAGAGAGTGGGCAAAATCTCTGAG 183
QY 238 AlAlIleIleAsnAlaLysAsnGlyValAlaLeuProLysProLeuGluLeuValAspAlaLys 257
Db 184 GCATTTCAGATGCAAGATGCAAGATGGGCTTTTACCAACCACTTGAGCTAGAGCCAAA 243
QY 258 G|YThrIleSTP|LeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 277
Db 244 GGTACCAAGTGCATAGTCTTTCAGAGTGCATAGTAAATCATCTGATGTGGCATCTCTTAG 303
QY 278 TyrValAsnGlyThrCysGlnThrThr 286
Db 304 TACGTTATGGAACCTGTCAAGCAACT 330
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RESULT 10

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US-09-978-274A-32
; Sequence 32, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelan, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent version 3.1
; SEQ ID NO 32
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-32
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Alignment Scores:

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Pred. No.: 3,28e-52 Length: 934
Score: 511.00 Matches: 130
Percent Similarity: 56.1% Conservative: 53
Best Local Similarity: 39.9% Mismatches: 111
Query Match: 31.6% Indels: 32
DB: 3 Gaps: 14
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US-09-978-274A-2 (1-314) x US-09-978-274A-32 (1-934)

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QY 1 MetIyValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaAlaProThr 20
Db 7 ATGAGAGGTGTTAGAGAGTGGTGGCATATGCATATGCGTGAAGCTTACCCACCA 66
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyr 40
Db 67 -----GCTTCTTCAAACATGTGTGTGACCTTGAGATGCACACCAAAACCTAC 117
QY 41 AlA|ThrPheMetGluSerLeuArgAsnGluAlaLysAspProLysLeuLysCysTyrGly 60
Db 118 TCTAATTTTTCGATGATGTTCCGAGAGCTGTGAAGACAGAAATTTGACATGCCATGA 177
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGly 80
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Db 178 ATGATATGGCCCAACCTCTCACTGAACCAACCAAGTATGTGTGACCTCAAAATTC 237

QY 81 AlA|AsnLeuYsrThrIleThrLeuMetLeuArgArgAsnLeuTyrValMetGlyTyr 100

Db 238 GGAATC---GGAACCTTCACATTTAGCAATGAGAGGGGAACCTTATTTTGGAGGGCTAT 294

QY 101 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120

Db 295 TCTGACATTTTACATGGA---AAATGCTTTATCGGATCTTCAAGAT----- 339

QY 121 GluArgThrAspAlaGluAsnThrLeuCysSerSerSerSerArg-----ValAla 138

Db 340 TCGAATCCGATGCGCCAGAGACCGTTGCCCCGGGGGCAAAAGCAAGCTGGACATCAG 399

QY 139 MetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysAlaGluValAsnSer 158

Db 400 AATATATTCCTTCATGAAAAAGATTACAAAGGATGAATCAAAAGGCT-----GGGGCT 453

QY 159 ArgAsnGluValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGly 178

Db 454 AGAATCTAATTTAGGGTTAGAGAAAGATACCTCAAGATGCAATGGTAAATCTTACGCG 513

QY 179 ValAspSerPhePro-----ValIleThrGluAlaPhePheLeuValAla 194

Db 514 AAGATGCAACGGATCAGAGCAGTATCAAAAAAGAGGCTGAATTTCTTTATAGCC 573

QY 195 IleGlnMetValSerGluAlaAlaArgPheLeuTyrIleGluAlaValIleThAsn 214

Db 574 GTTCAAAATGTTACTGAGGATCAAGGTTCAAAATTCATTCAGAACCAAGTAAAGGCTAAA 633

QY 215 PheAsnArgAla-----PheTyrProAspProLysValIleAsnLeuGluGlyTyr 232

Db 634 TTTGATATCTCCATAGGTGATTCAGCCAGATCTTAACTTATTCCTTAGGAAAAATTTGG 693

QY 233 GlyLysIleSerGluAlaIleHisAsnAlaLysAsnGly-----AlaLeu 247

Db 694 GACAGGTTCCTTCAAGTCATTT-----GCAAAAGTTGGACCTCCGGTGAATGACTGT 747

QY 248 ProLysProLeuGluLeuValAspAlaLysGlyThrLysThrIleValLeuArgValAsp 267

Db 748 ACTTACCTCGAACCCTTAAAGATGAGATATATTAACCTTGACCTACGGCACCATCAAC 807

QY 268 GluIleAsnArgAspVal-----AlaLeuLeuLysTyrValAsnGlyThrCysGlnThr 286

Db 808 GACCTTAAAGACACATATATGCACTCTTACCCACGTT-----ACTTCAAGCTT--- 858

QY 287 TyrGlnAsnAlaMetPheSerGluValIleIleSerThrTyrTyrAsnTyrMetSerAsn 306

Db 859 ---AAAAGTCCATGTTCCCTGAAATTAATCTCTATTATATAGCACTACTATTAAGTAC 915

QY 307 LeuGlyAspLeuPheGlu 312

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

Db 916 CTGCGTGA---TTCCAG 930

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/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 3
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (1)..(75)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (76)..(930)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(930)
/ US-11-106-187-3

Alignment Scores:
Pred. No.: 3,28e-52 Length: 934
Score: 511.00 Matches: 130
Percent Similarity: 56.1% Conservative: 53
Best Local Similarity: 39.9% Mismatches: 111
Query Match: 31.6% Indels: 32
DB: 10 Gaps: 14

US-09-978-274a-2 (1-314) x US-11-106-187-3 (1-934)

QY 1 MetLysValMetLeuValValValThrLeuIleAlaThrLeuIleAlaProThr 20
   |||||
DB 7 ATCAAGGTGTAGAAAGTAGTTGGTGGCAATATCCATATGCTGATGCTTACACCA 66
   |||||

QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLys 40
   |||||
DB 67 -----GCTTCTTCAACATAGTGTGTTGACGTTGAGAAATGCCACAGAAACCTAC 117
   |||||

QY 41 AlaThrPheMetCysLeuLeuArgAsnAlaLysLeuAspProLysCysTyrGly 60
   |||||
DB 118 TCTAATTTCTGCTAGTGTGGCAGAACTGTGAAAGCAAAATTTGACATCCATCGA 177
   |||||

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
   |||||
DB 178 ATGATATGCGCCCAACCCCTCACTGAAACCCAGATGATGTGTGGTGTGACCTCAATTC 237
   |||||

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
   |||||
DB 238 GGATCT---GGAACATTCACATTAGCAATCAGAAAGGGAACCTTATATTGGAGGGCTAT 294
   |||||

QY 101 SerAspProPheAsnLysLeuLysCysArgTyrHisIlePheAsnProIleThrSerThr 120
   |||||
DB 295 TCTGACATTTTACATGAG---AAATGTCGTTATCGATCTTCAAGAT----- 339
   |||||

QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArg-----ValAla 138
   |||||
DB 340 TCGAATCCGATCCCAAGAGACCGTTGCCCGGGCAAAAGCCTGCGACTGAC 399
   |||||

QY 139 MetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysAlaGluValAsnSer 158
   |||||
DB 400 AATAATATCCCTATGAAAGAGTACAAAGGAGTGAATCAAAAGGCT-----GGGGCT 453
   |||||

QY 159 ArgAsnGlnValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGly 178
   |||||
DB 454 AGAAGCTAATATGAGGTAGGAAAGATACACTCAAGAGTCGATGGGTAAATCTACGGC 513
   |||||

QY 179 ValAspSerPhePro-----ValLysThrGluAlaPhePheLeuLeuValAla 194
   |||||
DB 514 AAGAGTCGAACGATCGAAGACGATACAAAAGAGAGGCTGAATTTCTTTATAGCC 573
   |||||

QY 195 IleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsn 214
   |||||
DB 574 GTTCAATGTTACTAGAGCATCAAGTTCATATACATTGAGAAACAAGTGAAGGCTAA 633
   |||||

QY 215 PheAsnArgAla-----PheTyrProAspProLysValIleAsnLeuGlnGlyLysTyr 232
   |||||
DB 634 TTTGATGATGCCAATGGGTATAGCCAGATCCTTAAAGCTATTTCCCTAGGAAAAATGG 693
   |||||
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QY 233 GlyLysIleSerGluAlaIleHisAsnAlaLysAsnGly-----AlaLeu 247
   |||||
DB 694 GACAGTGTTCCTAAGGTCACTT-----GCCAAAGTTGGGACCTCCGGTATGACTGTT 747
   |||||

QY 248 ProLysProLeuGluLeuValAspAlaLysGlyThrLysThrIleValLeuArgValAsp 267
   |||||
DB 748 ACTTATCCTGAGACCTTAAGATGAGATTAATTAACCTTGACCTACGGCCACCATGAAC 807
   |||||

QY 268 GluIleAsnArgAspAla---AlaLeuLeuLysTyrValAsnGlyThrCysGlnThrThr 286
   |||||
DB 808 GACCTTAAGAACCACTATATGCACTCTACCCACAGTT-----ACTTGCAAGT--- 858
   |||||

QY 287 TyrGlnAsnAlaMetPheSerGlnValIleIleSerThrTyrTyrAsnTyrMetSerAsn 306
   |||||
DB 859 ---AAAGTTCATGTTCCTGAAATATATGCTATATATATGACCTGATATGCTAAC 915
   |||||

QY 307 LeuGlyAspLeuPheGlu 312
   |||||
DB 916 CTGGTGAA---TTCGAG 930
   |||||

RESULT 12
US-11-106-187-20
/ Sequence 20, Application US/11106187
/ Publication No. US20050183162A1
/ GENERAL INFORMATION:
/ APPLICANT: WANG, PINGR
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/11106,187
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 20
/ LENGTH: 855
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(855)
/ US-11-106-187-20

Alignment Scores:
Pred. No.: 1.67e-48 Length: 855
Score: 480.50 Matches: 121
Percent Similarity: 56.5% Conservative: 48
Best Local Similarity: 40.5% Mismatches: 101
Query Match: 29.7% Indels: 29
DB: 10 Gaps: 13

US-09-978-274a-2 (1-314) x US-11-106-187-20 (1-855)

QY 28 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetCysLeu 47
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DB 4 ATAGTGTTCGATGAGTGAAGATGCCACACCAAGAACTACTCTAATTTCTGACTAGTTG 63
   |||||

QY 48 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 67
   |||||
DB 64 CGAGAACTGTGAAAGCAAGAAATTTGACATGCCATGGAATGATATATGCGCAACACCTC 123
   |||||

QY 68 AsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
   |||||
DB 124 ACTGAACAAACCAAGTATGTGTGGTGGACCTCAATTTGGATCT---GAAACATTGACA 180
   |||||

QY 88 LeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlnLys 107
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Db 181 TTACCAATCAGAGGGGAACTTATATTGGAGGCTATTCTGACATTATACATGA--- 237
 Qy 108 LysCySATgTyrHsIlePheAsnAspIleThrSerThrgluArgThrAspValGluasn 127
 Db 238 AAATGCTTATTCGATCTTCAGAGT-----TCGAATTCGATGCCAAGANG 285
 Qy 128 ThrLeuCySerSerSerSerSerArg-----ValAlaMetSerIleAsnTyrAsnSer 145
 Db 286 ACCGTTTGCCTCCGGGACAAAGAGAGCGCTGCACTGAAATATATCCCTATGAAAG 345
 Qy 146 LeuTyrProthMetGluLysLeuValaGluValaAsnSerArgAsnGluValaGluLeuGly 165
 Db 346 AGTTACAAAGGAGATGGAATCAAAAGGCT-----GGGCTAGAACTTAAATTTAGGTTAGGA 399
 Qy 166 IleGluIleLeuSerSerSerAspIleGlyLysIleSerGlyValaAspSerPhePro----- 183
 Db 400 AAGATACACTCAAGAGTCGAATGGATGATTAATCAAGCAAGAGATGCAAGATCAGAG 459
 Qy 184 -----ValLysThrgluAlaPhePheLeuValaIleGluMetValSerGluVala 201
 Db 460 CAGTATCAAAAATAATGAGCTGGAATTTCTTATAGCGCTTCAAAATGTTACTAGAGCA 519
 Qy 202 AlaArgPheLysTyrIleGluAsnGluValLysThraPheAsnArgAla-----Phe 219
 Db 520 TCAAGGTTCAAAATCAATTGAGAGAACAAAGTGAAGGCTTAAATTTGATGATGCCAATGGCTAT 579
 Qy 220 TyrProAspProLysValaIleAsnLeuGluGluLysTyrGlyLysIleSerGluValaIle 239
 Db 580 CAGCAGATCTCAAGATCTATTTCTCTAGAGAAAATTTGGACAGCTGTTCTTAAAGCTCAT 639
 Qy 240 HisAsnAlaLysAsnGly-----AlaLeuProLysProLeuGluLeuVal 254
 Db 640 -----GCAAAAGTTGGACCTCCGGTATAGTACTGTACTTACTTACCTGAGACTTAA 693
 Qy 255 AspAlaLysGlyThrLysTyrIleValaLeuArgValaAspGluIleAsnArgAspVala--- 273
 Db 694 GATAGATATATTAACCTTGACTGACGACCATGAAAGCATTAAGAACAGACATTTATG 753
 Qy 274 AlaLeuLeuLysTyrValaAsnGlyThrCysGluInThrThryrGluAsnAlaMetPheSer 293
 Db 754 GCATCTCTTACCCACGTT-----ACTTGAAGGTT-----AAAAGTTCAATGTTCCCT 801
 Qy 294 GluValaIleIleSerThryrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlu 312
 Db 802 GAATTTATGCTCTTATATATAGACATGATTAAGTAACTTGGTGA---TTGAG 855

RESULT 13
 US-10-919-750-4
 ; Sequence 4, Application US/10919750
 ; Publication No. US20050120414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Diamond, Paul
 ; TITLE OR INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
 ; FILE REFERENCE: P1100-40S
 ; CURRENT APPLICATION NUMBER: US/10/919, 750
 ; PRIOR FILING DATE: 2004-08-16
 ; PRIOR APPLICATION NUMBER: US 10/644, 288
 ; PRIOR FILING DATE: 2003-08-20
 ; PRIOR APPLICATION NUMBER: US 10/354, 903
 ; PRIOR FILING DATE: 2003-01-29
 ; PRIOR APPLICATION NUMBER: US 60/352, 705
 ; PRIOR FILING DATE: 2002-01-29
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Microsoft Wordpad
 ; SEQ ID NO 4
 ; LENGTH: 935
 ; TYPE: DNA
 ; ORGANISM: Saponaria officinalis
 US-10-919-750-4

Alignment Scores: 7.82e-36 Length: 935
 Pred. No.: 378.50 Matches: 104
 Score:

Percent Similarity: 56.1% Conservative: 57
 Best Local Similarity: 36.2% Mismatches: 101
 Query Match: 23.4% Indels: 25
 Db: 9 Gaps: 11

US-09-978-274a-2 (1-314) x US-10-919-750-4 (1-935)

Qy 4 MetLeuValValValValThrLeuIleAlaThrLeuIle-----AlaAlaProthr 20
 Db 85 ATGAAGATATATGTTGTTAGCCACATATGATGATCTCGCTTCAATTTTCAAGCTTGACA 144
 Qy 21 SerThrcysAlaIleAsnThrIleThrPheAspAlaGluAsnAlaThrIleAsnLysTyr 40
 Db 145 ACAATGATGCGGTACATCAATCAATTAATGATCTTAATTAATCCGACCGCGGTCAATAC 204
 Qy 41 AlaThrPheMetGluSerLeuArgAsnGluAlaLysAspProLysLysCysTyrGly 60
 Db 205 TCATCTTTTGGATTAATAATCCGAACACGCTAAGGATCCAAACTGAATATACGGTGGT 264
 Qy 61 IleProMet---LeuProAspThrAsnSerThryrProLysTyrLeuLeuValaLysLeuGlu 79
 Db 265 ACCGACATAGCCGATGATAGGCCCACTTCAAGAAAATAATCTTAAATTAATTTCCAA 324
 Qy 80 GluValaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnLeuLysTyrValaMetGly 99
 Db 325 AGTCCCGA---GGAACGCTCTCATCTGGCTTAAACCGCATTAATCTGTATGTGTCGCG 381
 Qy 100 Tyr-----SerAspProPheAsnGlyAsnLysCysArgTyrHsIlePheAsnAspIle 117
 Db 382 TATCTTCATATGATTAACAGAAATGTTAAATCGGCA---TATTAATTCAGATCAGAAAT 438
 Qy 118 ThrSerThrgluArgThraPheValaGluAsnThrLeuCySerSerSerSerSerArgVal 137
 Db 439 ACTTCCCGCAGTCAACC-----GCCCTTTTCCAGAGGCCACACGCAAT 486
 Qy 138 AlaMetSerIleAsnTyrAsnSerLeuTyrProthMetGluLysValaGluVala--- 156
 Db 487 CAGAAACCTTTAGAAATACACAGAAATTAACAGTCAATGAAAAGAAATGCCCAATACAA 546
 Qy 157 -----AsnSerArgAsnGluValaGluLeuGlyIleGluIleLeuSerSerAspIle 173
 Db 547 CAAAGAGATCAAAAGTAAAGAAAGAACTCGGTGGGATGACTTAATTTCAACGTCATG 606
 Qy 174 GlyLysIleSerGlyValaAspSerPheProValLysThrgluAlaPhePheLeuVal 193
 Db 607 GAACGAGTGAAC---AAGAAAGCACGTGGTATTAAGACAGAGTCAATTCCTTATATC 663
 Qy 194 AlaIleGluMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGluValaLysThr 213
 Db 664 GCTATTTAGATGACGCTGAGGAGCGCCGATTTAGTACATCAAACTTGATATCAAG 723
 Qy 214 AsnPheAsnArgAlaPheTyrProAspProLysValaIleAsnLeuGluGluLysTyrGly 233
 Db 724 AACTTTCACAAAGTTCAACTCGGAAAACAAAGATGATTCAGTTTGAAGTTAACTGAAAA 783
 Qy 234 LysIleSerGluAlaIleHs---AsnAlaLysAsnGlyAlaLeuProLysProLeuGlu 252
 Db 784 AAAATTTCTACGGAATATACGGGAGATGCCAAAACGGCGTTTAAATTAAGATTATGAT 843
 Qy 253 LeuValaAspAlaLysGlyThrLysTyrIleValaLeuArgValaAspGluIleAsnArgAsp 272
 Db 844 TTCCGGTTTGGAAA-----GTTAGCAGATGAGAGACTTG-----CAA 882
 Qy 273 ValAlaLeuLeuLysTyrVal 279
 Db 883 ATGGACTCTTATGATTTG 903

RESULT 14
 US-09-861-257-38
 ; Sequence 38, Application US/09861257
 ; Publication No. US20030040496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chandler, Lois Ann


```

      / APPLICANT: Sosnowski, Barbara A.
      / APPLICANT: Baird, J. Andrew
      / APPLICANT: Pierce, Glenn
      / TITLE OF INVENTION: TREATMENT OF TUMORS USING
      / TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
      / NUMBER OF SEQUENCES: 103
      / CORRESPONDENCE ADDRESSES:
      / ADDRESSER: Seed Intellectual Property Law Group
      / STREET: 701 Fifth Avenue, Suite 6300
      / CITY: Seattle
      / STATE: Washington
      / COUNTRY: USA
      / ZIP: 98104
      / COMPUTER READABLE FORM:
      / MEDIUM TYPE: floppy disk
      / COMPUTER: IBM PC compatible
      / OPERATING SYSTEM: PC-DOS/MS-DOS
      / SOFTWARE: PatentIn Release #1.0, Version #1.30
      / CURRENT APPLICATION DATA:
      / APPLICATION NUMBER: US/09/861,257
      / FILING DATE: 17-MAY-2001
      / CLASSIFICATION:
      / ATTORNEY/AGENT INFORMATION:
      / NAME: Christensen Ph.D., William T.
      / REGISTRATION NUMBER: 44,614
      / REFERENCE/DOCKET NUMBER: 760100.423C1
      / TELECOMMUNICATION INFORMATION:
      / TELEPHONE: (206) 622-4900
      / TELEFAX: (206) 682-6031
      / INFORMATION FOR SEQ ID NO: 38:
      / SEQUENCE CHARACTERISTICS:
      / LENGTH: 804 base pairs
      / TYPE: nucleic acid
      / STRANDEDNESS: double
      / TOPOLOGY: unknown
      / MOLECULE TYPE: cDNA
      / FEATURE:
      / NAME/KEY: CDS
      / LOCATION: 1..804
      / FEATURE:
      / NAME/KEY: misc feature
      / LOCATION: 1..804
      / OTHER INFORMATION: /note= "Nucleotide sequence
      / OTHER INFORMATION: corresponding to the clone M13 mp18-g9"
      / FEATURE:
      / NAME/KEY: mat_peptide
      / LOCATION: 46..804
      / OTHER INFORMATION: /product= "Saporin"
      / US-09-861-257-38
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      Pred. No.: 7,69e-34 Length: 804
      Score: 361.50 Matches: 100
      Percent Similarity: 56.1% Conservative: 56
      Best Local Similarity: 36.0% Mismatches: 97
      Query Match: 22.4% Indels: 25
      DB: 3 Gaps: 11
      US-09-978-274A-2 (1-314) x US-09-861-257-38 (1-804)
      Qy 13 AlaTPlPLeuile-----AlaaIaProThSerThCySaIaiIeaThrIleThr 29
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      Db 1 GCATGGATCTGCGCTTCATATTTCAGCTTGGAACAACATGATCGGCATCATCA 60
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      Qy 30 PheaPaalagIYAsnaIathrrIleaenlySYrAlathrPhemctGIusErLeuaYasn 49
         |||||:::|||||:::|||||:::|||||:::|||||:::|||||
      Db 61 TTAgATCTTAAGTAATCCGACC CGCGGTCAATACTCATCTTTTGATTAATAATCCGAAC 120
         |||||:::|||||:::|||||:::|||||:::|||||
      Qy 50 GlnaIayASPPrOlylsEulySyCYrTYGLYLlEPromet---LeuPoaApThRasn 68
         |||||:::|||||:::|||||:::|||||:::|||||
      Db 121 AACGTAAAGACTCCAACCTGAAATKACGGGTGCCAGCACATAGCCGGAATAGGCCCACT 180
         |||||:::|||||:::|||||:::|||||
      Qy 69 SerThirProLyryrIeuLeuValIylvLeuGlngIyAlaIsnleulySrThrIleThrLeu 88

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Dh      181 TCTAAAGAAAATTCCTTGAAATTAATTTCCAAAGTCCGA---GGAGCGGTCACTT 237
Oy      89 MetLeuArgArgAsnAsnLeuTyrValMetGlyTyr-----SerAspProPheAsnGly 106
Dh      238 GGCCTTAAACGCAATTAATTATGTGTGGTCCGGTATCTTGCATAGATTAACAACAATGTT 297
Oy      107 AsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspValGlu 126
Dh      298 AATCGGCGCA---TATTACTTCAGATCGAATAATTACTTTCGCCGAGTTAAACC----- 345
Oy      127 AsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeu 146
Dh      346 ---GCCCTTTTCCAGAGCCACAACATCGAATAATCGAAGACTTTAGAAATACACAGAAAT 402
Oy      147 TyrProThrMetGlnLysLysValIadValA-----AsnSerArgAsnGlnVal 162
Dh      403 TATCAGCTGCAATGTGAAAAGAAATGCCAGATTAACACAGAGAGATCAAAATGAAAGAACTC 462
Oy      163 GlnLeuGlyIleGlnIleLeuSerSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
Dh      463 GGGTTGGGGATTGACTTACTTCAACGCCATCGAAGACAGATGAAAC---AAGAGCGCACGT 519
Oy      183 ProValLysThrGlnLysPhePheLeuLeuValAlaIleGlnMetValSerGlnAla 202
Dh      520 GTGGTTAAAGACGAAGCTGATTCCTCTTATCGCTATTCCAGATGACGCGTGAAGCGACGC 579
Oy      203 ArgPheLysTyrIleGlnLysGlnValLysThrAsnPheAsnArgAlaPheTyrProAsp 222
Dh      580 CGATTTAGGTACATACAAACTTGGTATTCAGAAACTTCCCAACAAGTTCAACTCGGAA 639
Oy      223 ProLysValIleLeuLeuGlnGluLysTyrGlyLysIleSerGlnAlaIleHis--Asn 241
Dh      640 AACAAAGTATTCAGTTTGAGGTTAACGTGAAAAAAATTTCTACGCAATATACGGGGAT 699
Oy      242 AlaLysAsnGlnAlaLeuLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTyr 261
Dh      700 GCCAAAAGACGGCGGTGTTTAATTAATAATTATATATATTCGGGTTTGAAAA----- 747
Oy      262 IleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuLysTyrVal 279
Dh      748 ---GTAGGCAAGTGAAGACACTTG-----CAATGGGACCTCTTAGTATTTTG 792

RESULT 15
; US-10-189-360-23
; Sequence 23, Application US/10189360
; Publication No. US20030143217A1
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
Chandler, Lois Ann
SosenowSKI, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/189,360
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996

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ATTORNEY/AGENT INFORMATION:
 NAME: No. US20030143217Altenburg Ph.D., Carol
 REGISTRATION NUMBER: 39,317
 REFERENCE/DOCKET NUMBER: 760100.415C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 804 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..804
 NAME/KEY: misc feature
 LOCATION: 1..804
 OTHER INFORMATION: /note= "Nucleotide sequence
 corresponding to the clone M13 mp18-69 in Example 1.B.2."
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 46..804
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 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-10-189-360-23

Alignment Scores:

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Percent Similarity:	56.1%	Conservative:	56
Best Local Similarity:	36.0%	Mismatches:	97
Query Match:	22.4%	Indels:	25
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US-09-978-274A-2 (1-314) x US-10-189-360-23 (1-804)

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Db 1 GCATGATCCGCTTCAATTTCTAGCTTGACAACTGATGCGTCACTCATATCACA 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 30 PheAspAlaGlyAsnAlaThrIleAsnLeuTyAlaThrPheMetGluSerLeuArgAsn 49
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 TTGATCTAGTAATTCGACCGCGGTCATATCTCTTTGTGATTAATTCGAAC 120
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 50 GluAlaIysAspProLysLeuLysCysTyrgIyIleProMet---LeuProAspThrAsn 68
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 AAGTAAAGATCCAAACCTGAATACGGGTACCGACATAGCCGTGATAGCCCACT 180
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Qy 69 SerThProLysTyIleLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeu 88
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Qy 89 MetLeuArgArgAsnAsnLeuTyValMetGlyTyI---SerAspProPheAsnGly 106
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Db 238 GGCCTAAACCGCATTAATCTGTATGTGCGGTATCTTGCAATGATTAACGATGTT 297
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Qy 107 AsnLysCysArgTyIleIlePheAsnAspIleThrSerThrgIuArgThrAspValGlu 126
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Qy 163 GlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
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Qy 203 ArgPheLysTyIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTyIleProAsp 222
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Db 580 CGATTAGGTACATACAAACTTGTGATATCAAGAACTTCCCAACAAGTTCACTCGGA 639
Qy 223 ProLysValIleAsnLeuGlnGluLysTyrgIyLysIleSerGluAlaIleHis---Asn 241
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Db 640 AACAAAGTATTCAGTTTGAGGTTACTGAAAAAAATTTCTACGGCAATATACGGGAGT 699
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Db 700 GCCAAAAACGCGGTGTTTAATTAAGATTATGATTTCCGGTTTGAAAA----- 747
Qy 262 IleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyIleVal 279
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Db 748 ---GTGAGCGAGGTGAAGACTTG-----CAATGGCACTCTTATGTAATTGG 792

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 Job time : 1129.2 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 823.643 Seconds
(without alignments)
1525.144 Million cell updates/sec

Title: US-09-978-274A-2
Perfect score: 1617
Sequence: 1 MKWLVVVVTLTAMLIAPF.....VISTYYNYSNGLDIFEGP 314

Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TAANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAHSIZE=500 -MINLEN=0
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-USER=US09978274.OCN_1_1_2451@runat_07042006_173042_28604 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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2: /SID5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1235.5	76.4	1360	US-11-010-795-19	Sequence 19, Appl
2	511	31.6	934	US-11-010-795-21	Sequence 21, Appl

3	315.5	19.5	1855	8	US-10-893-584-95	Sequence 95, Appl
4	313.5	19.4	1855	8 <th>US-10-893-584-92</th> <th>Sequence 92, Appl</th>	US-10-893-584-92	Sequence 92, Appl
5	311	19.2	1855	8 <th>US-10-893-584-35</th> <th>Sequence 35, Appl</th>	US-10-893-584-35	Sequence 35, Appl
6	311	19.2	1855	8 <th>US-10-893-584-74</th> <th>Sequence 74, Appl</th>	US-10-893-584-74	Sequence 74, Appl
7	310.5	19.2	1855	8 <th>US-10-893-584-39</th> <th>Sequence 39, Appl</th>	US-10-893-584-39	Sequence 39, Appl
8	310.5	19.2	1855	8 <th>US-10-893-584-50</th> <th>Sequence 50, Appl</th>	US-10-893-584-50	Sequence 50, Appl
9	310	19.2	1855	8 <th>US-10-893-584-125</th> <th>Sequence 125, Appl</th>	US-10-893-584-125	Sequence 125, Appl
10	309	19.1	1813	8 <th>US-10-893-584-245</th> <th>Sequence 245, Appl</th>	US-10-893-584-245	Sequence 245, Appl
11	307.5	19.0	1810	8 <th>US-10-893-584-168</th> <th>Sequence 168, Appl</th>	US-10-893-584-168	Sequence 168, Appl
12	307.5	19.0	1855	8 <th>US-10-893-584-80</th> <th>Sequence 80, Appl</th>	US-10-893-584-80	Sequence 80, Appl
13	307.5	19.0	1807	8 <th>US-10-893-584-196</th> <th>Sequence 196, Appl</th>	US-10-893-584-196	Sequence 196, Appl
14	306.5	19.0	1855	8 <th>US-10-893-584-3</th> <th>Sequence 3, Appl</th>	US-10-893-584-3	Sequence 3, Appl
15	306.5	19.0	1855	8 <th>US-10-893-584-5</th> <th>Sequence 5, Appl</th>	US-10-893-584-5	Sequence 5, Appl
16	306.5	19.0	1855	8 <th>US-10-893-584-7</th> <th>Sequence 7, Appl</th>	US-10-893-584-7	Sequence 7, Appl
17	306.5	19.0	1855	8 <th>US-10-893-584-9</th> <th>Sequence 9, Appl</th>	US-10-893-584-9	Sequence 9, Appl
18	306.5	19.0	1855	8 <th>US-10-893-584-13</th> <th>Sequence 13, Appl</th>	US-10-893-584-13	Sequence 13, Appl
19	306.5	19.0	1855	8 <th>US-10-893-584-15</th> <th>Sequence 15, Appl</th>	US-10-893-584-15	Sequence 15, Appl
20	306.5	19.0	1855	8 <th>US-10-893-584-17</th> <th>Sequence 17, Appl</th>	US-10-893-584-17	Sequence 17, Appl
21	306.5	19.0	1855	8 <th>US-10-893-584-19</th> <th>Sequence 19, Appl</th>	US-10-893-584-19	Sequence 19, Appl
22	306.5	19.0	1855	8 <th>US-10-893-584-21</th> <th>Sequence 21, Appl</th>	US-10-893-584-21	Sequence 21, Appl
23	306.5	19.0	1855	8 <th>US-10-893-584-23</th> <th>Sequence 23, Appl</th>	US-10-893-584-23	Sequence 23, Appl
24	306.5	19.0	1855	8 <th>US-10-893-584-25</th> <th>Sequence 25, Appl</th>	US-10-893-584-25	Sequence 25, Appl
25	306.5	19.0	1855	8 <th>US-10-893-584-27</th> <th>Sequence 27, Appl</th>	US-10-893-584-27	Sequence 27, Appl
26	306.5	19.0	1855	8 <th>US-10-893-584-29</th> <th>Sequence 29, Appl</th>	US-10-893-584-29	Sequence 29, Appl
27	306.5	19.0	1855	8 <th>US-10-893-584-31</th> <th>Sequence 31, Appl</th>	US-10-893-584-31	Sequence 31, Appl
28	306.5	19.0	1855	8 <th>US-10-893-584-33</th> <th>Sequence 33, Appl</th>	US-10-893-584-33	Sequence 33, Appl
29	306.5	19.0	1855	8 <th>US-10-893-584-37</th> <th>Sequence 37, Appl</th>	US-10-893-584-37	Sequence 37, Appl
30	306.5	19.0	1855	8 <th>US-10-893-584-48</th> <th>Sequence 48, Appl</th>	US-10-893-584-48	Sequence 48, Appl
31	306.5	19.0	1855	8 <th>US-10-893-584-52</th> <th>Sequence 52, Appl</th>	US-10-893-584-52	Sequence 52, Appl
32	306.5	19.0	1855	8 <th>US-10-893-584-54</th> <th>Sequence 54, Appl</th>	US-10-893-584-54	Sequence 54, Appl
33	306.5	19.0	1855	8 <th>US-10-893-584-77</th> <th>Sequence 77, Appl</th>	US-10-893-584-77	Sequence 77, Appl
34	306.5	19.0	1855	8 <th>US-10-893-584-83</th> <th>Sequence 83, Appl</th>	US-10-893-584-83	Sequence 83, Appl
35	306.5	19.0	1855	8 <th>US-10-893-584-86</th> <th>Sequence 86, Appl</th>	US-10-893-584-86	Sequence 86, Appl
36	306.5	19.0	1855	8 <th>US-10-893-584-89</th> <th>Sequence 89, Appl</th>	US-10-893-584-89	Sequence 89, Appl
37	306.5	19.0	1855	8 <th>US-10-893-584-98</th> <th>Sequence 98, Appl</th>	US-10-893-584-98	Sequence 98, Appl
38	306.5	19.0	1855	8 <th>US-10-893-584-101</th> <th>Sequence 101, Appl</th>	US-10-893-584-101	Sequence 101, Appl
39	306.5	19.0	1855	8 <th>US-10-893-584-104</th> <th>Sequence 104, Appl</th>	US-10-893-584-104	Sequence 104, Appl
40	306.5	19.0	1855	8 <th>US-10-893-584-110</th> <th>Sequence 110, Appl</th>	US-10-893-584-110	Sequence 110, Appl
41	306.5	19.0	1855	8 <th>US-10-893-584-113</th> <th>Sequence 113, Appl</th>	US-10-893-584-113	Sequence 113, Appl
42	306.5	19.0	1855	8 <th>US-10-893-584-116</th> <th>Sequence 116, Appl</th>	US-10-893-584-116	Sequence 116, Appl
43	306.5	19.0	1855	8 <th>US-10-893-584-119</th> <th>Sequence 119, Appl</th>	US-10-893-584-119	Sequence 119, Appl
44	306.5	19.0	1855	8 <th>US-10-893-584-122</th> <th>Sequence 122, Appl</th>	US-10-893-584-122	Sequence 122, Appl
45	306.5	19.0	1855	8 <th>US-10-893-584-111</th> <th>Sequence 11, Appl</th>	US-10-893-584-111	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NITGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCINS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1145)
US-11-010-795-19

Alignment Scores:

Pred. No. : 1,586-132 Length: 1360
 Score: 1235.50 Matches: 239
 Percent Similarity: 86.3% Conservative: 33
 Best Local Similarity: 75.9% Mismatches: 40
 Query Match: 76.4% Indels: 3
 DB: 14 Gaps: 2

US-09-978-274A-2 (1-314) x US-11-010-795-19 (1-1360)

```

QY 1 MetLysValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaIleProThr 20
DB 207 ATGAAGTCATGCTTGTGGTACAAATACAAAT-----TGCTTCATTTCTTGACCAACT 260
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLys 40
DB 261 TCAACTGGCGTGTGAATCAATCACTACATGTTGAAGTACCACTTACCAATATC 320
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTrpGly 60
DB 321 GCCACTTTTCTGAATGATCTTGTGAATGAGCGAAAGATCCAAAGTTTAAATGCTATGGA 380
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTrpLeuLeuValLysLeuGlnGly 80
DB 381 ATACCAATGCTGCCCAATACAAATACAAATCCAAAGTACGTTGTTGAGCTCCAAAGT 440
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTrpValMetGlyTrp 100
DB 441 TCAAAATAAACCAATACATACATGCTGAGCGAAACATTTGATGATGGGTTAT 500
QY 101 SerAspProPheAsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThr 120
DB 501 TCTGAATCCCTTGGAAACCAATAAATGCTGTACAAATCTTAAATGATATCTCAGGTACT 560
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140
DB 561 GAAACCGCAAGATGTAGAGACTACTCTTCCCAAGCCCAATCTCTGTGTAGTAAAC 620
QY 141 IleAsnTrpAsnSerLeuTrpProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
DB 621 ATAACTTTTGAATGATGATATCCAAATGGAATCAAAAGCGGAGTAAATCAAGAG 680
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 681 CAGGTCACACTGGGAATTCAAATATCCGACAGTAAATTTGGAAGATTTCTGGAGGTAG 740
QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB 741 TCATTCACAGAAACCAAGCCCAATCTCTATTTGTCGACCAATGATGATGAG 800
QY 201 AlaAlaAspPheLysTrpIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTrp 220
DB 801 GCAGCAAGATTCAGATACATAGAGATCAGGTGAAACCTAATTTTAAACAGAGCATTCAC 860
QY 221 ProAspProLysValIleAsnLeuGlnGluLysTrpGlyLysIleSerGluAlaIleHis 240
DB 861 CCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGTAAGATTTCCAAACAGCAATTCAT 920
QY 241 AsnAlaLysAsnGlyValAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
DB 921 GATGCCAAGATGAGATTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGTGCGAAG 980
QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsn 280
DB 981 TGGAGATGTTGAGATGATGAATCAAGCTGATGACACTTTAAATACATGCTGAT 1040
QY 281 GlyThrCysGlnThrThrTrp---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1041 GGGAGCTGTCAGCAACTTAATACCAAAATGCCATGTTTCTCAACTTAAATATGCTACT 1100
QY 300 TrpTrpAsnTrpMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
DB 1101 TATTAATTAATCATGTTAATCTTGTGATCTATTTTGAAGGATTC 1145

```

RESULT 2

US-11-010-795-21

; Sequence 21, Application US/11010795

; Publication No. US20060005271A1

; GENERAL INFORMATION:

; APPLICANT: TUMER, NILGUN E.

; APPLICANT: DI, RONG

; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE

; FILE REFERENCE: OCIRS 3.0-085

; CURRENT APPLICATION NUMBER: US/11/010,795

; PRIOR FILING DATE: 2004-12-13

; PRIOR APPLICATION NUMBER: 60/529,348

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 21

; LENGTH: 934

; TYPE: DNA

; ORGANISM: Phytolacca americana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(930)

US-11-010-795-21

Alignment Scores:

Pred. No. : 7,486-49 Length: 934
 Score: 511.00 Matches: 130
 Percent Similarity: 56.1% Conservative: 53
 Best Local Similarity: 39.9% Mismatches: 111
 Query Match: 31.6% Indels: 32
 DB: 14 Gaps: 14

US-09-978-274A-2 (1-314) x US-11-010-795-21 (1-934)

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QY 1 MetLysValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaIleProThr 20
DB 7 ATGAAGTCTTGAAGTGTGGTGGCAATATGATATGCTGATGCTTACACCACCA 66
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLys 40
DB 67 -----GCTTCTCAACATATGATGTTGAGTGGCAATATGATATGCTGATGCTTACACCACCA 117
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTrpGly 60
DB 118 TCTAATTTTCTGACTATGTTGCGAAGCTGTGAAAGCAAGAAATTGACATGCCATGGA 177
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTrpLeuLeuValLysLeuGlnGly 80
DB 178 ATGATATATGCGCAACCTCTCACTGACCAACCAAGTATGCTGTGATGACCTCAAAATTC 237
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTrpValMetGlyTrp 100
DB 238 GGATCT---GGAACATTCATTCATTCACATCAAGAGGCAACTTAATTTGAGAGGCTAT 294
QY 101 SerAspProPheAsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThr 120
DB 295 TCTGACATTTACAAATGGA---AAATGTGTTATGCAATCTTCAAGAT----- 339
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArg-----ValAla 138
DB 340 TCGAATCCGATGCCAAGAGACCGTTTGGCCCGGGGCAAAAGCAAGCTGCGACTCAG 399
QY 139 MetSerIleAsnTrpAsnSerLeuTrpProThrMetGluLysLysAlaGluValAsnSer 158
DB 400 AATAATATCCCTTAAGAAAGATTAACAAAGGATGAAATCAAGGCT-----GGGGCT 453
QY 159 ArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGly 178
DB 454 ACAACATAATTAATGGTTAGGAAGATTAACATCAAGAGTCAAGTGGTAAATATTCACGC 513
QY 179 ValAspSerPhePro-----ValLysThrGluAlaPhePheLeuLeuValAla 194

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Db 514 AAGAGTCAACGAGTCAAGACAGTATCAAAAAATGAGCTGAATTTCTTATAGCC 573
Qy 195 IlegImetValSerGluAlaAlaArgPheLysTyrIleGluAengInValIleThraSn 214
Db 574 GTTCAATGGTATCTGAGGCTCAAGGTTCAATTCATTGGAACAAAGTGAAGGCTTAA 633
Qy 215 PheAsnArgAla-----PheTyrProAspProLysValIleAenLeuGluGlyLysTyr 232
Db 634 TTTGATGATGCGCAATGGGTATCAGCCAGATCTTAAGCTATTTCTTGAAGAAAAATTGG 693
Qy 233 GLyValSerGluAlaIleHisAsnAlaLysAengLy-----AlaLeu 247
Db 694 GACAGTGTTCATAGGTCATT-----GCAAAAGTTGCACTCCGGTGAATGATGACTT 747
Qy 248 ProLysProLeuGluLeuValAspAlaLysGlyThrLysTrrPileValIleuArgValAsp 267
Db 748 ACTTACTTGGAGGCTTAAAGATGAGATTAATTAACCTTGAGCTAGCGCCACCATGAC 807
Qy 268 GluIleAsnArgAspVal-----AlaLeuLysLysTyrValAengLyThrCysGlnThrThr 286
Db 808 GACCTTAAGAAGCATTAATGAGCACTCTTAACCAAGCTT-----ACTTGAAGGTT--- 858
Qy 287 TyrGlnAsnAlaMetPheSerGlnValIleIleSerThrTyrTyrAsnTyrMetSerAsn 306
Db 859 ---AAAGTTCAGATTCCTCGAAATATGCTTATTAATAGACTAGATTAATGATAC 915
Qy 307 LeuGlyAspLeuPheGlu 312
Db 916 CTGGTGAA---TTGAG 930
RESULT 3
US-10-893-584-95
; Sequence 95, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR APPLICATION NUMBER: 2004-07-19
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-276 insert
US-10-893-584-95
Alignment Scores:
Pred. No.: 7,93e-26 Length: 1855
Score: 315.50 Matches: 95
Percent Similarity: 44.4% Conservative: 52
Best Local Similarity: 28.7% Mismatches: 115
Query Match: 19.5% Indels: 69
DB: 8 Gaps: 13
US-09-978-274A-2 (1-314) x US-10-893-584-95 (1-1855)
Qy 10 ThrLeuIleAlaTrrPheLeuIleAlaAlaProThSerThrCysAlaIleAsnThr----- 27
Db 25 ACTATTGTATATATGATGATGATGAGTGGCAACATGGCTTGTGTTGATCACCCTCAGGG 84

Qy 28 -----IleThrPhe 30
Db 85 TGGCTTTTCATTAGAGATTAACAATATTTCCCAACAATACCAATATTAATACTT 144
Qy 31 AspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeuArgAsnGln 50
Db 145 ACCAAGCGGGGTGCTGAGCAAGCTTACCAAACTTTATCAGAGCTGTGGGGTCTG 204
Qy 51 AlaLysAspProLysLysCysTyrGlyIleProMetLeuProAspThrAsnSerThr 70
Db 205 TTAACAACTGAGCTGATGAGACATGATATACAGTGTGGCCAAACAGAGTGGTTTG 264
Qy 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLysTrrPileThr 87
Db 265 CTTATTAACCAACGGTTATTTATGTTGAATCTCAAAATCATGACAGACTTCTGTATCA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsn 107
Db 325 TTAGCGCTGATGATGACAAATGATATGATGTGGTACCGT-----GCTGAAAT 375
Qy 108 LysCysArgTyr-----HisIlePhe 114
Db 376 AGCGCATATTTCTTTCATCTCGAACAATCAGAAAGATCAGAAAGCATCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysAla 154
Db 451 ---CGATATACATTCGCTTGGTGGTAAAT-----TATATAGACTTGAACAATGCT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyTyrIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATCGAGTTGGAAATGTCACCTAGAGAGAGCATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATTAATTAACGATCTGAGTGGTGCATCGACTTCAACTGCTGCTGCTCTT--- 615
Qy 191 LeuLeuValAlaIlegImetValSerGluAlaAlaArgPheLysTyrIleGluAengIn 210
Db 616 ---ATATTTGCATTCCAATATGATTCAGAGCAAGATTCCAATATATTTGAGGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
Db 673 ATGGGCAAGCAATTAAGTACCAACCGAGATCTGCAACAGATCTTACGTAATTAACATT 732
Qy 229 GluGluLysTrrPglyLysIleSerGluAlaIleHisAsnAlaLysAengLyAlaLeuPro 248
Db 733 GAGAAATAGTGGGGAGACTTTCACCTGCACTGCAATTCAGAGCTTAACAGAGAGCTTTGCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTrrPileValIleuArgValAspGlu 268
Db 793 AGTCCAAATTCATGCAAGCAAGCATTAATGTTCCAAATTCAGTGTACATGAGATATA 852
Qy 269 IleAsnArgAspValAlaLeuLysLysTyrValAengLyThrCysGlnThrTyrGln 288
Db 853 TTAATCCCTATCATAGCTCTCATGTGTAT-----AGATGCGCAACTTCA---CCA 900
RESULT 4
US-10-893-584-92
; Sequence 92, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr

```
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
US-10-893-584-92
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Alignment Scores:

Pred. No.:	1,35e-25	Length:	1855
Score:	313.50	Matches:	94
Percent Similarity:	44.5%	Conservative:	57
Best Local Similarity:	27.7%	Mismatches:	119
Query Match:	19.4%	Indels:	69
DB:	8	Gaps:	13

US-09-978-274A-2 (1-314) x US-10-893-584-92 (1-1855)

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QY 10 ThrLeuIleAlaTrpLeuIleAlaProThrSerThrCysAlaIleAenThr-----27
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DB 25 ACTATTGTATATGATGTATGATGTCAGTGGCAACATGGCTTTGTTGGATCCACTCAGG 84
QY 28 -----11eThrPhe 30
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 85 TGGCTTTTCACATTAGAGATTAACAATATTCCTCCCAACATACCAATATTAATTAACCTTT 144
QY 31 AspAlaGlyAsnAlaThrIleAenLysTyraIleThrPheMetGluSerLeuAryAangIn 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 145 ACCACAGCGGGTCCACTGTGCAAGCTACCAAACTTTATCAGAGCTGTTCGGCGTGT 204
QY 51 AlaLysAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAenSerThr 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 205 TTAAACAACGTGAGCTGATGAGACATGATATACAGTGTGGCAACAGATTGGTTTG 264
QY 71 Pro-----LysTyrlleuLeuValLysLeuGlnGlyAlaAenLysThrIleThr 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 265 CCTATAAACCAACGGTTTATTATTAGTTGAACCTCAATCATCAGAGCTTCTGTAC 324
QY 88 LeuMetLeuAryAryAangAenLysTyraIleMetGlyTySerAspProPheAangIn 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 325 TTAGCGCTGATGTCAACATGATGTCGAGTCCGCTACCGT-----GCTGAAT 375
QY 108 LysCysArgTy-----ACTGATGTTCAAAAT-----HisIlePhe 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 376 ACCGCAATATTTCTTCATCCCTGACAATCAGAAATGACAGAACATCACTCATCTTTTC 435
QY 115 AenAspIleThrSerThrGluArgThrAspValGluAenThrLeuCysSerSerSer 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 436 -----ACTGATGTTCAAAAT-----450
QY 135 SerArgValAlaMetSerIleAenTyraAenSerLeuTyProThrMetGluLysVal 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 451 ---CGATTATACATTCGCTTTGGTGTAAAT-----TATGATGACTTGAACAACCTTGCT 501
QY 155 GluValAsnSerArgAangInValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 502 GGT---AATCTGAGAGAAATATCGAGTTCGGAAATGATGCATTAAGAGAGCTATCTCA 558
QY 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
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DB 559 GCCCTTATATTATACAGTACTGGTGGCACTCAGCTTCCAACTCGGCTGCTCTT---615
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrlleGluAangIn 210
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 616 ---ATAATTGTCATCCAAATGATTTCAAGAGCAGAAAGATTCATATATTTAGGGAGAA 672
QY 211 ValIleThr-----AenPheAenArgAlaPheTyProAspProLysValIleAenLeu 228
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 673 ATGCGCAGAGAAATTAGTTCACACCGAGATCTGCACAGATCTTACCGTATTAACCTT 732
QY 229 GluGluLysTyrglyLysIleSerGluAlaIleHisAsnAlaLysAangInValAeuPro 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 733 GAGAAATAGTTGGGGGAGACTTTCACCTGCATTCAGAGTCAACAGTCAACAGAGCTTGTCT 792
QY 249 LysPheLeuGluLeuValAspAlaLysGlyThyIleTyrlleValIleuAryValAargIn 268
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 793 AGTCAATTCACATCGCAAGACGTAATGTTCCAAATTCAGTGTACAGATGAGATATA 852
QY 269 IleAsnArgAspValAlaLeuLeuLysTyraIleAangIlyThrCysGlnThrThrTyrgIn 288
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 853 TTATCCCTATCATCTCTCATGCTGTAT-----AGATGCCACTCCA---CCA 900
QY 289 AsnAlaMetPheSerGlnValIleIleSerThrTyraAenTyraMetSerAenLeu 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 901 TCGTCACAGTTTCTTGTCTTATATTCGGGTCAATGGCTAATTTTATGCTGATGTT 957
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RESULT 5

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US-10-893-584-35
Sequence 35, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
```

```
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Burac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
US-10-893-584-35
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Alignment Scores:

Pred. No.:	2.63e-25	Length:	1855
Score:	311.00	Matches:	92
Percent Similarity:	43.2%	Conservative:	50
Best Local Similarity:	28.0%	Mismatches:	109
Query Match:	19.2%	Indels:	78
DB:	8	Gaps:	12

US-09-978-274A-2 (1-314) x US-10-893-584-35 (1-1855)

```
QY 10 ThrLeuIleAlaTrpLeuIleAlaProThrSerThrCysAlaIleAenThr-----27
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 25 ACTATTGTATATGATGTATGATGTCAGTGGCAACATGGCTTTGTTGGATCCACTCAGG 84
QY 28 -----11eThrPhe 30
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```



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Qy 108 LysCysArgTyr-----HisIlePhe 114
Db 376 AGCCGATATTTCTTTCATCTGACAAATGAGAAATGAGAAAGCAATCATCTATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValAla 154
Db 451 ---CGATATACATTCGCTTGGTGGTGAAT---TATGATAGACCTTGAAACAATTTGCT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATGCAATGTTGGAAATGCTCCATGAGAGAGCTATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATTTATTCAGTACTGCTGGCACTCAGCTTCCAACTTGGCTCGTTCTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaIleAsnGlyPheLysTyrIleGluAsnGln 210
Db 616 ---ATAATTTGCATCCAAATATATTTCAAGACAGACAGATTCATATATTGAGGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
Db 673 ATGGCAGCAGAAATTAGGTACACCGAGATCTGCACAGATCTTAGGTATTTACACTT 732
Qy 229 GluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyValAlaLeuPro 248
Db 733 GAGAAATAGTTGGGGAGACTTCCACTGCAATTCAGATTCAGCAAGAGAGCTTTGCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAspGlu 268
Db 793 AGTCCAAATTCACATGCAAAAGACGTAAATGTTCCAAATTCAGTGTACGATGAGATATA 852
Qy 269 IleAsnArgAspValAlaLeuLeuLysTyr-----ValAsnGlyThrCys 283
Db 853 TTATTCCTATCATAGCTCTCATAGTGTATAGATGCCAGACAGATGATGCGGGGTGT 912

RESULT 14
US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richn-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893, 584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Cathepsin B linker regions of PAP-214
US-10-893-584-3

Alignment Scores: 8,74e-25 Length: 1855
Pred. No.: 306,50 Matches: 89

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Percent Similarity: 44.2% Conservative: 48
Best Local Similarity: 28.7% Mismatches: 108
Query Match: 19.0% Indels: 65
DB: 8 Gaps: 11

US-09-978-274A-2 (1-314) x US-10-893-584-3 (1-1855)

Qy 10 ThrLeuIleAlaTProLeuIleAlaLProThrSerThrCysAlaIleAsnThr----- 27
Db 25 ACTATGTATATATGATGATGATGAGTGCACACAGCTTGTGTGATGCACCTCAGGG 84
Qy 28 -----IleThrPhe 30
Db 85 TGGCTTTCACATTAGAGATTAACAATATATCCCAACAATCCCAATATTAATTAATCTT 144
Qy 31 AspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeuArgAsnGln 50
Db 145 ACCACAGCGGGGTGCACCTGCAAGCTACCAAACTTTATCAGAGCTGTTGGGGTCTG 204
Qy 51 AlaLysAspProLysLysLysCysTyrGlyIleProMetLeuProAspThrAsnSerThr 70
Db 205 TTAACAACGTGAGCTGATGTGACACATATATACAGTGTGGCCAAACAGAGTTGGTTTG 264
Qy 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
Db 265 CCTATTAACCAACGCTTATTTATTTAGTGAATCTCAATCATGACAGAGCTTCTGTACA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsn 107
Db 325 TTAGCGCTGATGTCACCAATGCAATATGATGTGGCTACCGT-----GCTGAAAT 375
Qy 108 LysCysArgTyr-----HisIlePhe 114
Db 376 AGCCGATATTTCTTTCATCTGACAAATGAGAAATGAGAAAGCAATCACTCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValAla 154
Db 451 ---CGATATACATTCGCTTGGTGGTGAAT---TATGATAGACTTGAACAATCTGCT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATGCAATGTTGGAAATGCTCCACTGAGAGAGCTATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATTTATTCAGTACTGCTGGCACTCAGCTTCCAACTTGGCTCGTTCTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaIleAsnArgPheLysTyrIleGluAsnGln 210
Db 616 ---ATAATTTGCATCCAAATGATTTCAAGACAGACAGATTCCAATATATTGAGGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
Db 673 ATGGCAGCAGAAATTAGGTACACCGAGATCTGCACCAATATCTTAGCGTAAATTAACCTT 732
Qy 229 GluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyValAlaLeuPro 248
Db 733 GAGAAATAGTTGGGGAGACTTCCACTGCAATTCAGAGCTTAACCAAGAGCTTTGCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAspGlu 268
Db 793 AGTCCAAATTCACATGCAAAAGACGTAAATGTTCCAAATTCAGTGTATGATGAGATATA 852
Qy 269 IleAsnArgAspValAlaLeuLeuLysTyr-----ValAsnGlyThrCys 283
Db 853 TTATTCCTATCATAGCTCTCATAGTGTAT 882

RESULT 15
US-10-893-584-5

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